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(54) Title: PROTEIN KINASES

(57) Abstract: The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypep-  
tides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

DESCRIPTION

## PROTEIN KINASES

FIELD OF THE INVENTION

5           The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

BACKGROUND OF THE INVENTION

10           The following description of the background of the invention is provided to aid in understanding the invention, but is not admitted to be or to describe prior art to the invention.

          Cellular signal transduction is a fundamental mechanism whereby external stimuli that regulate diverse cellular processes are relayed to the interior of cells. One of the key  
15       biochemical mechanisms of signal transduction involves the reversible phosphorylation of proteins, which enables regulation of the activity of mature proteins by altering their structure and function.

          Protein phosphorylation plays a pivotal role in biological signal transduction. Among the biological functions controlled by protein phosphorylation are the following:  
20       cell division; differentiation and death (apoptosis); cell motility and cytoskeletal structure; control of DNA replication, transcription, splicing and translation; protein translocation events from the endoplasmic reticulum and Golgi apparatus to the membrane and extracellular space; protein nuclear import and export; regulation of metabolic reactions, etc. Abnormal protein phosphorylation is widely recognized to be causally linked to the  
25       etiology of many diseases including cancer as well as immunologic, neuronal and metabolic disorders.

          The most common phospho-acceptor amino acid residues are serine, threonine and tyrosine. Phosphorylation in histidine has also been observed in bacteria. The presence of a phosphate moiety modulates protein function in multiple ways. A common mechanism  
30       includes changes in the catalytic properties ( $V_{\max}$  and  $K_m$ ) of an enzyme leading to its activation or inactivation. A second widely recognized mechanism involves promoting protein-protein interactions. An example of this is the tyrosine autophosphorylation of the

ligand-activated EGF receptor tyrosine kinase. This event triggers the high-affinity binding to the phosphotyrosine residue on the receptor's C-terminal intracellular domain to the SH2 motif of the adaptor molecule Grb2. Grb2 in turn binds through its SH3 motif to a second adaptor molecule, such as SHC. The formation of this ternary complex  
5 activates the signaling events that are responsible for the biological effects of EGF. Serine and threonine phosphorylation events have also been recently recognized to exert their biological function through protein-protein interaction events mediated by the high-affinity binding of phosphoserine and phosphothreonine to WW motifs present in a large variety of proteins (Lu, P.J. *et al.* (1999) *Science* 283:1325-1328). A third important  
10 outcome of protein phosphorylation is changes in the subcellular localization of the substrate. As an example, nuclear import and export events in a large diversity of proteins are regulated by protein phosphorylation (Drier E.A. *et al.* (1999) *Genes Dev* 13: 556-568).

Protein kinases are one of the largest families of eukaryotic proteins with several  
15 hundred known members. These proteins share a 250-300 amino acid domain that can be subdivided into 12 distinct subdomains that comprise the common catalytic core structure. These conserved protein motifs have recently been exploited using PCR-based and bioinformatic strategies leading to a significant expansion of the known kinases. Multiple  
20 alignment of the sequences in the catalytic domain of protein kinases and subsequent parsimony analysis permits their segregation into a dendrogram reflecting the relatedness of their catalytic domains (Fig. 1). In this manner, related kinases are clustered into distinct branches or subfamilies including: tyrosine kinases, cyclic-nucleotide-dependent kinases, calcium/calmodulin kinases, cyclin-dependent kinases and MAP-kinases, serine-threonine kinase receptors, and several other less defined subfamilies.

25 We have recently completed a systematic analysis of the protein kinases present in *C. elegans*, the multicellular organism whose entire DNA sequence has been determined. We identified 473 unique kinase profiles including 398 full-length conventional kinases, and 20 additional proteins that may function as atypical protein kinases. (Plowman G.D. *et al.* (1999), *Proc. Natl. Acad. Sci.* 96:13603-13610).

30 Using parsimony analysis, the protein kinases may be divided into 4 major groups: AGC, CAMK, CMGC and tyrosine kinases. In addition, there are a number of minor yet distinct families, including the STE and casein kinase 1, families related to worm- or

fungus-specific kinases, and a family designated "other" to represent several smaller families. In addition, we designate an "atypical" family to represent protein kinases whose catalytic domain has little or no primary sequence homology to conventional kinases, including the A6 kinases and PI3 kinases.

5           The AGC kinases are basic amino acid-directed enzymes that phosphorylate residues found proximal to Arg and Lys. Examples of this group are the cyclic nucleotide-dependent kinases, G protein kinases, NDR or DBF2 and the ribosomal S6 kinases.

          The CAMK group kinases are also basic amino acid-directed kinases. They include the Ca<sup>2+</sup>/calmodulin-regulated and AMP-dependent protein kinases, myosin light chain  
10          kinases, checkpoint 2 kinases (CHK2) and EMK-related protein kinases. The EMK family of STK are involved in the control of cell polarity, microtubule stability and cancer. One member of the EMK family, C-TAK1 has been reported to control entry into mitosis by activating Cdc25C which in turn dephosphorylates Cdc2.

          CMGC group kinases are "proline-directed" enzymes phosphorylating residues  
15          that exist in a proline-rich context. They include the cyclin-dependent kinases (CDKs), mitogen-activated kinases (MAPKs), GSK3s and CLKs. Most CMGC kinases have larger-than-average kinase domains owing to the presence of insertions within subdomains X and XI.

          The tyrosine kinase group encompass both cytoplasmic (i.e. src) as well as  
20          transmembrane receptor tyrosine kinases (i.e. EGF receptor). These kinases play a pivotal role in the signal transduction processes that mediate cell proliferation, differentiation and apoptosis.

          Group members that define smaller, yet distinct phylogenetic branches of conventional kinases include the elongation factor 2 kinases (EIFKs); homologues of the  
25          yeast sterile family kinases (STE) which refers to 3 classes of kinases which lie sequentially upstream of the MAPKs; mixed lineage kinases (MLKs); Lim-domain containing kinases (LIMKs); Calcium-calmodulin kinase kinases (CAMKK), dual-specific tyrosine kinases (DYRK), integrin receptor associated kinase (IRAK); testis-specific kinases (TSK); UNC-51 related kinases (UNC); several families that are close  
30          homologues to worm (C26C2.1, YQ09, ZC581.9, YFL033c, C24A1.3), Drosophila (SLOB), or yeast (YDOD\_sp, YGR262\_sc) kinases, and others that are "unique" and don't cluster into any obvious family.



### SUMMARY OF THE INVENTION

Through a search of the EST database for homologies to the conserved catalytic kinase domain of protein kinases, hundreds of mammalian members of known and previously unidentified protein kinase families and groups have been identified as part of the present invention. Multiple alignment and parsimony analysis of the catalytic domain reveals that approximately half of these protein kinases cluster into 10 known groups, with the other half perhaps defining novel groups. Classification in this manner has proven highly accurate not only in predicting motifs present in the remaining non-catalytic portion of each protein, but also in their regulation, substrates, and signaling pathways. The present invention includes the partial or complete sequence of new protein kinases, their classification, predicted or deduced protein structure, and a strategy for elucidating their biologic and therapeutic relevance.

Thus, a first aspect of the invention features an isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,

SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,  
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,  
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,  
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,  
5 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,  
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,  
and SEQ ID NO:242.

By "isolated" in reference to nucleic acid is meant a polymer of nucleotides  
conjugated to each other, including DNA and RNA, that is isolated from a natural source  
10 or that is synthesized. The isolated nucleic acid of the present invention is unique in the  
sense that it is not found in a pure or separated state in nature. Use of the term "isolated"  
indicates that a naturally occurring sequence has been removed from its normal cellular  
(i.e., chromosomal) environment. Thus, the sequence may be in a cell-free solution or  
placed in a different cellular environment. The term does not imply that the sequence is  
15 the only nucleotide chain present, but that it is essentially free (about 90 - 95% pure at  
least) of non-nucleotide material naturally associated with it, and thus is distinguished  
from isolated chromosomes.

By the use of the term "enriched" in reference to nucleic acid is meant that the  
specific DNA or RNA sequence constitutes a significantly higher fraction (2 - 5 fold) of  
20 the total DNA or RNA present in the cells or solution of interest than in normal or  
diseased cells or in the cells from which the sequence was taken. This could be caused by  
a person by preferential reduction in the amount of other DNA or RNA present, or by a  
preferential increase in the amount of the specific DNA or RNA sequence, or by a  
combination of the two. However, it should be noted that enriched does not imply that  
25 there are no other DNA or RNA sequences present, just that the relative amount of the  
sequence of interest has been significantly increased. The term "significant" is used to  
indicate that the level of increase is useful to the person making such an increase, and  
generally means an increase relative to other nucleic acids of about at least 2 fold, more  
preferably at least 5 to 10 fold or even more. The term also does not imply that there is no  
30 DNA or RNA from other sources. The other source DNA may, for example, comprise  
DNA from a yeast or bacterial genome, or a cloning vector such as pUC19. This term  
distinguishes from naturally occurring events, such as viral infection, or tumor type

growths, in which the level of one mRNA may be naturally increased relative to other species of mRNA. That is, the term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

It is also advantageous for some purposes that a nucleotide sequence be in purified form. The term "purified" in reference to nucleic acid does not require absolute purity (such as a homogeneous preparation). Instead, it represents an indication that the sequence is relatively more pure than in the natural environment (compared to the natural level this level should be at least 2-5 fold greater, *e.g.*, in terms of mg/mL). Individual clones isolated from a cDNA library may be purified to electrophoretic homogeneity. The claimed DNA molecules obtained from these clones could be obtained directly from total DNA or from total RNA. The cDNA clones are not naturally occurring, but rather are preferably obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The construction of a cDNA library from mRNA involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection of the cells carrying the cDNA library. Thus, the process which includes the construction of a cDNA library from mRNA and isolation of distinct cDNA clones yields an approximately  $10^6$ -fold purification of the native message. Thus, purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

By a "kinase polypeptide" is meant 10 (preferably 20, more preferably 40, most preferably 75) or more contiguous amino acids set forth in an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,

SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,  
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,  
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,  
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,  
5 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,  
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,  
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,  
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SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,  
10 SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,  
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,  
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,  
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,  
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional  
15 derivatives thereof as described herein. For sequences for which the full-length sequence  
is not given, the remaining sequences can be determined using methods well-known to  
those in the art and are intended to be included in the invention. In certain aspects,  
polypeptides of 100, 200, 300 or more amino acids are preferred. The kinase polypeptide  
can be encoded by a full-length nucleic acid sequence or any portion of the full-length  
20 nucleic acid sequence, so long as a functional activity of the polypeptide is retained. By  
“functional” domain is meant any region of the polypeptide that may play a regulatory or  
catalytic role as predicted from amino acid sequence homology to other proteins or by the  
presence of amino acid sequences that may give rise to specific structural conformations  
(*i.e.*, coiled-coils). For some purposes, polypeptide domains are preferred, including, but  
25 not limited to, N-terminal, catalytic/kinase and C-terminal.

The amino acid sequence will be substantially similar to a sequence selected from  
the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID  
NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID  
NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID  
30 NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID  
NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID  
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15 NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID  
NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID  
NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID  
NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID  
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding  
20 full-length amino acid sequence, or fragments thereof. A sequence that is substantially  
similar to a sequence selected from the group consisting of those set forth in SEQ ID  
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID  
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ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 or portions of or the entire corresponding full-length amino acid sequences.

By "identity" is meant a property of sequences that measures their similarity or relationship. Identity is measured by dividing the number of identical residues between two sequences (either full-length or a defined domain) by the total number of residues in the known sequence, or the domain of the known sequence, and multiplying the product by 100. Thus, two copies of exactly the same sequence have 100% identity, but sequences that are less highly conserved, and have replacements and substitutions, have a lower degree of identity. "Gaps" are spaces in an alignment that can result from aligning a novel sequence with a known sequence when the novel sequence has additions or deletions of amino acids in comparison with the known sequence. These gaps do not factor into the assessment of % identity using the above calculation.

Those skilled in the art will recognize that several computer programs are also available for determining sequence identity using standard parameters, for example, Blast (Altschul, *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402), Blast2 (Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410), and Smith-Waterman (Smith, *et al.* (1981) *J. Mol. Biol.* 147:195-197).

In preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding a kinase polypeptide comprising a nucleotide sequence that: (a) encodes a polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID



NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID  
NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID  
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NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID  
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NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID  
NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will  
15 have at least 75% identity (preferably 90%, more preferably at least 95% and most  
preferably 99-100%) to the sequence selected from the group consisting of those set forth  
in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID  
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID  
NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID  
20 NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID  
NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID  
NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID  
NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID  
NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID  
25 NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID  
NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID  
NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID  
NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID  
NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID  
30 NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID  
NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID  
NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID

NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID

NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID

NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (e) is the complement of the nucleotide sequence of (d); (f) encodes a polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID

NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. (The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.) A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID

NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ

ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID

NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

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SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, where the domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (g) is the complement of the nucleotide sequence of (f); (h) encodes a polypeptide having an amino acid sequence selected from the group consisting

of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,

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SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,  
5 SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,  
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,  
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,  
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,  
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10 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,  
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SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,  
15 SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,  
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,  
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,  
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,  
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at  
20 least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-  
100%) to the sequence selected from the group consisting of those set forth in SEQ ID  
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID  
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID  
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID  
25 NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID  
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID  
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NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID  
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID  
30 NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID  
NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID  
NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID

NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID

NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,

SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at

5 least 95% and most preferably 99-100%) to the sequence of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID  
10 NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID  
15 NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID  
20 NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID  
25 NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242,

30 except that it lacks one or more of the domains selected from the group consisting of a N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; or (i) is the

complement of the nucleotide sequence of (h). The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.

The term "complement" refers to two nucleotides that can form multiple favorable interactions with one another. For example, adenine is complementary to thymine as they can form two hydrogen bonds. Similarly, guanine and cytosine are complementary since they can form three hydrogen bonds. A nucleotide sequence is the complement of another nucleotide sequence if all of the nucleotides of the first sequence are complementary to all of the nucleotides of the second sequence.

The term "domain" refers to a region of a polypeptide that contains a particular function. For instance, N-terminal or C-terminal domains of signal transduction proteins can serve functions including, but not limited to, binding molecules that localize the signal transduction molecule to different regions of the cell or binding other signaling molecules directly responsible for propagating a particular cellular signal. Some domains can be expressed separately from the rest of the protein and function by themselves, while others must remain part of the intact protein to retain function. The latter are termed functional regions of proteins and also relate to domains.

The term "N-terminal domain" refers to the extracatalytic region located between the initiator methionine and the catalytic domain of the protein kinase. The N-terminal domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the N-terminal boundary of the catalytic domain. Depending on its length, the N-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose N-terminal domain has been shown to play a regulatory role is PAK65, which contains a CRIB motif used for Cdc42 and rac binding (Burbelo, P.D. *et al.* (1995) *J. Biol. Chem.* 270, 29071-29074). The N-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the amino-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. Further, in some cases, portions of the N-terminal domains of the protein kinases of the invention have not been identified since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined and using the approaches described herein the N-terminal domain can be identified.

The term "catalytic domain" or "kinase domain" refers to a region of the protein kinase that is typically 25-300 amino acids long and is responsible for carrying out the phosphate transfer reaction from a high-energy phosphate donor molecule such as ATP or GTP to itself (autophosphorylation) or to other proteins (exogenous phosphorylation).

5 The catalytic domain of protein kinases is made up of 12 subdomains that contain highly conserved amino acid residues, and are responsible for proper polypeptide folding and for catalysis. The catalytic domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database. The catalytic/kinase domains of the protein kinases of the invention are identified in Table 2, herein. Further,  
10 in some cases, the complete sequence of the catalytic/kinase domains of the protein kinases of the invention may not have been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the catalytic/kinase domain can be identified.

15 The term "catalytic activity", as used herein, defines the rate at which a kinase catalytic domain phosphorylates a substrate. Catalytic activity can be measured, for example, by determining the amount of a substrate converted to a phosphorylated product as a function of time. Catalytic activity can be measured by methods of the invention by holding time constant and determining the concentration of a phosphorylated substrate  
20 after a fixed period of time. Phosphorylation of a substrate occurs at the active-site of a protein kinase. The active-site is normally a cavity in which the substrate binds to the protein kinase and is phosphorylated.

The term "substrate" as used herein refers to a molecule phosphorylated by a kinase of the invention. Kinases phosphorylate substrates on serine/threonine or tyrosine  
25 amino acids. The molecule may be another protein or a polypeptide.

The term "C-terminal domain" refers to the region located between the catalytic domain and the carboxy-terminal amino acid residue of the protein kinase. The C-terminal domain can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C-terminal boundary of  
30 the catalytic domain or of any functional C-terminal extracatalytic domain. Depending on its length and amino acid composition, the C-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose C-terminal



domain may play a regulatory role is PAK3 which contains a heterotrimeric G<sub>b</sub> subunit-binding site near its C-terminus (Leeuw, T. *et al.* (1998) *Nature*, 391, 191-195). The C-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the carboxy-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. In some cases, the C-terminal domains of the protein kinases of the invention have not been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the C-terminal domain can be identified.

The term "signal transduction pathway" refers to the molecules that propagate an extracellular signal through the cell membrane to become an intracellular signal. This signal can then stimulate a cellular response. The polypeptide molecules involved in signal transduction processes are typically receptor and non-receptor protein tyrosine kinases, receptor and non-receptor protein phosphatases, SRC homology 2 and 3 domains, phosphotyrosine binding proteins (SRC homology 2 (SH2) and phosphotyrosine binding (PTB and PH) domain containing proteins), proline-rich binding proteins (SH3 domain containing proteins), nucleotide exchange factors, and transcription factors.

The term "coiled-coil structure region" as used herein, refers to a polypeptide sequence that has a high probability of adopting a coiled-coil structure as predicted by computer algorithms such as COILS (Lupas, A. (1996) *Meth. Enzymology* 266:513-525). Coiled-coils are formed by two or three amphipathic  $\alpha$ -helices in parallel. Coiled-coils can bind to coiled-coil domains of other polypeptides resulting in homo- or heterodimers (Lupas, A. (1991) *Science* 252:1162-1164). Coiled-coil-dependent oligomerization has been shown to be necessary for protein function including catalytic activity of serine/threonine kinases (Roe, J. *et al.* (1997) *J. Biol. Chem.* 272:5838-5845). Coiled-coil regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "proline-rich region" as used herein, refers to a region of a protein kinase whose proline content over a given amino acid length is higher than the average content of this amino acid found in proteins (*i.e.*, >10%). Proline-rich regions are easily discernable by visual inspection of amino acid sequences and quantitated by standard computer

sequence analysis programs such as the DNASTar program EditSeq. Proline-rich regions have been demonstrated to participate in regulatory protein-protein interactions. Among these interactions, those that are most relevant to this invention involve the "PxxP" proline rich motif found in certain protein kinases (*i.e.*, human PAK1) and the SH3 domain of the adaptor molecule Nck (Galisteo, M.L. *et al.* (1996) J. Biol. Chem. 271:20997-21000).

Other regulatory interactions involving "PxxP" proline-rich motifs include the WW domain (Sudol, M. (1996) Prog. Biophys. Mol. Bio. 65:113-132). Proline rich regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "spacer region" as used herein, refers to a region of the protein kinase located between predicted functional domains. The spacer region has no detectable homology to any amino acid sequence in the database, and can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C- and N-terminal boundaries of the flanking functional domains. Spacer regions may or may not play a fundamental role in protein kinase function. Precedence for the regulatory role of spacer regions in kinase function is provided by the role of the src kinase spacer in inter-domain interactions (Xu, W. *et al.* (1997) Nature 385:595-602). Spacer regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "insert" as used herein refers to a portion of a protein kinase that is absent from a close homolog. Inserts may or may not be the product alternative splicing of exons. Inserts can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Inserts may play a functional role by presenting a new interface for protein-protein interactions, or by interfering with such interactions. Insert regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "C-terminal tail" as used herein, refers to a C-terminal domain of a protein kinase, that by homology extends or protrudes past the C-terminal amino acid of its closest homolog. C-terminal tails can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Depending on its length, a C-terminal tail may or may not play a regulatory role in kinase function. C-terminal tail regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

Various low or high stringency hybridization conditions may be used depending upon the specificity and selectivity desired. These conditions are well-known to those skilled in the art. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides, more preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 50 contiguous nucleotides, most preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 100 contiguous nucleotides. In some instances, the conditions may prevent hybridization of nucleic acids having more than 5 mismatches in the full-length sequence.

By stringent hybridization assay conditions is meant hybridization assay conditions at least as stringent as the following: hybridization in 50% formamide, 5X SSC, 50 mM  $\text{NaH}_2\text{PO}_4$ , pH 6.8, 0.5% SDS, 0.1 mg/mL sonicated salmon sperm DNA, and 5X Denhart solution at 42 °C overnight; washing with 2X SSC, 0.1% SDS at 45 °C; and washing with 0.2X SSC, 0.1% SDS at 45 °C. Under some of the most stringent hybridization assay conditions, the second wash can be done with 0.1X SSC at a temperature up to 70 °C (pg. 421, Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein including any figures, tables, or drawings.). However, other applications may require the use of conditions falling between these sets of conditions. Methods of determining the conditions required to achieve desired hybridizations are well-known to those with ordinary skill in the art, and are based on several factors, including but not limited to, the sequences to be hybridized and the samples to be tested.

In other preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding kinase polypeptides, further comprising a vector or promoter effective to initiate transcription in a host cell. The invention also features recombinant nucleic acid, preferably in a cell or an organism. The recombinant nucleic acid may contain a sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a functional derivative thereof and a vector or a promoter effective to initiate transcription in a host cell. The recombinant nucleic acid can alternatively contain a transcriptional initiation region functional in a cell, a sequence complementary to an RNA sequence encoding a kinase polypeptide and a transcriptional termination region functional in a cell. Specific

vectors and host cell combinations are discussed herein. The recombinant nucleic acid can also contain the full-length sequence encoding the protein kinase, or a domain, for example.

The term "vector" relates to a single or double-stranded circular nucleic acid molecule that can be transfected into cells and replicated within or independently of a cell genome. A circular double-stranded nucleic acid molecule can be cut and thereby linearized upon treatment with restriction enzymes. An assortment of nucleic acid vectors, restriction enzymes, and the knowledge of the nucleotide sequences cut by restriction enzymes are readily available to those skilled in the art. A nucleic acid molecule encoding a kinase can be inserted into a vector by cutting the vector with restriction enzymes and ligating the two pieces together.

The term "transfecting" defines a number of methods to insert a nucleic acid vector or other nucleic acid molecules into a cellular organism. These methods involve a variety of techniques, such as treating the cells with high concentrations of salt, an electric field, detergent, or DMSO to render the outer membrane or wall of the cells permeable to nucleic acid molecules of interest or use of various viral transduction strategies.

The term "promoter" as used herein, refers to nucleic acid sequence needed for gene sequence expression. Promoter regions vary from organism to organism, but are well known to persons skilled in the art for different organisms. For example, in prokaryotes, the promoter region contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

In preferred embodiments, the isolated nucleic acid comprises, consists essentially of, or consists of a nucleic acid sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35,

SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, encodes an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID

NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID  
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID  
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID  
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID  
5 NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID  
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID  
NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID  
NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID  
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID  
10 NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ  
ID NO:242, or the corresponding full-length amino acid sequence, a functional derivative  
thereof, or at least 10, 20, 40, 50, 75, 100, 200, 300 or 500 contiguous amino acids of a  
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID  
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID  
15 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID  
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID  
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID  
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID  
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID  
20 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID  
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID  
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID  
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID  
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID  
25 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID  
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID  
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID  
NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID  
NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID  
30 NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID  
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID  
NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID

NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length sequences or derivatives thereof. The nucleic acid may be isolated from a natural source by cDNA cloning or by subtractive hybridization. The natural source may be mammalian, preferably human, blood, semen, or tissue, and the nucleic acid may be synthesized by the triester method or by using an automated DNA synthesizer.

The term "mammal" refers preferably to such organisms as mice, rats, rabbits, guinea pigs, sheep, and goats, more preferably to cats, dogs, monkeys, and apes, and most preferably to humans.

In yet other preferred embodiments, the nucleic acid is a conserved or unique region, for example those useful for: the design of hybridization probes to facilitate identification and cloning of additional polypeptides, the design of PCR probes to facilitate cloning of additional polypeptides, obtaining antibodies to polypeptide regions, and designing antisense oligonucleotides.

By "conserved nucleic acid regions", are meant regions present on two or more nucleic acids encoding a kinase polypeptide, to which a particular nucleic acid sequence can hybridize under lower stringency conditions. Examples of lower stringency conditions suitable for screening for nucleic acid encoding kinase polypeptides are provided in Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables. Preferably, conserved regions differ by no more than 5 out of 20 nucleotides, even more preferably 2 out of 20 nucleotides or most preferably 1 out of 20 nucleotides.

By "unique nucleic acid region" is meant a sequence present in a nucleic acid coding for a kinase polypeptide that is not present in a sequence coding for any other naturally occurring polypeptide. Such regions preferably encode 10 (preferably 25, more preferably 50, most preferably 75) or more contiguous amino acids selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,



SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,  
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,  
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,  
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,  
5 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,  
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,  
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,  
SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,  
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,  
10 SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,  
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,  
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,  
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,  
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,  
15 SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,  
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,  
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,  
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,  
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,  
20 SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,  
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,  
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,  
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,  
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional derivatives thereof.  
25 In particular, a unique nucleic acid region is preferably of mammalian origin and  
preferably human.

A second aspect of the invention features a nucleic acid probe for the detection of  
nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is  
selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,  
30 SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,  
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,  
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,

SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,  
SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,  
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,  
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,  
5 SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,  
SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,  
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,  
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,  
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,  
10 SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,  
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,  
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,  
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,  
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,  
15 SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,  
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,  
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,  
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,  
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,  
20 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,  
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the nucleic acid  
probe encodes a kinase polypeptide that is a fragment of the protein encoded by an amino  
acid sequence selected from the group consisting of those set forth in SEQ ID NO:122,  
SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,  
25 SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132,  
SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137,  
SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142,  
SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147,  
SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152,  
30 SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157,  
SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162,  
SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167,

SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172,  
SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177,  
SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,  
SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,  
5 SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,  
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,  
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,  
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,  
SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,  
10 SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,  
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,  
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,  
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,  
SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,  
15 SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID  
NO:242, or the corresponding full-length amino acid sequences. The nucleic acid probe  
contains a nucleotide base sequence that will hybridize to a sequence selected from the  
group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ  
ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9,  
20 SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ  
ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID  
NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25,  
SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ  
ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID  
25 NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41,  
SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ  
ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID  
NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57,  
SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ  
30 ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID  
NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73,  
SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ

ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, or a functional derivative thereof.

In preferred embodiments, the nucleic acid probe hybridizes to nucleic acid encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID

NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or functional derivatives thereof.

Methods for using the probes include detecting the presence or amount of kinase RNA in a sample by contacting the sample with a nucleic acid probe under conditions such that hybridization occurs and detecting the presence or amount of the probe bound to kinase RNA. The nucleic acid duplex formed between the probe and a nucleic acid sequence coding for a kinase polypeptide may be used in the identification of the sequence of the nucleic acid detected (Nelson *et al.*, in *Nonisotopic DNA Probe Techniques*, Academic Press, San Diego, Kricka, ed., p. 275, 1992, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables). Kits for performing such methods may be constructed to include a container means having disposed therein a nucleic acid probe.

In a third aspect, the invention describes a recombinant cell or tissue comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,

SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,  
SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,  
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,  
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,  
5 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,  
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,  
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,  
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,  
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,  
10 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,  
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,  
and SEQ ID NO:242. In such cells, the nucleic acid may be under the control of the  
genomic regulatory elements, or may be under the control of exogenous regulatory  
elements including an exogenous promoter. By "exogenous" it is meant a promoter that is  
15 not normally coupled *in vivo* transcriptionally to the coding sequence for the kinase  
polypeptides.

The polypeptide is preferably a fragment of the protein encoded by an amino acid  
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID  
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID  
20 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID  
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID  
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID  
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID  
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID  
25 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID  
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID  
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID  
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID  
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID  
30 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID  
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID  
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID

NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID  
NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID  
NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID  
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID  
5 NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID  
NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID  
NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID  
NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID  
NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID  
10 NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the  
corresponding full-length amino acid sequence. By "fragment," is meant an amino acid  
sequence present in a kinase polypeptide. Preferably, such a sequence comprises at least  
10, 20, 40, 50, 75, 100, 200, or 300 contiguous amino acids a sequence selected from the  
group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,  
15 SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,  
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,  
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,  
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,  
SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,  
20 SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,  
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,  
SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,  
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,  
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,  
25 SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,  
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,  
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,  
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,  
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,  
30 SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,  
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,  
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,

SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,  
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,  
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,  
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,  
5 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,  
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or of the corresponding full-  
length amino acid sequence, or a functional derivative thereof.

In a fourth aspect, the invention features an isolated, enriched, or purified kinase  
polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ  
10 ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ  
ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ  
ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ  
ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ  
ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ  
15 ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ  
ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ  
ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ  
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ  
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ  
20 ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ  
ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ  
ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ  
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ  
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ  
25 ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ  
ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ  
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ  
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ  
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ  
30 ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ  
ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ



ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

By "isolated" in reference to a polypeptide is meant a polymer of amino acids (2 or more amino acids) conjugated to each other, including polypeptides that are isolated from a natural source or that are synthesized. The isolated polypeptides of the present invention are unique in the sense that they are not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only amino acid chain present, but that it is essentially free (about 90 - 95% pure at least) of non-amino acid material naturally associated with it.

By the use of the term "enriched" in reference to a polypeptide is meant that the specific amino acid sequence constitutes a significantly higher fraction (2 - 5 fold) of the total amino acid sequences present in the cells or solution of interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other amino acid sequences present, or by a preferential increase in the amount of the specific amino acid sequence of interest, or by a combination of the two. However, it should be noted that enriched does not imply that there are no other amino acid sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term significant here is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other amino acid sequences of about at least 2-fold, more preferably at least 5- to 10-fold or even more. The term also does not imply that there is no amino acid sequence from other sources. The other source of amino acid sequences may, for example, comprise amino acid sequence encoded by a yeast or bacterial genome, or a cloning vector such as pUC19. The term is meant to cover only those situations in which man has intervened to increase the proportion of the desired amino acid sequence.

It is also advantageous for some purposes that an amino acid sequence be in purified form. The term "purified" in reference to a polypeptide does not require absolute purity (such as a homogeneous preparation); instead, it represents an indication that the sequence is relatively purer than in the natural environment. Compared to the natural level

this level should be at least 2-5 fold greater (*e.g.*, in terms of mg/mL). Purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. The substance is preferably free of contamination at a functionally significant level, for example 90%, 95%, or 99% pure.

5           In preferred embodiments, the kinase polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,  
10       SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,  
15       SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,  
20       SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,  
25       SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,  
30       SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequences. Preferably, the kinase polypeptide contains at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous

amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof.

In preferred embodiments, the kinase polypeptide comprises an amino acid sequence having (a) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ

ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ

ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (c) an amino acid sequence of a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,  
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,  
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,  
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,  
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,  
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,  
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,  
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,  
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,  
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,  
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID  
NO:242 where the domain is selected from the group consisting of an N-terminal domain,  
a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich  
region, a spacer region, an insert, and a C-terminal tail; or (d) an amino acid sequence  
15 selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123,  
SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,  
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,  
SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,  
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,  
20 SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,  
SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,  
SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,  
SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,  
SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,  
25 SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,  
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,  
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,  
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,  
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,  
30 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,  
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,  
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,

SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,  
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,  
SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,  
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,  
5 SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,  
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,  
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it  
lacks one or more, but not all, of the domains selected from the group consisting of a C-  
terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich  
10 region, a coiled-coil structure region, an insert, and a C-terminal tail. (The domain  
demarcations of the polypeptides of the invention are indicated in Table 2 by reference to  
the kinase domain.)

The polypeptide can be isolated from a natural source by methods well-known in  
the art. The natural source may be mammalian, preferably human, blood, semen, or tissue,  
15 and the polypeptide may be synthesized using an automated polypeptide synthesizer. The  
isolated, enriched, or purified kinase polypeptide is preferably selected from the group  
consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ  
ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ  
ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ  
20 ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ  
ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ  
ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ  
ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ  
ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ  
25 ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ  
ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ  
ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ  
ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ  
ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ  
30 ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ  
ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ  
ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ

ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242A.

In some embodiments the invention includes a recombinant kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,



SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. By “recombinant kinase polypeptide” is meant a polypeptide produced by recombinant DNA techniques such that it is distinct from a naturally occurring polypeptide either in its location (*e.g.*, present in a different cell or tissue than found in nature), purity or structure. Generally, such a recombinant polypeptide will be present in a cell in an amount different from that normally observed in nature.

In a fifth aspect, the invention features an antibody (*e.g.*, a monoclonal or polyclonal antibody) having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain or fragment where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ

ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. In preferred embodiments, the antibody binds specifically to domains of kinase polypeptides, that are defined *supra*.

By “specific binding affinity” is meant that the antibody binds to the target kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions. Antibodies or antibody fragments are polypeptides that contain regions that can bind other polypeptides. The term “specific binding affinity” describes an antibody that binds to a kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions.

The term “polyclonal” refers to antibodies that are heterogenous populations of antibody molecules derived from the sera of animals immunized with an antigen or an antigenic functional derivative thereof. For the production of polyclonal antibodies, various host animals may be immunized by injection with the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species.

“Monoclonal antibodies” are substantially homogenous populations of antibodies to a particular antigen. They may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture. Monoclonal antibodies may be obtained by methods known to those skilled in the art (Kohler *et al.*, Nature 256:495-497, 1975, and U.S. Patent No. 4,376,110, both of which are hereby incorporated by reference herein in their entirety including any figures, tables, or drawings).

The term “antibody fragment” refers to a portion of an antibody, often the hyper variable region and portions of the surrounding heavy and light chains, that displays specific binding affinity for a particular molecule. A hyper variable region is a portion of an antibody that physically binds to the polypeptide target.

Antibodies or antibody fragments having specific binding affinity to a kinase polypeptide or domains of a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by probing the sample with the antibody under conditions suitable for kinase-antibody immunocomplex formation and detecting the presence and/or amount of the antibody conjugated to the

kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include antibodies or antibody fragments specific for the kinase as well as a conjugate of a binding partner of the antibodies or the antibodies themselves.

An antibody or antibody fragment with specific binding affinity to a kinase polypeptide of the invention can be isolated, enriched, or purified from a prokaryotic or eukaryotic organism. Routine methods known to those skilled in the art enable production of antibodies or antibody fragments, in both prokaryotic and eukaryotic organisms. Purification, enrichment, and isolation of antibodies, which are polypeptide molecules, are described above.

Antibodies having specific binding affinity to a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by contacting the sample with the antibody under conditions such that an immunocomplex forms and detecting the presence and/or amount of the antibody conjugated to the kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include a first container containing the antibody and a second container having a conjugate of a binding partner of the antibody and a label, such as, for example, a radioisotope. The diagnostic kit may also include notification of an FDA approved use and instructions therefor.

In a sixth aspect, the invention features a hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain, where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID

NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; and where the domains are defined as above. By “hybridoma” is meant an immortalized cell line that is capable of secreting an antibody, for example an antibody to a kinase of the invention. In preferred embodiments, the antibody to the kinase comprises a sequence of amino acids that is able to specifically bind a kinase polypeptide of the invention.

In a seventh aspect, the invention features a kinase polypeptide binding agent able to bind to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,  
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,  
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,  
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,  
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,  
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,  
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,  
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,  
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,  
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,  
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID  
NO:242. The binding agent is preferably a purified antibody that recognizes an epitope  
present on a kinase polypeptide of the invention. Other binding agents include molecules  
that bind to kinase polypeptides and analogous molecules that bind to a kinase  
15 polypeptide. Such binding agents may be identified by using assays that measure kinase  
binding partner activity, such as those that measure PDGFR activity.

The invention also features a method for screening for human cells containing a  
kinase polypeptide of the invention or an equivalent sequence. The method involves  
identifying the novel polypeptide in human cells using techniques that are routine and  
20 standard in the art, such as those described herein for identifying the kinases of the  
invention (*e.g.*, cloning, Southern or Northern blot analysis, in situ hybridization, PCR  
amplification, etc.).

In an eighth aspect, the invention features methods for identifying a substance that  
modulates kinase activity comprising the steps of: (a) contacting a kinase polypeptide  
25 selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,  
SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,  
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,  
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,  
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,  
30 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,  
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,  
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,

SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,  
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,  
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,  
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,  
5 SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,  
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,  
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,  
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,  
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,  
10 SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,  
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,  
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,  
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,  
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,  
15 SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,  
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,  
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 with a test substance; (b)  
measuring the activity of said polypeptide; and (c) determining whether said substance  
modulates the activity of said polypeptide.

20       The term “modulates” refers to the ability of a compound to alter the function of a  
kinase of the invention. A modulator preferably activates or inhibits the activity of a  
kinase of the invention.

      The term “activates” refers to increasing the cellular activity of the kinase. The  
term inhibit refers to decreasing the cellular activity of the kinase. Kinase activity is  
25 preferably the interaction with a natural binding partner.

      The term “modulates” also refers to altering the function of kinases of the  
invention by increasing or decreasing the probability that a complex forms between the  
kinase and a natural binding partner. A modulator preferably increases the probability that  
such a complex forms between the kinase and the natural binding partner, more preferably  
30 increases or decreases the probability that a complex forms between the kinase and the  
natural binding partner depending on the concentration of the compound exposed to the

kinase, and most preferably decreases the probability that a complex forms between the kinase and the natural binding partner.

The term “complex” refers to an assembly of at least two molecules bound to one another. Signal transduction complexes often contain at least two protein molecules  
5 bound to one another. For instance, a protein tyrosine receptor protein kinase, GRB2, SOS, RAF, and RAS assemble to form a signal transduction complex in response to a mitogenic ligand.

The term “natural binding partner” refers to polypeptides, lipids, small molecules, or nucleic acids that bind to kinases in cells. A change in the interaction between a kinase  
10 and a natural binding partner can manifest itself as an increased or decreased probability that the interaction forms, or an increased or decreased concentration of kinase/natural binding partner complex.

The term “contacting” as used herein refers to mixing a solution comprising the test compound with a liquid medium bathing the cells of the methods. The solution  
15 comprising the compound may also comprise another component, such as dimethyl sulfoxide (DMSO), which facilitates the uptake of the test compound or compounds into the cells of the methods. The solution comprising the test compound may be added to the medium bathing the cells by utilizing a delivery apparatus, such as a pipet-based device or syringe-based device.

In a ninth aspect, the invention features methods for identifying a substance that modulates kinase activity in a cell comprising the steps of: (a) expressing a kinase  
20 polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,  
25 SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,  
30 SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,

SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,  
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,  
SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,  
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,  
5 SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,  
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,  
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,  
SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,  
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,  
10 SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,  
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,  
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,  
SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,  
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,  
15 and SEQ ID NO:242; (b) adding a test substance to said cell; and (c) monitoring a change  
in cell phenotype or the interaction between said polypeptide and a natural binding  
partner.

The term “expressing” as used herein refers to the production of kinases of the  
invention from a nucleic acid vector containing kinase genes within a cell. The nucleic  
20 acid vector is transfected into cells using well known techniques in the art as described  
herein.

In a tenth aspect, the invention provides methods for treating a disease or abnormal  
condition by administering to a patient in need of such treatment a substance that  
modulates the activity of a polypeptide selected from the group consisting of SEQ ID  
25 NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID  
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID  
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID  
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID  
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID  
30 NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID  
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID  
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID



NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the disease is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer. Also included are metabolic disorders, such as diabetes mellitus, and reproductive disorders, such as infertility.

Preferably, the disease or disorder is selected from the group consisting of rheumatoid arthritis, arteriosclerosis, autoimmune disorders, and organ transplantation. Preferably the disease or disorder is selected from the group consisting of immune-related diseases and disorders, myocardial infarction, cardiomyopathies, stroke, renal failure, and oxidative stress-related neurodegenerative disorders. Most preferably, the immune-related diseases and disorders are selected from the group consisting of rheumatoid arthritis, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, arteriosclerosis, rhinitis, autoimmunity, and organ transplantation.

Substances useful for treatment of disorders or diseases preferably show positive results in one or more in vitro assays for an activity corresponding to treatment of the disease or disorder in question. Substances that modulate the activity of the polypeptides

preferably include, but are not limited to, antisense oligonucleotides and inhibitors of protein kinases.

The term “preventing” refers to decreasing the probability that an organism contracts or develops an abnormal condition.

5       The term “treating” refers to having a therapeutic effect and at least partially alleviating or abrogating an abnormal condition in the organism.

10       The term “therapeutic effect” refers to the inhibition or activation factors causing or contributing to the abnormal condition. A therapeutic effect relieves to some extent one or more of the symptoms of the abnormal condition. In reference to the treatment of abnormal conditions, a therapeutic effect can refer to one or more of the following: (a) an increase in the proliferation, growth, and/or differentiation of cells; (b) inhibition (*i.e.*, slowing or stopping) of cell death; (c) inhibition of degeneration; (d) relieving to some extent one or more of the symptoms associated with the abnormal condition; and (e) enhancing the function of the affected population of cells. Compounds demonstrating efficacy against abnormal conditions can be identified as described herein.

15       The term “abnormal condition” refers to a function in the cells or tissues of an organism that deviates from their normal functions in that organism. An abnormal condition can relate to cell proliferation, cell differentiation or cell survival. An abnormal condition may also include irregularities in cell cycle progression, *i.e.*, irregularities in normal cell cycle progression through mitosis and meiosis.

20       Abnormal cell proliferative conditions include cancers such as fibrotic and mesangial disorders, abnormal angiogenesis and vasculogenesis, wound healing, psoriasis, diabetes mellitus, and inflammation.

25       Abnormal differentiation conditions include, but are not limited to neurodegenerative disorders, slow wound healing rates, and slow tissue grafting healing rates.

30       Abnormal cell survival conditions relate to conditions in which programmed cell death (apoptosis) pathways are activated or abrogated. A number of protein kinases are associated with the apoptosis pathways. Aberrations in the function of any one of the protein kinases could lead to cell immortality or premature cell death.

The term "aberration", in conjunction with the function of a kinase in a signal transduction process, refers to a kinase that is over- or under-expressed in an organism, mutated such that its catalytic activity is lower or higher than wild-type protein kinase activity, mutated such that it can no longer interact with a natural binding partner, is no longer modified by another protein kinase or protein phosphatase, or no longer interacts with a natural binding partner.

The term "administering" relates to a method of incorporating a compound into cells or tissues of an organism. The abnormal condition can be prevented or treated when the cells or tissues of the organism exist within the organism or outside of the organism. Cells existing outside the organism can be maintained or grown in cell culture dishes. For cells harbored within the organism, many techniques exist in the art to administer compounds, including (but not limited to) oral, parenteral, dermal, injection, and aerosol applications. For cells outside of the organism, multiple techniques exist in the art to administer the compounds, including (but not limited to) cell microinjection techniques, transformation techniques, and carrier techniques.

The abnormal condition can also be prevented or treated by administering a compound to a group of cells having an aberration in a signal transduction pathway to an organism. The effect of administering a compound on organism function can then be monitored. The organism is preferably a mouse, rat, rabbit, guinea pig, or goat, more preferably a monkey or ape, and most preferably a human.

In an eleventh aspect, the invention features methods for detection the expression of a polypeptide in a sample as a diagnostic tool for diseases or disorders, wherein the method comprises the steps of: (a) contacting the sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ

5 ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ  
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ  
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ  
ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ  
ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ  
ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ  
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ  
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ  
ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ  
10 ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ  
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ  
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ  
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ  
ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ  
15 ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ  
ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ  
ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe  
comprising the nucleic acid sequence encoding the polypeptide, fragments thereof, and the  
complements of the sequences and fragments; and (b) detecting the presence or amount of  
20 the probe:target region hybrid as an indication of the disease.

In preferred embodiments of the invention, the disease or disorder is selected from  
the group consisting of rheumatoid arthritis, arteriosclerosis, autoimmune disorders, organ  
transplantation, myocardial infarction, cardiomyopathies, stroke, renal failure, oxidative  
stress-related neurodegenerative disorders, metabolic disorder including diabetes,  
25 reproductive disorders including infertility, and cancer.

The kinase "target region" is a nucleotide base sequence selected from the group  
consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID  
NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ  
ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID  
30 NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20,  
SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ  
ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID

NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequences, a functional derivative thereof, or a fragment thereof to which the nucleic acid probe will specifically hybridize. Specific hybridization indicates that in the presence of other nucleic acids the probe only hybridizes detectably with the kinase of the invention's target region. Putative target regions can be identified by methods well known in the art consisting of alignment and comparison of the most closely related sequences in the database.

In preferred embodiments the nucleic acid probe hybridizes to a kinase target region encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of the sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID

NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof. Hybridization conditions should be such that hybridization occurs only with the kinase genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

Hybridization conditions should be such that hybridization occurs only with the genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

The diseases for which detection of kinase genes in a sample could be diagnostic include diseases in which kinase nucleic acid (DNA and/or RNA) is amplified in comparison to normal cells. By "amplification" is meant increased numbers of kinase

DNA or RNA in a cell compared with normal cells. In normal cells, kinases are typically found as single copy genes. In selected diseases, the chromosomal location of the kinase genes may be amplified, resulting in multiple copies of the gene, or amplification. Gene amplification can lead to amplification of kinase RNA, or kinase RNA can be amplified in the absence of kinase DNA amplification.

“Amplification” as it refers to RNA can be the detectable presence of kinase RNA in cells, since in some normal cells there is no basal expression of kinase RNA. In other normal cells, a basal level of expression of kinase exists, therefore in these cases amplification is the detection of at least 1-2-fold, and preferably more, kinase RNA, compared to the basal level.

The diseases that could be diagnosed by detection of kinase nucleic acid in a sample preferably include cancers. The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

Another aspect of the invention involves a method of agonizing (stimulating) or antagonizing a target of the invention and a natural binding partner associated activity in a mammal comprising administering to said mammal an agonist or antagonist to one of the above disclosed polypeptides in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of the protein of the present invention activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize associated functions is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein polypeptides. Some small organic molecules form a class of compounds that modulate the function of protein polypeptides. Examples of molecules that have been reported to inhibit the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published

November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzyolphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*), all of which are incorporated by reference herein, including any drawings.

Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein inhibitors only weakly inhibit function. In addition, many inhibit a variety of protein kinases and will therefore cause multiple side-effects as therapeutics for diseases.

Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin, naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar groups including hydroxylated alkyl, phosphate, and ether substituents. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon



& Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives, both of which are incorporated by reference herein, including any drawings.

5 Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722  
10 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5,316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris  
15 *et al.* J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.* J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J. Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*,  
20 Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); and Sikora *et al.*, Analytical Biochem. 172:344-355 (1988), all of which are incorporated  
25 herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432  
30 (1993); and Burke *et al.* BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen et al., Clin. Exp. Immunol. 91:141-156 (1993); Anafi et al., Blood 82:12:3524-3529 (1993); Baker et al., J. Cell Sci. 102:543-555 (1992); Bilder et al., Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton et al., Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert et al., Experimental Cell Research 199:255-261 (1992); Dong et al., J. Leukocyte Biology 53:53-60 (1993); Dong et al., J. Immunol. 151(5):2717-2724 (1993); Gazit et al., J. Med. Chem. 32:2344-2352 (1989); Gazit et al., " J. Med. Chem. 36:3556-3564 (1993); Kaur et al., Anti-Cancer Drugs 5:213-222 (1994); Kaur et al., King et al., Biochem. J. 275:413-418 (1991); Kuo et al., Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall et al., J. Biol. Chem. 264:14503-14509 (1989); Peterson et al., The Prostate 22:335-345 (1993); Pillemer et al., Int. J. Cancer 50:80-85 (1992); Posner et al., Molecular Pharmacology 45:673-683 (1993); Rendu et al., Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring et al., J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda et al., Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

#### Methods of Treating a Disease (Enablement - i.e., Dosing)

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be

The term "aberration", in conjunction with the function of a kinase in a signal transduction process, refers to a kinase that is over- or under-expressed in an organism, mutated such that its catalytic activity is lower or higher than wild-type protein kinase activity, mutated such that it can no longer interact with a natural binding partner, is no longer modified by another protein kinase or protein phosphatase, or no longer interacts with a natural binding partner.

The term "administering" relates to a method of incorporating a compound into cells or tissues of an organism. The abnormal condition can be prevented or treated when the cells or tissues of the organism exist within the organism or outside of the organism. Cells existing outside the organism can be maintained or grown in cell culture dishes. For cells harbored within the organism, many techniques exist in the art to administer compounds, including (but not limited to) oral, parenteral, dermal, injection, and aerosol applications. For cells outside of the organism, multiple techniques exist in the art to administer the compounds, including (but not limited to) cell microinjection techniques, transformation techniques, and carrier techniques.

The abnormal condition can also be prevented or treated by administering a compound to a group of cells having an aberration in a signal transduction pathway to an organism. The effect of administering a compound on organism function can then be monitored. The organism is preferably a mouse, rat, rabbit, guinea pig, or goat, more preferably a monkey or ape, and most preferably a human.

In an eleventh aspect, the invention features methods for detection the expression of a polypeptide in a sample as a diagnostic tool for diseases or disorders, wherein the method comprises the steps of: (a) contacting the sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ

ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding the polypeptide, fragments thereof, and the complements of the sequences and fragments; and (b) detecting the presence or amount of the probe:target region hybrid as an indication of the disease.

In preferred embodiments of the invention, the disease or disorder is selected from the group consisting of rheumatoid arthritis, atherosclerosis, autoimmune disorders, organ transplantation, myocardial infarction, cardiomyopathies, stroke, renal failure, oxidative stress-related neurodegenerative disorders, metabolic disorder including diabetes, reproductive disorders including infertility, and cancer.

The kinase "target region" is a nucleotide base sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID

NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequences, a functional derivative thereof, or a fragment thereof to which the nucleic acid probe will specifically hybridize. Specific hybridization indicates that in the presence of other nucleic acids the probe only hybridizes detectably with the kinase of the invention's target region. Putative target regions can be identified by methods well known in the art consisting of alignment and comparison of the most closely related sequences in the database.

In preferred embodiments the nucleic acid probe hybridizes to a kinase target region encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of the sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID

NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof. Hybridization conditions should be such that hybridization occurs only with the kinase genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

Hybridization conditions should be such that hybridization occurs only with the genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

The diseases for which detection of kinase genes in a sample could be diagnostic include diseases in which kinase nucleic acid (DNA and/or RNA) is amplified in comparison to normal cells. By "amplification" is meant increased numbers of kinase

DNA or RNA in a cell compared with normal cells. In normal cells, kinases are typically found as single copy genes. In selected diseases, the chromosomal location of the kinase genes may be amplified, resulting in multiple copies of the gene, or amplification. Gene amplification can lead to amplification of kinase RNA, or kinase RNA can be amplified in the absence of kinase DNA amplification.

"Amplification" as it refers to RNA can be the detectable presence of kinase RNA in cells, since in some normal cells there is no basal expression of kinase RNA. In other normal cells, a basal level of expression of kinase exists, therefore in these cases amplification is the detection of at least 1-2-fold, and preferably more, kinase RNA, compared to the basal level.

The diseases that could be diagnosed by detection of kinase nucleic acid in a sample preferably include cancers. The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

Another aspect of the invention involves a method of agonizing (stimulating) or antagonizing a target of the invention and a natural binding partner associated activity in a mammal comprising administering to said mammal an agonist or antagonist to one of the above disclosed polypeptides in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of the protein of the present invention activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize associated functions is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein polypeptides. Some small organic molecules form a class of compounds that modulate the function of protein polypeptides. Examples of molecules that have been reported to inhibit the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published

November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*), all of which are incorporated by reference herein, including any drawings.

Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein inhibitors only weakly inhibit function. In addition, many inhibit a variety of protein kinases and will therefore cause multiple side-effects as therapeutics for diseases.

Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin, naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar groups including hydroxylated alkyl, phosphate, and ether substituents. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon



& Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives, both of which are incorporated by reference herein, including any drawings.

5 Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722  
10 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris  
15 *et al.* J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.* J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J. Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*,  
20 Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); and Sikora *et al.*, Analytical Biochem. 172:344-355 (1988), all of which are incorporated  
25 herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432  
30 (1993); and Burke *et al.* BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen et al., Clin. Exp. Immunol. 91:141-156 (1993); Anafi et al., Blood 82:12:3524-3529 (1993); Baker et al., J. Cell Sci. 102:543-555 (1992); Bilder et al., Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton et al., Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert et al., Experimental  
5 Cell Research 199:255-261 (1992); Dong et al., J. Leukocyte Biology 53:53-60 (1993); Dong et al., J. Immunol. 151(5):2717-2724 (1993); Gazit et al., J. Med. Chem. 32:2344-2352 (1989); Gazit et al., "J. Med. Chem. 36:3556-3564 (1993); Kaur et al., Anti-Cancer Drugs 5:213-222 (1994); Kaur et al., King et al., Biochem. J. 275:413-418 (1991); Kuo et al., Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992);  
10 Lyall et al., J. Biol. Chem. 264:14503-14509 (1989); Peterson et al., The Prostate 22:335-345 (1993); Pillemer et al., Int. J. Cancer 50:80-85 (1992); Posner et al., Molecular Pharmacology 45:673-683 (1993); Rendu et al., Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring et al., J. Biol.  
15 Chem. 269(36):22470-22472 (1994); and Yoneda et al., Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996,  
20 incorporated herein by reference in its entirety, including any drawings.

Methods of Treating a Disease (Enablement - i.e., Dosing)

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number  
25 WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being  
30 treated, the particular composition being used and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be

formulated in animal models to achieve a circulating concentration range that initially takes into account the  $IC_{50}$  as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

5 Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors and major organs can also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan and MRI. Compounds that show potent inhibitory activity in the  
10 screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows:

15 1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is  
20 present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, Journal of American Veterinary Medical Assoc., 202:229-249, 1993).

25 Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness or toxicity. Gross abnormalities in tissue are noted and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse  
30 effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

In a final aspect, the invention features a method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein the method comprises: (a) comparing a nucleic acid target region encoding the kinase polypeptide in  
10 a sample, where the kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID  
15 NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID  
20 NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID  
25 NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID  
30 NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID

NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding the kinase polypeptide, or one or more fragments thereof; and (b) detecting  
5 differences in sequence or amount between the target region and the control target region, as an indication of the disease or disorder. Preferably, the disease or disorder is selected from the group consisting of immune-related diseases and disorders, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders, and cancer. Immune-related diseases and disorders include,  
10 but are not limited to, those discussed previously.

The term "comparing" as used herein refers to identifying discrepancies between the nucleic acid target region isolated from a sample, and the control nucleic acid target region. The discrepancies can be in the nucleotide sequences, *e.g.* insertions, deletions, or point mutations, or in the amount of a given nucleotide sequence. Methods to determine  
15 these discrepancies in sequences are well-known to one of ordinary skill in the art. The "control" nucleic acid target region refers to the sequence or amount of the sequence found in normal cells, *e.g.* cells that are not diseased as discussed previously.

The term also includes anti-sense molecules drawn thereto.

The invention has been described broadly and generically herein. Each of the  
20 narrower species and subgeneric groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein. For example, in some instances the nucleotide sequence of particular kinase polypeptides may not be part of a preferred  
25 embodiment.

The summary of the invention described above is not limiting and other features and advantages of the invention will be apparent from the following detailed description of the invention, and from the claims.

### BRIEF DESCRIPTION OF THE FIGURES

Figures 1A to 1BB shows the amino acid sequences of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

Figures 2A to 2MMMM shows the nucleic acid sequences of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID

NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34,  
SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ  
ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID  
NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50,  
5 SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ  
ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID  
NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66,  
SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ  
ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID  
10 NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82,  
SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ  
ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID  
NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98,  
SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103,  
15 SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108,  
SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113,  
SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118,  
SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121.

## 20 DETAILED DESCRIPTION OF THE INVENTION

The present invention relates in part to kinase polypeptides, nucleic acids encoding  
such polypeptides, cells containing such nucleic acids, antibodies to such polypeptides,  
assays utilizing such polypeptides, and methods relating to all of the foregoing. The  
present invention is based upon the isolation and characterization of new kinase  
25 polypeptides. The polypeptides and nucleic acids may be produced using well-known and  
standard synthesis techniques when given the sequences presented herein.

### I. The Nucleic Acids of the Invention

30 Included within the scope of this invention are the functional equivalents of the  
herein-described isolated nucleic acid molecules. The degeneracy of the genetic code  
permits substitution of certain codons by other codons that specify the same amino acid  
and hence would give rise to the same protein. The nucleic acid sequence can vary

substantially since, with the exception of methionine and tryptophan, the known amino acids can be coded for by more than one codon. Thus, portions or all of the kinase genes of the invention could be synthesized to give a nucleic acid sequence significantly different from one selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121. The encoded amino acid sequence thereof would, however, be preserved.

In addition, the nucleic acid sequence may comprise a nucleotide sequence which results from the addition, deletion or substitution of at least one nucleotide to the 5'-end and/or the 3'-end of the nucleic acid sequence shown in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID



NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13,  
SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ  
ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID  
NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29,  
5 SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ  
ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID  
NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45,  
SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ  
ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID  
10 NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61,  
SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ  
ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID  
NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77,  
SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ  
15 ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID  
NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93,  
SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ  
ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID  
NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID  
20 NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID  
NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID  
NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a derivative thereof. Any nucleotide  
or polynucleotide may be used in this regard, provided that its addition, deletion or  
substitution does not alter the amino acid sequence of SEQ ID NO:122, SEQ ID NO:123,  
25 SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,  
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,  
SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,  
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,  
SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,  
30 SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,  
SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,  
SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,

SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,  
SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,  
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,  
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,  
5 SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,  
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,  
SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,  
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,  
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,  
10 SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,  
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,  
SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,  
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,  
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,  
15 SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,  
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, that is encoded  
by the nucleotide sequence. For example, the present invention is intended to include any  
nucleic acid sequence resulting from the addition of ATG as an initiation codon at the 5'-  
end of the inventive nucleic acid sequence or its derivative, or from the addition of TTA,  
20 TAG or TGA as a termination codon at the 3'-end of the inventive nucleotide sequence or  
its derivative. Moreover, the nucleic acid molecule of the present invention may, as  
necessary, have restriction endonuclease recognition sites added to its 5'-end and/or 3'-  
end.

Such functional alterations of a given nucleic acid sequence afford an opportunity  
25 to promote secretion and/or processing of heterologous proteins encoded by foreign  
nucleic acid sequences fused thereto, for example. All variations of the nucleotide  
sequence of the kinase genes of the invention and fragments thereof permitted by the  
genetic code are, therefore, included in this invention.

Further, it is possible to delete codons or to substitute one or more codons with  
30 codons other than degenerate codons to produce a structurally modified polypeptide, but  
one which has substantially the same utility or activity as the polypeptide produced by the  
unmodified nucleic acid molecule. As recognized in the art, the two polypeptides are

functionally equivalent, as are the two nucleic acid molecules that give rise to their production, even though the differences between the nucleic acid molecules are not related to the degeneracy of the genetic code. This is discussed further in the "Functional Derivatives" section, herein.

5           Finally, many of the nucleic acid molecules of the invention are provided as a partial sequence only (Fig. 2A through 2QQ). However, it is standard for one of ordinary skill in the art to obtain a full-length sequence when provided with a partial sequence. Similarly, when provided with a partial or full-length sequence it is standard for one of ordinary skill in the art to obtain nucleic acid sequence coding for homologous proteins.  
10          Therefore, these nucleic acid molecules are also part of the invention.

          The characteristics of the protein kinase nucleic acid sequences of the invention are provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI, CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant number of protein kinases that do not belong to any of the known groups, and therefore  
15          presumably define new protein kinase groups.

          Additional characteristics may be found, *inter alia*, in the tables, namely Table 1, Table 2, Table 3 and Table 4, shown below.

## 20          II.    Nucleic Acid Probes, Methods, and Kits for Detection of Protein Kinases.

          A nucleic acid probe of the present invention may be used to probe an appropriate chromosomal or cDNA library by usual hybridization methods to obtain other nucleic acid molecules of the present invention. A chromosomal DNA or cDNA library may be prepared from appropriate cells according to recognized methods in the art (cf. "Molecular Cloning: A Laboratory Manual", second edition, Cold Spring Harbor Laboratory,  
25          Sambrook, Fritsch, & Maniatis, eds., 1989).

          In the alternative, chemical synthesis can be carried out in order to obtain nucleic acid probes having nucleotide sequences that correspond to N-terminal, kinase or C-terminal portions, for example, of the amino acid sequence of the polypeptide of interest. The synthesized nucleic acid probes may be used as primers in a polymerase chain  
30          reaction (PCR) carried out in accordance with recognized PCR techniques, essentially according to PCR Protocols, "A Guide to Methods and Applications", Academic Press,

Michael, *et al.*, eds., 1990, utilizing the appropriate chromosomal or cDNA library to obtain the fragment of the present invention.

One skilled in the art can readily design such probes based on the sequence disclosed herein using methods of computer alignment and sequence analysis known in the art ("Molecular Cloning: A Laboratory Manual", 1989, *supra*). The hybridization probes of the present invention can be labeled by standard labeling techniques such as with a radiolabel, enzyme label, fluorescent label, biotin-avidin label, chemiluminescence, and the like. After hybridization, the probes may be visualized using known methods.

The nucleic acid probes of the present invention include RNA, as well as DNA probes, such probes being generated using techniques known in the art. The nucleic acid probe may be immobilized on a solid support. Examples of such solid supports include, but are not limited to, plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, and acrylic resins, such as polyacrylamide and latex beads. Techniques for coupling nucleic acid probes to such solid supports are well known in the art.

The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

One method of detecting the presence of nucleic acids of the invention in a sample comprises (a) contacting said sample with the above-described nucleic acid probe under conditions such that hybridization occurs, and (b) detecting the presence of said probe bound to said nucleic acid molecule. One skilled in the art would select the nucleic acid probe according to techniques known in the art as described above. Samples to be tested include but should not be limited to RNA samples of human tissue.

A kit for detecting the presence of nucleic acids of the invention in a sample comprises at least one container means having disposed therein the above-described nucleic acid probe. The kit may further comprise other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound nucleic acid probe. Examples of detection reagents include, but are not limited to

radiolabelled probes, enzymatic labeled probes (horseradish peroxidase, alkaline phosphatase), and affinity labeled probes (biotin, avidin, or streptavidin).

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allow the efficient transfer of reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the probe or primers used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, and the like), and containers which contain the reagents used to detect the hybridized probe, bound antibody, amplified product, or the like. One skilled in the art will readily recognize that the nucleic acid probes described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

### III. DNA Constructs Comprising a Protein Kinase Nucleic Acid Molecule and Cells Containing These Constructs.

The present invention also relates to a recombinant DNA molecule comprising, 5' to 3', a promoter effective to initiate transcription in a host cell and the above-described nucleic acid molecules. In addition, the present invention relates to a recombinant DNA molecule comprising a vector and an above-described nucleic acid molecule. The present invention also relates to a nucleic acid molecule comprising a transcriptional region functional in a cell, a sequence complementary to an RNA sequence encoding an amino acid sequence corresponding to the above-described polypeptide, and a transcriptional termination region functional in said cell. The above-described molecules may be isolated and/or purified DNA molecules.

The present invention also relates to a cell or organism that contains an above-described nucleic acid molecule and thereby is capable of expressing a polypeptide. The polypeptide may be purified from cells that have been altered to express the polypeptide. A cell is said to be "altered to express a desired polypeptide" when the cell, through genetic manipulation, is made to produce a protein which it normally does not produce or

which the cell normally produces at lower levels. One skilled in the art can readily adapt procedures for introducing and expressing either genomic, cDNA, or synthetic sequences into either eukaryotic or prokaryotic cells.

A nucleic acid molecule, such as DNA, is said to be "capable of expressing" a polypeptide if it contains nucleotide sequences which contain transcriptional and translational regulatory information and such sequences are "operably linked" to nucleotide sequences which encode the polypeptide. An operable linkage is a linkage in which the regulatory DNA sequences and the DNA sequence sought to be expressed are connected in such a way as to permit gene sequence expression. The precise nature of the regulatory regions needed for gene sequence expression may vary from organism to organism, but shall in general include a promoter region which, in prokaryotes, contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

If desired, the non-coding region 3' to the sequence encoding a kinase of the invention may be obtained by the above-described methods. This region may be retained for its transcriptional termination regulatory sequences, such as termination and polyadenylation. Thus, by retaining the 3'-region naturally contiguous to the DNA sequence encoding a kinase of the invention, the transcriptional termination signals may be provided. Where the transcriptional termination signals are not satisfactorily functional in the expression host cell, then a 3' region functional in the host cell may be substituted.

Two DNA sequences (such as a promoter region sequence and a sequence encoding a kinase of the invention) are said to be operably linked if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region sequence to direct the transcription of a gene sequence encoding a kinase of the invention, or (3) interfere with the ability of the gene sequence of a kinase of the invention to be transcribed by the promoter region sequence. Thus, a promoter region would be operably linked to a DNA sequence if the promoter were capable of effecting transcription of that DNA sequence.

Thus, to express a gene encoding a kinase of the invention, transcriptional and translational signals recognized by an appropriate host are necessary.

The present invention encompasses the expression of a gene encoding a kinase of the invention (or a functional derivative thereof) in either prokaryotic or eukaryotic cells.

5 Prokaryotic hosts are, generally, very efficient and convenient for the production of recombinant proteins and are, therefore, one type of preferred expression system for kinases of the invention. Prokaryotes most frequently are represented by various strains of *E. coli*. However, other microbial strains may also be used, including other bacterial strains.

10 In prokaryotic systems, plasmid vectors that contain replication sites and control sequences derived from a species compatible with the host may be used. Examples of suitable plasmid vectors may include pBR322, pUC118, pUC119 and the like; suitable phage or bacteriophage vectors may include  $\gamma$ gt10,  $\gamma$ gt11 and the like; and suitable virus vectors may include pMAM-neo, pKRC and the like. Preferably, the selected vector of the present invention has the capacity to replicate in the selected host cell.

15 Recognized prokaryotic hosts include bacteria such as *E. coli*, *Bacillus*, *Streptomyces*, *Pseudomonas*, *Salmonella*, *Serratia*, and the like. However, under such conditions, the polypeptide will not be glycosylated. The prokaryotic host must be compatible with the replicon and control sequences in the expression plasmid.

20 To express a kinase of the invention (or a functional derivative thereof) in a prokaryotic cell, it is necessary to operably link the sequence encoding the kinase of the invention to a functional prokaryotic promoter. Such promoters may be either constitutive or, more preferably, regulatable (*i.e.*, inducible or derepressible). Examples of constitutive promoters include the *int* promoter of bacteriophage  $\lambda$ , the *bla* promoter of the  $\beta$ -lactamase gene sequence of pBR322, and the *cat* promoter of the chloramphenicol acetyl transferase gene sequence of pPR325, and the like. Examples of inducible prokaryotic promoters include the major right and left promoters of bacteriophage  $\lambda$  ( $P_L$  and  $P_R$ ), the *trp*, *recA*, *lacZ*, *lacI*, and *gal* promoters of *E. coli*, the  $\alpha$ -amylase (Ulmanen *et al.*, J. Bacteriol. 162:176-182, 1985) and the  $\zeta$ -28-specific promoters of *B. subtilis* (Gilman *et*  
25 *al.*, Gene Sequence 32:11-20, 1984), the promoters of the bacteriophages of *Bacillus* (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, Inc., NY, 1982), and *Streptomyces* promoters (Ward *et al.*, Mol. Gen. Genet. 203:468-478, 1986). Prokaryotic  
30

promoters are reviewed by Glick (Ind. Microbiol. 1:277-282, 1987), Cenatiempo (Biochimie 68:505-516, 1986), and Gottesman (Ann. Rev. Genet. 18:415-442, 1984).

Proper expression in a prokaryotic cell also requires the presence of a ribosome-binding site upstream of the gene sequence-encoding sequence. Such ribosome-binding sites are disclosed, for example, by Gold *et al.* (Ann. Rev. Microbiol. 35:365-404, 1981). The selection of control sequences, expression vectors, transformation methods, and the like, are dependent on the type of host cell used to express the gene. As used herein, "cell", "cell line", and "cell culture" may be used interchangeably and all such designations include progeny. Thus, the words "transformants" or "transformed cells" include the primary subject cell and cultures derived therefrom, without regard to the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. However, as defined, mutant progeny have the same functionality as that of the originally transformed cell.

Host cells which may be used in the expression systems of the present invention are not strictly limited, provided that they are suitable for use in the expression of the kinase polypeptide of interest. Suitable hosts may often include eukaryotic cells. Preferred eukaryotic hosts include, for example, yeast, fungi, insect cells, mammalian cells either *in vivo*, or in tissue culture. Mammalian cells which may be useful as hosts include HeLa cells, cells of fibroblast origin such as VERO or CHO-K1, or cells of lymphoid origin and their derivatives. Preferred mammalian host cells include SP2/0 and J558L, as well as neuroblastoma cell lines such as IMR 332, which may provide better capacities for correct post-translational processing.

In addition, plant cells are also available as hosts, and control sequences compatible with plant cells are available, such as the cauliflower mosaic virus 35S and 19S, and nopaline synthase promoter and polyadenylation signal sequences. Another preferred host is an insect cell, for example the *Drosophila* larvae. Using insect cells as hosts, the *Drosophila* alcohol dehydrogenase promoter can be used (Rubin, Science 240:1453-1459, 1988). Alternatively, baculovirus vectors can be engineered to express large amounts of kinases of the invention in insect cells (Jasny, Science 238:1653, 1987; Miller *et al.*, In: Genetic Engineering, Vol. 8, Plenum, Setlow *et al.*, eds., pp. 277-297, 1986).



Any of a series of yeast expression systems can be utilized which incorporate promoter and termination elements from the actively expressed sequences coding for glycolytic enzymes that are produced in large quantities when yeast are grown in mediums rich in glucose. Known glycolytic gene sequences can also provide very efficient transcriptional control signals. Yeast provides substantial advantages in that it can also carry out post-translational modifications. A number of recombinant DNA strategies exist utilizing strong promoter sequences and high copy number plasmids which can be utilized for production of the desired proteins in yeast. Yeast recognizes leader sequences on cloned mammalian genes and secretes peptides bearing leader sequences (*i.e.*, pre-peptides). Several possible vector systems are available for the expression of kinases of the invention in a mammalian host.

A wide variety of transcriptional and translational regulatory sequences may be employed, depending upon the nature of the host. The transcriptional and translational regulatory signals may be derived from viral sources, such as adenovirus, bovine papilloma virus, cytomegalovirus, simian virus, or the like, where the regulatory signals are associated with a particular gene sequence which has a high level of expression. Alternatively, promoters from mammalian expression products, such as actin, collagen, myosin, and the like, may be employed. Transcriptional initiation regulatory signals may be selected which allow for repression or activation, so that expression of the gene sequences can be modulated. Of interest are regulatory signals which are temperature-sensitive so that by varying the temperature, expression can be repressed or initiated, or are subject to chemical (such as metabolite) regulation.

Expression of kinases of the invention in eukaryotic hosts requires the use of eukaryotic regulatory regions. Such regions will, in general, include a promoter region sufficient to direct the initiation of RNA synthesis. Preferred eukaryotic promoters include, for example, the promoter of the mouse metallothionein I gene sequence (Hamer *et al.*, J. Mol. Appl. Gen. 1:273-288, 1982); the TK promoter of Herpes virus (McKnight, Cell 31:355-365, 1982); the SV40 early promoter (Benoist *et al.*, Nature (London) 290:304-31, 1981); and the yeast gal4 gene sequence promoter (Johnston *et al.*, Proc. Natl. Acad. Sci. (USA) 79:6971-6975, 1982; Silver *et al.*, Proc. Natl. Acad. Sci. (USA) 81:5951-5955, 1984).

Translation of eukaryotic mRNA is initiated at the codon that encodes the first methionine. For this reason, it is preferable to ensure that the linkage between a eukaryotic promoter and a DNA sequence which encodes a kinase of the invention (or a functional derivative thereof) does not contain any intervening codons which are capable of encoding a methionine (*i.e.*, AUG). The presence of such codons results either in the formation of a fusion protein (if the AUG codon is in the same reading frame as the kinase of the invention coding sequence) or a frame-shift mutation (if the AUG codon is not in the same reading frame as the kinase of the invention coding sequence).

A nucleic acid molecule encoding a kinase of the invention and an operably linked promoter may be introduced into a recipient prokaryotic or eukaryotic cell either as a nonreplicating DNA or RNA molecule, which may either be a linear molecule or, more preferably, a closed covalent circular molecule. Since such molecules are incapable of autonomous replication, the expression of the gene may occur through the transient expression of the introduced sequence. Alternatively, permanent expression may occur through the integration of the introduced DNA sequence into the host chromosome.

A vector may be employed which is capable of integrating the desired gene sequences into the host cell chromosome. Cells which have stably integrated the introduced DNA into their chromosomes can be selected by also introducing one or more markers which allow for selection of host cells which contain the expression vector. The marker may provide for prototrophy to an auxotrophic host, biocide resistance, *e.g.*, antibiotics, or heavy metals, such as copper, or the like. The selectable marker gene sequence can either be directly linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection. Additional elements may also be needed for optimal synthesis of mRNA. These elements may include splice signals, as well as transcription promoters, enhancers, and termination signals. cDNA expression vectors incorporating such elements include those described by Okayama (*Mol. Cell. Biol.* 3:280-, 1983).

The introduced nucleic acid molecule can be incorporated into a plasmid or viral vector capable of autonomous replication in the recipient host. Any of a wide variety of vectors may be employed for this purpose. Factors of importance in selecting a particular plasmid or viral vector include: the ease with which recipient cells that contain the vector may be recognized and selected from those recipient cells which do not contain the vector;

the number of copies of the vector which are desired in a particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

Preferred prokaryotic vectors include plasmids such as those capable of replication in *E. coli* (such as, for example, pBR322, ColEI, pSC101, pACYC 184,  $\pi$ VX; "Molecular Cloning: A Laboratory Manual", 1989, *supra*). *Bacillus* plasmids include pC194, pC221, pT127, and the like (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, NY, pp. 307-329, 1982). Suitable *Streptomyces* plasmids include p1J101 (Kendall *et al.*, J. Bacteriol. 169:4177-4183, 1987), and streptomyces bacteriophages such as  $\phi$ C31 (Chater *et al.*, In: Sixth International Symposium on Actinomycetales Biology, Akademiai Kaido, Budapest, Hungary, pp. 45-54, 1986). *Pseudomonas* plasmids are reviewed by John *et al.* (Rev. Infect. Dis. 8:693-704, 1986), and Izaki (Jpn. J. Bacteriol. 33:729-742, 1978).

Preferred eukaryotic plasmids include, for example, BPV, vaccinia, SV40, 2-micron circle, and the like, or their derivatives. Such plasmids are well known in the art (Botstein *et al.*, Miami Wntr. Symp. 19:265-274, 1982; Broach, In: "The Molecular Biology of the Yeast *Saccharomyces*: Life Cycle and Inheritance", Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, p. 445-470, 1981; Broach, Cell 28:203-204, 1982; Bollon *et al.*, J. Clin. Hematol. Oncol. 10:39-48, 1980; Maniatis, In: Cell Biology: A Comprehensive Treatise, Vol. 3, Gene Sequence Expression, Academic Press, NY, pp. 563-608, 1980).

Once the vector or nucleic acid molecule containing the construct(s) has been prepared for expression, the DNA construct(s) may be introduced into an appropriate host cell by any of a variety of suitable means, *i.e.*, transformation, transfection, conjugation, protoplast fusion, electroporation, particle gun technology, calcium phosphate-precipitation, direct microinjection, and the like. After the introduction of the vector, recipient cells are grown in a selective medium, which selects for the growth of vector-containing cells. Expression of the cloned gene(s) results in the production of a kinase of the invention, or fragments thereof. This can take place in the transformed cells as such, or following the induction of these cells to differentiate (for example, by administration of bromodeoxyuracil to neuroblastoma cells or the like). A variety of incubation conditions can be used to form the peptide of the present invention. The most preferred conditions are those which mimic physiological conditions.

#### IV. The Proteins of the Invention

A variety of methodologies known in the art can be utilized to obtain the polypeptides of the present invention. The polypeptides may be purified from tissues or cells that naturally produce the polypeptides. Alternatively, the above-described isolated nucleic acid fragments could be used to express the kinases of the invention in any  
5 organism. The samples of the present invention include cells, protein extracts or membrane extracts of cells, or biological fluids. The samples will vary based on the assay format, the detection method, and the nature of the tissues, cells or extracts used as the sample.

10 Any eukaryotic organism can be used as a source for the polypeptides of the invention, as long as the source organism naturally contains such polypeptides. As used herein, "source organism" refers to the original organism from which the amino acid sequence of the subunit is derived, regardless of the organism the subunit is expressed in and ultimately isolated from.

15 One skilled in the art can readily follow known methods for isolating proteins in order to obtain the polypeptides free of natural contaminants. These include, but are not limited to: size-exclusion chromatography, HPLC, ion-exchange chromatography, and immuno-affinity chromatography.

Further, the polypeptides of the invention include the full-length polypeptides that  
20 can be identified from the full-length or partial sequences encoded by SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142,  
25 SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167,  
30 SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,

SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,  
SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,  
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,  
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,  
5 SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,  
SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,  
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,  
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,  
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,  
10 SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,  
SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,  
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID  
NO:242 (Figure 1). In addition, the polypeptides of the invention include the domains of  
these polypeptides, including, but not limited to, the N-terminal, kinase/catalytic, and C-  
15 terminal domains.

The characteristics of the protein kinase nucleic acid sequences of the invention are  
provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI,  
CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant  
number of protein kinases that do not belong to any of the known groups, and therefore  
20 presumably define new protein kinase groups.

Additional characteristics are shown in, *inter alia*, the tables, namely Table 1,  
Table 2, Table 3 and Table 4, provided below.

V. Antibodies, Hybridomas, Methods of Use and Kits for Detection of Protein  
25 Kinases

The present invention relates to an antibody having binding affinity to a kinase of  
the invention. The polypeptide may have an amino acid sequence selected from the group  
consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ  
ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ  
30 ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ  
ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ  
ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or a functional derivative thereof, or at least 9 contiguous amino acids thereof (preferably, at least 20, 30, 35, or 40 or more contiguous amino acids thereof). Alternatively, the antibody may bind to a part of the polypeptide not provided in the sequences above, but that is present in the full-length sequence of the polypeptide and that is easily obtained using methods standard in the art. Further, the antibody may bind specifically to particular domains of one or more of the kinases of the invention, including, but not limited to, the N-terminal, kinase/catalytic, or C-terminal domains.

The present invention also relates to an antibody having specific binding affinity to a kinase or kinase domain of the invention. Such an antibody may be isolated by comparing its binding affinity to a kinase of the invention with its binding affinity to other polypeptides. Those that bind selectively to a kinase of the invention would be chosen for use in methods requiring a distinction between a kinase of the invention and other

polypeptides. Such methods could include, but should not be limited to, the analysis of altered kinase expression in tissue containing other polypeptides.

The kinases of the present invention can be used in a variety of procedures and methods, such as for the generation of antibodies, for use in identifying pharmaceutical compositions, and for studying DNA/protein interaction.

The kinases of the present invention can be used to produce antibodies or hybridomas. One skilled in the art will recognize that if an antibody is desired, such a peptide could be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well fragments of these antibodies, and humanized forms. Humanized forms of the antibodies of the present invention may be generated using one of the procedures known in the art such as chimerization or CDR grafting.

The present invention also relates to a hybridoma that produces the above-described monoclonal antibody, or binding fragment thereof. A hybridoma is an immortalized cell line that is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1984; St. Groth *et al.*, J. Immunol. Methods 35:1-21, 1980).

Any animal (mouse, rabbit, and the like) which is known to produce antibodies can be immunized with the selected polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of polypeptide used for immunization will vary based on the animal that is immunized, the antigenicity of the polypeptide and the site of injection.

The polypeptide may be modified or administered in an adjuvant in order to increase the peptide antigenicity. Methods of increasing the antigenicity of a polypeptide are well known in the art. Such procedures include coupling the antigen with a heterologous protein (such as globulin or  $\beta$ -galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Agl4 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell that produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al.*, Exp. Cell Res. 175:109-124, 1988). Hybridomas secreting the desired antibodies are cloned and the class and subclass are determined using procedures known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology", *supra*, 1984).

For polyclonal antibodies, antibody-containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The above-described antibodies may be detectably labeled. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, and the like), enzymatic labels (such as horse radish peroxidase, alkaline phosphatase, and the like) fluorescent labels (such as FITC or rhodamine, and the like), paramagnetic atoms, and the like. Procedures for accomplishing such labeling are well-known in the art, for example, see Stemberger *et al.*, J. Histochem. Cytochem. 18:315, 1970; Bayer *et al.*, Meth. Enzym. 62:308-, 1979; Engval *et al.*, Immunol. 109:129-, 1972; Goding, J. Immunol. Meth. 13:215-, 1976. The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues that express a specific peptide.

The above-described antibodies may also be immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10, 1986; Jacoby *et al.*, Meth. Enzym. 34, Academic Press, N.Y., 1974). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as in immunochromatography.



Furthermore, one skilled in the art can readily adapt currently available procedures, as well as the techniques, methods and kits disclosed herein with regard to antibodies, to generate peptides capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides (Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides", In Synthetic Peptides, A User's Guide, W.H. Freeman, NY, pp. 289-307, 1992; Kaspczak *et al.*, Biochemistry 28:9230-9238, 1989).

Anti-peptide peptides can be generated by replacing the basic amino acid residues found in the peptide sequences of the kinases of the invention with acidic residues, while maintaining hydrophobic and uncharged polar groups. For example, lysine, arginine, and/or histidine residues are replaced with aspartic acid or glutamic acid and glutamic acid residues are replaced by lysine, arginine or histidine.

The present invention also encompasses a method of detecting a kinase polypeptide in a sample, comprising: (a) contacting the sample with an above-described antibody, under conditions such that immunocomplexes form, and (b) detecting the presence of said antibody bound to the polypeptide. In detail, the methods comprise incubating a test sample with one or more of the antibodies of the present invention and assaying whether the antibody binds to the test sample. Altered levels of a kinase of the invention in a sample as compared to normal levels may indicate disease.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion based Ouchterlony, or rocket immunofluorescent assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be found in Chard ("An Introduction to Radioimmunoassay and Related Techniques" Elsevier Science Publishers, Amsterdam, The Netherlands, 1986), Bullock *et al.* ("Techniques in Immunocytochemistry," Academic Press, Orlando, FL Vol. 1, 1982; Vol. 2, 1983; Vol. 3, 1985), Tijssen ("Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1985).

The immunological assay test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as blood, serum, plasma, or urine. The test samples used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is testable with the system utilized.

A kit contains all the necessary reagents to carry out the previously described methods of detection. The kit may comprise: (i) a first container means containing an above-described antibody, and (ii) second container means containing a conjugate comprising a binding partner of the antibody and a label. In another preferred embodiment, the kit further comprises one or more other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound antibodies.

Examples of detection reagents include, but are not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents that are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits. One skilled in the art will readily recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

#### VI. Isolation of Compounds That Interact With Protein Kinases

The present invention also relates to a method of detecting a compound capable of binding to a protein kinase of the invention, comprising incubating the compound with a kinase of the invention and detecting the presence of the compound bound to the kinase. The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts.

The present invention also relates to a method of detecting an agonist or antagonist of kinase activity or kinase binding partner activity comprising incubating cells that produce a kinase of the invention in the presence of a compound and detecting changes in the level of kinase activity or kinase binding partner activity. The compounds thus identified would produce a change in activity indicative of the presence of the compound.

The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts. Once the compound is identified it can be isolated using techniques well known in the art.

5 The present invention also encompasses a method of agonizing (stimulating) or antagonizing kinase associated activity in a mammal comprising administering to said mammal an agonist or antagonist to a kinase of the invention in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of kinase activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize kinase associated functions  
10 is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein kinases. Some small organic molecules form a class of compounds that modulate the function of protein kinases. Examples of molecules that have been reported to inhibit  
15 the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S.  
20 Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*).

25 Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein kinase inhibitors only weakly inhibit the function of protein kinases. In addition, many inhibit a variety of protein kinases and will cause multiple side-effects as therapeutics for diseases.

30 Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin,

naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar moieties including hydroxylated alkyl, phosphate, and ether moieties. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives.

Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris *et al.*, J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.*, J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J.

Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*, Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); Sikora *et al.*, Analytical Biochem. 172:344-355 (1988); all of which are incorporated herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432 (1993); and Burke *et al.*, BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen *et al.*, Clin. Exp. Immunol. 91:141-156 (1993); Anafi *et al.*, Blood 82:12:3524-3529 (1993); Baker *et al.*, J. Cell Sci. 102:543-555 (1992); Bilder *et al.*, Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton *et al.*, Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert *et al.*, Experimental Cell Research 199:255-261 (1992); Dong *et al.*, J. Leukocyte Biology 53:53-60 (1993); Dong *et al.*, J. Immunol. 151(5):2717-2724 (1993); Gazit *et al.*, J. Med. Chem. 32:2344-2352 (1989); Gazit *et al.*, J. Med. Chem. 36:3556-3564 (1993); Kaur *et al.*, Anti-Cancer Drugs 5:213-222 (1994); Kaur *et al.*, King *et al.*, Biochem. J. 275:413-418 (1991); Kuo *et al.*, Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall *et al.*, J. Biol. Chem. 264:14503-14509 (1989); Peterson *et al.*, The Prostate 22:335-345 (1993); Pillemer *et al.*, Int. J. Cancer 50:80-85 (1992); Posner *et al.*, Molecular Pharmacology 45:673-683 (1993); Rendu *et al.*, Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring *et al.*, J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda *et al.*, Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

VII. Biological Significance, Applications and Clinical Relevance of Novel Protein  
5 Kinases

For each protein kinase in this application, we provide a classification of the protein class and family to which it belongs, a summary of non-catalytic protein motifs, a profile of its expression in several hundred tissue and cell sources, and a chromosomal location. This information can be used to suggest potential function, regulation or  
10 therapeutic utility for each of the proteins.

The kinase classification and protein domains often reflect pathways, cellular roles, or mechanisms of up- or down-stream regulation. Also disease-relevant genes often occur in families of related genes. For example if one member of a kinase family functions as an oncogene, a tumor suppressor, or has been found to be disrupted in an immune,  
15 neurologic, cardiovascular, or metabolic disorder, frequently other family members may play a related role.

The expression analysis organizes kinases into groups that are transcriptionally upregulated in tumors and those that are more restricted to specific tumor types such as melanoma or prostate. This analysis also identifies genes that are regulated in a cell cycle  
20 dependent manner, and are therefore likely to be involved in maintaining cell cycle checkpoints, entry, progression, or exit from mitosis, oversee DNA repair, or are involved in cell proliferation and genome stability. Expression data also can identify genes expressed in endothelial sources or other tissues that suggest a role in angiogenesis, thereby implicating them as targets for control of diseases that have an angiogenic  
25 component, such as cancer, endometriosis, retinopathy and macular degeneration, and various ischemic or vascular pathologies. A proteins' role in cell survival can also be suggested based on restricted expression in cells subjected to external stress such as oxidative damage, hypoxia, drugs such as cisplatin, or irradiation. Metastases-associated genes can be implicated when expression is restricted to invading regions of a  
30 tumor, or is only seen in local or distant metastases compared to the primary tumor, or when a gene is upregulated during cell culture models of invasion, migration, or motility.

Chromosomal location can identify candidate targets for a tumor amplicon or a tumor-suppressor locus. Summaries of prevalent tumor amplicons are available in the literature, and can identify tumor types to experimentally be confirmed to contain amplified copies of a kinase gene which localizes to an adjacent region.

Based on these criteria several kinases immediately stand out as being of potential therapeutic relevance. The protein kinases can be divided into the following disease-relevant categories (nucleotide Seq ID #s in parentheses):

Tumor associated: Mok (SEQ ID NO:57), EPK2, AA316804 (SEQ ID NO:11), AA435956 (SEQ ID NO:48), AA278842 (SEQ ID NO:88), AA599286 (SEQ ID NO:89), AA826850 (SEQ ID NO:3), HRI (SEQ ID NO:73), MLK4 AA232253 (SEQ ID NO:82), AA883975 SGK 235 (SEQ ID NO:95), AA311714 (SEQ ID NO:101), MPSK1 (SEQ ID NO:110), R19609 (Seq ID111), AA383293 (SEQ ID NO:26).

Prostate-specific: AA234451 (SEQ ID NO:47), TSK4 (SEQ ID NO:93), RIP4 (SEQ ID NO:84), KIAA0965 (SEQ ID NO:8).

Oncogenic or proliferation associated: KIAA0781 (SEQ ID NO:38), AA789239 (SEQ ID NO:52), CCRK (SEQ ID NO:54), CLK4 (SEQ ID NO:55), H85389 (SEQ ID NO:97).

Neuronal restricted: CAMKKB (SEQ ID NO:66)

Hematopoietic expressed: PTK9L (SEQ ID NO:22), DRAK2 (SEQ ID NO:29), AI025291 (SEQ ID NO:94)

Angiogenic or endothelial expressed: DRAK1 (SEQ ID NO:31), MAK-V (SEQ ID NO:40), TRAD (SEQ ID NO:44), MOK (SEQ ID NO:57), AA08847 (SEQ ID NO:78), HGP\_66444466 (SEQ ID NO:79), RSK4 (SEQ ID NO:16).

Cell cycle regulated: AA454060 (SEQ ID NO:45), KIAA0999 (Mitotic – SEQ ID NO:32), AA579641 (Mitotic – SEQ ID NO:60), AA305176 (Mitotic – SEQ ID NO:6), AA018361 (S1 phase – SEQ ID NO:100).

#### VIII. Transgenic Animals.

A variety of methods are available for the production of transgenic animals associated with this invention. DNA can be injected into the pronucleus of a fertilized egg before fusion of the male and female pronuclei, or injected into the nucleus of an embryonic cell (*e.g.*, the nucleus of a two-cell embryo) following the initiation of cell division (Brinster *et al.*, Proc. Nat. Acad. Sci. USA 82: 4438-4442, 1985). Embryos can

be infected with viruses, especially retroviruses, modified to carry inorganic-ion receptor nucleotide sequences of the invention.

Pluripotent stem cells derived from the inner cell mass of the embryo and stabilized in culture can be manipulated in culture to incorporate nucleotide sequences of the invention. A transgenic animal can be produced from such cells through implantation into a blastocyst that is implanted into a foster mother and allowed to come to term. Animals suitable for transgenic experiments can be obtained from standard commercial sources such as Charles River (Wilmington, MA), Taconic (Germantown, NY), Harlan Sprague Dawley (Indianapolis, IN), etc.

The procedures for manipulation of the rodent embryo and for microinjection of DNA into the pronucleus of the zygote are well known to those of ordinary skill in the art (Hogan *et al.*, *supra*). Microinjection procedures for fish, amphibian eggs and birds are detailed in Houdebine and Chourrout (Experientia 47: 897-905, 1991). Other procedures for introduction of DNA into tissues of animals are described in U.S. Patent No., 4,945,050 (Sanford *et al.*, July 30, 1990).

By way of example only, to prepare a transgenic mouse, female mice are induced to superovulate. Females are placed with males, and the mated females are sacrificed by CO<sub>2</sub> asphyxiation or cervical dislocation and embryos are recovered from excised oviducts. Surrounding cumulus cells are removed. Pronuclear embryos are then washed and stored until the time of injection. Randomly cycling adult female mice are paired with vasectomized males. Recipient females are mated at the same time as donor females. Embryos then are transferred surgically. The procedure for generating transgenic rats is similar to that of mice (Hammer *et al.*, Cell 63:1099-1112, 1990).

Methods for the culturing of embryonic stem (ES) cells and the subsequent production of transgenic animals by the introduction of DNA into ES cells using methods such as electroporation, calcium phosphate/DNA precipitation and direct injection also are well known to those of ordinary skill in the art (Teratocarcinomas and Embryonic Stem Cells, A Practical Approach, E.J. Robertson, ed., IRL Press, 1987).

In cases involving random gene integration, a clone containing the sequence(s) of the invention is co-transfected with a gene encoding resistance. Alternatively, the gene encoding neomycin resistance is physically linked to the sequence(s) of the invention.



Transfection and isolation of desired clones are carried out by any one of several methods well known to those of ordinary skill in the art (E.J. Robertson, *supra*).

DNA molecules introduced into ES cells can also be integrated into the chromosome through the process of homologous recombination (Capecchi, Science 244: 1288-1292, 1989). Methods for positive selection of the recombination event (*i.e.*, neo resistance) and dual positive-negative selection (*i.e.*, neo resistance and gancyclovir resistance) and the subsequent identification of the desired clones by PCR have been described by Capecchi, *supra* and Joyner *et al.* (Nature 338: 153-156, 1989), the teachings of which are incorporated herein in their entirety including any drawings. The final phase of the procedure is to inject targeted ES cells into blastocysts and to transfer the blastocysts into pseudopregnant females. The resulting chimeric animals are bred and the offspring are analyzed by Southern blotting to identify individuals that carry the transgene. Procedures for the production of non-rodent mammals and other animals have been discussed by others (Houdebine and Chourrout, *supra*; Pursel *et al.*, Science 244:1281-1288, 1989; and Simms *et al.*, Bio/Technology 6:179-183, 1988).

Thus, the invention provides transgenic, nonhuman mammals containing a transgene encoding a kinase of the invention or a gene effecting the expression of the kinase. Such transgenic nonhuman mammals are particularly useful as an *in vivo* test system for studying the effects of introduction of a kinase, or regulating the expression of a kinase (*i.e.*, through the introduction of additional genes, antisense nucleic acids, or ribozymes).

A "transgenic animal" is an animal having cells that contain DNA which has been artificially inserted into a cell, which DNA becomes part of the genome of the animal which develops from that cell. Preferred transgenic animals are primates, mice, rats, cows, pigs, horses, goats, sheep, dogs and cats. The transgenic DNA may encode human STE20-related kinases. Native expression in an animal may be reduced by providing an amount of anti-sense RNA or DNA effective to reduce expression of the receptor.

#### IX. Gene Therapy

Protein kinases of the invention, or their genetic sequences will also be useful in gene therapy (reviewed in Miller, Nature 357:455-460, 1992). Miller states that advances have resulted in practical approaches to human gene therapy that have demonstrated

positive initial results. The basic science of gene therapy is described in Mulligan (Science 260:926-931, 1993).

In one preferred embodiment, an expression vector containing protein kinase coding sequence is inserted into cells, the cells are grown *in vitro*, and then are infused in large numbers into patients. In another preferred embodiment, a DNA segment containing a promoter of choice (for example a strong promoter) is transferred into cells containing an endogenous gene encoding kinases of the invention in such a manner that the promoter segment enhances expression of the endogenous kinase gene (for example, the promoter segment is transferred to the cell such that it becomes directly linked to the endogenous kinase gene).

The gene therapy may involve the use of an adenovirus containing kinase cDNA targeted to a tumor, systemic kinase increase by implantation of engineered cells, injection with kinase-encoding virus, or injection of naked kinase DNA into appropriate tissues.

Target cell populations may be modified by introducing altered forms of one or more components of the protein complexes in order to modulate the activity of such complexes. For example, by reducing or inhibiting a complex component activity within target cells, an abnormal signal transduction event(s) leading to a condition may be decreased, inhibited, or reversed. Deletion or missense mutants of a component, that retain the ability to interact with other components of the protein complexes but cannot function in signal transduction may be used to inhibit an abnormal, deleterious signal transduction event.

Expression vectors derived from viruses such as retroviruses, vaccinia virus, adenovirus, adeno-associated virus, herpes viruses, several RNA viruses, or bovine papilloma virus, may be used for delivery of nucleotide sequences (*e.g.*, cDNA) encoding recombinant kinase of the invention protein into the targeted cell population (*e.g.*, tumor cells). Methods which are well known to those skilled in the art can be used to construct recombinant viral vectors containing coding sequences (Maniatis *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y., 1989; Ausubel *et al.*, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, N.Y., 1989). Alternatively, recombinant nucleic acid molecules encoding protein sequences can be used as naked DNA or in a reconstituted system *e.g.*, liposomes or other lipid systems for delivery to target cells (*e.g.*, Felgner *et al.*, Nature 337:387-8,

1989). Several other methods for the direct transfer of plasmid DNA into cells exist for use in human gene therapy and involve targeting the DNA to receptors on cells by complexing the plasmid DNA to proteins (Miller, *supra*).

5 In its simplest form, gene transfer can be performed by simply injecting minute amounts of DNA into the nucleus of a cell, through a process of microinjection (Capecchi, Cell 22:479-88, 1980). Once recombinant genes are introduced into a cell, they can be recognized by the cell's normal mechanisms for transcription and translation, and a gene product will be expressed. Other methods have also been attempted for introducing DNA into larger numbers of cells. These methods include: transfection, wherein DNA is  
10 precipitated with  $\text{CaPO}_4$  and taken into cells by pinocytosis (Chen *et al.*, Mol. Cell Biol. 7:2745-52, 1987); electroporation, wherein cells are exposed to large voltage pulses to introduce holes into the membrane (Chu *et al.*, Nucleic Acids Res. 15:1311-26, 1987); lipofection/liposome fusion, wherein DNA is packaged into lipophilic vesicles which fuse with a target cell (Felgner *et al.*, Proc. Natl. Acad. Sci. USA. 84:7413-7417, 1987); and  
15 particle bombardment using DNA bound to small projectiles (Yang *et al.*, Proc. Natl. Acad. Sci. 87:9568-9572, 1990). Another method for introducing DNA into cells is to couple the DNA to chemically modified proteins.

It has also been shown that adenovirus proteins are capable of destabilizing endosomes and enhancing the uptake of DNA into cells. The admixture of adenovirus to  
20 solutions containing DNA complexes, or the binding of DNA to polylysine covalently attached to adenovirus using protein crosslinking agents substantially improves the uptake and expression of the recombinant gene (Curiel *et al.*, Am. J. Respir. Cell. Mol. Biol., 6:247-52, 1992).

As used herein "gene transfer" means the process of introducing a foreign nucleic acid molecule into a cell. Gene transfer is commonly performed to enable the expression  
25 of a particular product encoded by the gene. The product may include a protein, polypeptide, anti-sense DNA or RNA, or enzymatically active RNA. Gene transfer can be performed in cultured cells or by direct administration into animals. Generally gene transfer involves the process of nucleic acid contact with a target cell by non-specific or  
30 receptor mediated interactions, uptake of nucleic acid into the cell through the membrane or by endocytosis, and release of nucleic acid into the cytoplasm from the plasma membrane or endosome. Expression may require, in addition, movement of the nucleic

acid into the nucleus of the cell and binding to appropriate nuclear factors for transcription.

As used herein "gene therapy" is a form of gene transfer and is included within the definition of gene transfer as used herein and specifically refers to gene transfer to express  
5 a therapeutic product from a cell *in vivo* or *in vitro*. Gene transfer can be performed *ex vivo* on cells which are then transplanted into a patient, or can be performed by direct administration of the nucleic acid or nucleic acid-protein complex into the patient.

In another preferred embodiment, a vector having nucleic acid sequences encoding a protein kinase polypeptide of the invention is provided in which the nucleic acid  
10 sequence is expressed only in specific tissue. Methods of achieving tissue-specific gene expression are set forth in International Publication No. WO 93/09236, filed November 3, 1992 and published May 13, 1993.

In all of the preceding vectors set forth above, a further aspect of the invention is that the nucleic acid sequence contained in the vector may include additions, deletions or  
15 modifications to some or all of the sequence of the nucleic acid, as defined above.

In another preferred embodiment, a method of gene replacement is set forth. "Gene replacement" as used herein means supplying a nucleic acid sequence which is capable of being expressed *in vivo* in an animal and thereby providing or augmenting the function of an endogenous gene that is missing or defective in the animal.

#### 20 X. Administration of Substances

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by  
25 reference in their entirety, including any drawings, figures, or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used, and the size and physiological condition of  
30 the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be formulated in animal models to achieve a circulating concentration range that initially

takes into account the  $IC_{50}$  as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors, and major organs can be also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan, and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows: 1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition, and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, *Journal of American Veterinary Medical Assoc.*, 202:229-249, 1993). Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness, or toxicity. Gross abnormalities in tissue are noted, and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

### EXAMPLES

10 The examples below are not limiting and are merely representative of various aspects and features of the present invention. The examples below demonstrate the isolation and characterization of the protein kinases of the invention.

#### EXAMPLE 1: Isolation of cDNA clones Encoding Novel Mammalian Protein Kinases Materials and Methods Identification from cDNA databases and isolation of clones encoding novel protein kinases

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Novel kinases were identified from the public EST databases using a Hidden Markov model, abbreviated HMM (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. 1994. Hidden Markov models in computational biology: Applications to protein modeling. *J. Mol. Biol.*, 235:1501-1531). The model was built with 70 mammalian and yeast kinase catalytic domain sequences. These sequences were chosen from a comprehensive collection of kinases such that no two sequences had more than 50% sequence identity. ESTs were translated in six open reading frames and were searched against the model. ESTs that had a score of at least 10 against the HMM were then masked for repetitive sequences and vectors and were clustered using MSA. The resulting contigs were searched against known kinases to identify EST clones that encode novel kinases.

20

25

Approximately 40% of the ESTs encoding potentially novel kinases did not correspond to the correct EST upon sequence analysis. Most of these discrepancies were resolved by ordering additional clones, however, 14 remained unavailable. These 14 ESTs were amplified from a variety of single-stranded cDNA sources with primers derived from the corresponding EST entry as shown on Table 5. The PCR product was subcloned into a bluescript vector, digested to confirm the presence of a correct size insert and sequenced. Full sequencing of EST and PCR was carried out using a cycle sequencing Big-dye kit

30

with AmpliTaq DNA Polymerase, FS (ABI, Foster City, CA). Sequencing reaction products were run on an ABI Prism 377 DNA Sequencer.

Table 5: Primers used to clone PCR products corresponding to novel kinases

	ID#	ID#	Parent	5' primer	3' primer
sp	na	aa	Sequence	Sequence*	Sequence*
H	33	153	2R22-5-11	GAGATCGRNTTYAARGA RTTYGA	TGTCACNCCNAGNSWCCAN AYRTT
M	81	200	5R57_10_2_ m TESK2_m	GCTGCTGGACAGTGACT TGTATTT	GAAAGCAAAGCCTTCACAC CTT
H	67	187	5R69_17_2_h	CTCTCACCTCAGGAACT GG	GCTTGCGGATCTTCTCA
H	46	166	SGK309_h	GACATCCTGCCGGCCAA CTACG	CGGCCCTGGAGCTGCATCA CTA
M	67	228	5R72_16_2_h	TGCGCGACACCATTGAC CAG	CTCAGGGCTTACATACAGA G
H	45	165	5R72_8_2_h	AAAGGAGAACTACATTT TGAAAAT	CTTCATCATCTCTAATACAT TGGTTGG
H	41	161	Z36720	CAAATTAAGATCATTGA CTTTGGG	GGAAACAAAGTCCTTGGCC TC
H	115	234	AL031652 – Pak6	GTGGACATCTGGTCCCT CG	GTAGGTCCTTCACTCTTGG AG

- degenerate oligonucleotide residue designation:

5 N= A,C,G or T

R= A or G

Y= C or T

S = C or G

W= A or T

10

#### Full-length sequence extension of protein kinases using cDNA and genomic databases

Extension of partial cDNA sequences to encompass the full-length open-reading frame was carried out by iterative blastn searching of the cDNA databases listed in Table 6. All blastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1. The gapped blast algorithm is described in: (Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and

15

PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402).

Table 6. Databases used for cDNA-based sequence extensions

Database	Database Date
LifeGold templates	Feb 2000
LifeGold compseqs	Feb 2000
LifeGold compseqs	Mar 2000
LifeGold compseqs	Apr 2000
LifeGold fl	Feb 2000
LifeGold flt	Apr 2000
NCBI human Ests	May 2000
NCBI murine Ests	May 2000
NCBI nonredundant	May 2000

Extension of partial cDNA sequences to encompass the full-length open-reading frame was also carried out by iterative searches of genomic databases. Three methods were used. The first method made use of the Smith-Waterman algorithm to carry out protein-protein searches of the closest homologue or orthologue to the partial kinase. The target databases consisted of Genescan and open-reading frame (ORF) predictions of all human genomic sequence derived from the human genome project (HGP) as well as from Celera. The complete set of genomic databases searched is shown in Table 7 below. Genomic sequences encoding potential extensions were further assessed by blastp analysis against the NCBI nonredundant to confirm the novelty of the hit. The extending genomic sequences were incorporated into the cDNA sequence after removal of potential introns using the Seqman program from DNASTar. The default parameters used for Smith-Waterman searches were as shown next. Matrix: blosum 62; gap-opening penalty: 12; gap extension penalty: 2. Genescan predictions were made using the Genescan program as detailed in (Chris Burge and Sam Karlin "Prediction of Complete Gene Structures in Human Genomic DNA", JMB (1997) 268(1):78-94). ORF predictions from genomic DNA were made using a standard 6-frame translation.



The second method for genomic sequence-based extensions made use of tBlastn searches of the homologue or orthologue to the partial kinase against the cDNA databases listed in Table 7. The recognition of significant hits in these databases made possible to identify bridging partial cDNA clones. The iterative application of the two methods made possible the assemblage of the virtual full-length sequence for a large number of the kinases presented in this application. All tblastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1.

The last method for defining cDNA extensions from genomic sequence used iterative searches of genomic databases through the Genescan program to predict exon splicing and the Genewise program (<http://www.sanger.ac.uk/Software/Wise2/>) to predict potential ORFs based on homology to the closest orthologue/homologue.

Table 7. Databases used for genomic-based sequence extensions

Database	Number of entries	Database Date
Celera v. 1-5	5,306,158	Jan 19/00
Celera v. 6-10	4,209,980	Mar 24/00
Celera v. 11-14	7,222,425	Apr 24/00
Celera v. 15	243,044	May 14/00
HGP all Genescan	25,885	Apr 04/00
HGP; Phase 0	4,944	May 04/00
HGP; Phase 1	28,478	May 05/00
HGP; Phase 2	1,508	May 04/00
HGP; Phase 3	9,971	May 05/00

#### Virtual Extensions

Human AA826850 (SEQ ID NO: 3, SEQ ID NO:124)

Blastn analysis of the partial AA826850 sequence revealed an extension to encompass the complete ORF in the Incyte EST 238299.1. A frame-shift correction at position 595 of this EST (marked by X in NA sequence) generated an uninterrupted ORF.

Human AA960957 (SEQ ID NO: 4, SEQ ID NO:125)

Since the initial filing of this application, the partial AA960957 sequence appeared in the public database as the full-length gene for a protein kinase encoded by a gene that maps adjacent to the evc (AJ250839) (ellis-van creveld syndrome and weyers acrodermal dysostosis) gene from 4p16.1.

5 Human 5R79-46-1\_h (SEQ ID NO: 5, SEQ ID NO:126)

Blastn analysis of the partial 5R79-46-1 sequence revealed an extension to encompass the complete ORF in the Incyte EST 463894.6. Since the initial filing of this application, the full-length virtual 5R79-46-1 appeared in the public database as the full-length gene for the TANK-binding kinase (TBK1) (Pomerantz, J.L. and Baltimore, D. (1999) EMBO J. 18 (23), 6694-6704). TBK1 participates in NF- $\kappa$ B activation through the formation of a signaling complex with TRAF2 and TANK.

Human AA305176 (SEQ ID NO: 6, SEQ ID NO:127)

Blastn analysis of the partial AA305176 sequence revealed an extension to encompass the complete ORF in the Incyte EST 220937.1.

15 Human AA256100 (SEQ ID NO: 8, SEQ ID NO:129)

Blastn analysis of the partial AA256100 sequence revealed an extension to encompass the complete ORF through the assembly of three partial clones: Incyte EST 480815.6, KIAA0965 (BAA76809) and AA256100.

Human AA210825 (SEQ ID NO: 9, SEQ ID NO: 130)

20 Blastn analysis of the partial AA210825 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte EST 014721.7, and the NCBI EST's AW01158 and AA210825. An insertion of two "N's" at positions 1915 and 1916 generated an uninterrupted ORF. Blastx analysis indicated the possibility of a start Met in the range of 400-450 nucleotides (i.e. compared to the closest homolog, human PKCmu (CAA53384.1). However, no Met was found in this region; rather ORF ends in an in-frame stop preceeded by the sequence  
25 "RGL LAPGDPPCPPNPAPATPPSSRLPTLFSNFCDS". It is possible that part of the sequence covered by nucleotide positions 1-400 derived from AW01158 comes from an intron, explaining the absence of a start Met.

30 Human AA127299 (SEQ ID NO:10, SEQ ID NO:131)

No entries in the database extended this sequence. The 1684 bp insert of this EST contains a 1369 bp intron at the 3' end. Blastx and SW analysis of the 315 bp coding

region revealed homology to the extracatalytic C2 domain of PKC. This EST, may or may not encode a kinase.

Human AA316804 (SEQ ID NO:11, SEQ ID NO:132)

5 Since the initial filing of this application, the partial AA316804 sequence appeared in the public database as the full-length gene for the PKC family protein kinase EPK2 or PKC $\epsilon$  (AB015982).

Human H19102 (SEQ ID NO:14, SEQ ID NO:135)

10 Genewise and Genescan analyses of the partial H19102 sequence revealed an extension from the HGP phase 3 contig 3810672 to encompass the complete catalytic domain of this EST. Blastn analysis against the non-redundant database revealed that this gene is found in the cosmid AC005726 from chromosome 17. H19102 may encode a dual catalytic kinase given the homology to S6 kinase. Analysis of genomic sequence upstream of the 5' end of H19102 revealed a non-kinase gene oriented in the same polarity as H19102 suggestive of the start Met for H19102 being close to the 5' end of the H19102  
15 sequence. From this analysis it is deduced that the second catalytic domain of H19102, if present, is most likely located within the 47334-185,215 bp region of the genomic sequence of AC005726.

Human AA476563 (SEQ ID NO:15, SEQ ID NO:136)

20 Since the initial filing of this application, the partial AA476563 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KC1 (NM\_012424) (Zhang, H. et al Genomics (1999) 61, 314-318), which is an S6 kinase mapping to 12q12-q13.1.

Human AA626690 (SEQ ID NO:16, SEQ ID NO:137)

25 Since the initial filing of this application, the partial AA626690 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KA6 (AF184965) (Yntema, H.G et al (1999) Genomics 62, 332-343), an S6 kinase commonly deleted in patients with complex X-linked (Xq21.1 ) mental retardation.

Human AI215680 (SEQ ID NO: 17, SEQ ID NO:138)

30 Since the initial filing of this application, the partial AI215680 sequence appeared in the public database as the full-length gene encoding a hypothetical protein (AAD30182) from the locus AC006530.4 from chromosome 14.

Human AA887783 (SEQ ID NO:21, SEQ ID NO:142)

Blastn analysis of the partial AA887783 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte 415390R6 and the NCBI EST's AA887783 and N94726. Since the initial filing of this application, the nearly full-length virtual AA887783 sequence appeared in the public database as the full-length gene encoding SGK3 (AF169035), a serum- and glucocorticoid-induced protein kinase (Kobayashi, T. et al (1999) Biochemical J. 344, 189-197.

Human R47805 (SEQ ID NO:22, SEQ ID NO:143)

A cDNA clone encoding the full-length ORF of R47805 was isolated using R47805 as a screening probe. A full-length form for R47805 has also appeared in the public database as

PTK9L (NM\_007284), an A6-related protein kinase.

Human H60215 (SEQ ID NO:23, SEQ ID NO:144)

Blastn analysis of the partial H60215 sequence revealed an extension to encompass the complete ORF in the public EST AI275726. This was confirmed through the full insert sequencing of this EST (2,310 bp) which corresponds to the sequence under SEQ ID NO:144.

A different stop codon was predicted for AI275726 compared to H60215 due to a single nucleotide insertion at position 1586 in AI275726. Evidence for the extra nucleotide comes from EST AI191922.

SGK324\_h orthologue of W30246\_m (SEQ ID NO:24, SEQ ID NO:145)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding to the human orthologue of murine W30246. Exons predicted from the following sequences were used for contig construction: Celera 17000189645083, 17000057549105 and 11000501939981; Incyte142404.1, HGP\_7249119, Incyte 7196489H1, Celera 11000501939981, 17000028165594; Incyte 7249119\_3, Celera 17000035772368, 11000502081575 and 17000140274329. The latter Celera sequence provides the N-terminus.

Human AA383293 (SEQ ID NO:26, SEQ ID NO:147)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding for AA383293. Exons predicted from the following sequences were used for contig construction: (numbers in parenthesis

refer to the aa sequence of the closest homolog (RU2S, NP\_057440) used for the Smith-Waterman query): N-term from Incyte 6010175\_2 (14-97), Incyte 6981981 (134-184) 7596749 (186-232) Celera 17000020789545 (243-301) CAB75619.1 (310-341)--(56-145 DCX homology) 6010175\_2, Celera 17000030058129 (241-262 DCX homology).

5 Human AA021445 (SEQ ID NO:32, SEQ ID NO:152)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. Contig reconstruction was as follows: nucleotides 1-802 from KIAA0999 (AB023216); nucleotides 803-4321 from full-insert sequence of AA021445. A pairwise alignment between the AA021445 and KIAA0999 revealed three  
10 inserts in the extracatalytic C-terminus of 48, 48 and 161 aminoacids. In addition, both AA021445 and KIAA0999 have 15 copies of a CAG repeat. Trinucleotide repeats are often found in genes that linked to neurodegenerative diseases.

Human 2R22-55-1 (SEQ ID NO:33, SEQ ID NO:153)

Blastn analysis revealed an extension in the Incyte EST clone 321074.1 to  
15 encompass the complete ORF corresponding to 2R22-55-1.

Human orthologue of AA544838\_m (SEQ ID NO:36, SEQ ID NO:156)

tBlastn analysis identified the partial human KIAA0135 (U79240) clone as the human orthologue of murine AA544838. Blastn revealed an extension KIAA0135\_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from  
20 Incyte406786.5, KFZp430051 and KIAA0135 (U79240).

Human orthologue of AI785735\_m (SEQ ID NO:38, SEQ ID NO:158)

tBlastn analysis identified the partial human KIAA0781 (AB018324) clone as the human orthologue of murine AI785735. Blastn revealed an extension KIAA0135\_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from Incyte  
25 986123.37 KIAA0781 (AB018324).

Human AA207220 (SEQ ID NO: 39, SEQ ID NO:159)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. The full ORF was reconstructed from Incyte 402740.1 and AA207220. Frame corrections: deletion of 441 and 595 over Inc402740.1 seq based on  
30 blastx to keep frame open; two n insertions 940, 941 over AA207220 to keep frame open.

Human AA426580 (SEQ ID NO:40, SEQ ID NO:160)

Since the initial filing of this application, the partial AA426580 sequence appeared in the public database as the full-length gene encoding MAK-V (AJ271722) from chromosome 21q22.1.

Human 5R79-54-1 (SEQ ID NO: 41, SEQ ID NO:161)

5 Genewise and Genescan analyses of the partial 5R79-54-1 sequence revealed an extension from genomic sequence to encode the full ORF for 5R79-54-1.

Human orthologue of AA542015\_m (SEQ ID NO: 42, SEQ ID NO:162)

10 tBlastn analysis identified KIAA1297 (AB037718). Blastn extended the KIAA1297 sequence to provide the C-terminus through the Incyte 224074.1 EST. The partial ORF consists of a dual catalytic domain flanked by 6 Ig domains and 2 fibronectin repeats. Based on homology to the bt drosophila protein (AAF59316.1), the human form of AA542015 is expected to be missing 16 Ig domains.

Human R19772 (SEQ ID NO:44, SEQ ID NO:164)

15 The full-length ORF for R19772 was isolated by screening a cDNA library using a probe derived from R19772. Since the initial filing of this application, the R19772 sequence appeared in the public database as the full-length gene encoding Trio (Duet) (AB011422). CDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

20 Table 8. Isoforms for R19772

Kestrl Name	Kestrl AA Acc #	Isoform type	Source	Description*
Trad (Duet)	R19772	B	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762
		C	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762

				Deletion of 32 aa (160-191)
		D	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)
		E	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)

\* reference amino acid position are with respect to sequence of Trad (AB011422)

Human AA435956 (SEQ ID NO:48, SEQ ID NO:168)

5        Blastn analysis revealed an extension to encompass the nearly complete catalytic region of AA435956. 5' end sequence extension was provided by genomic locus AC007242.3\_h (range 44880-43801). Based on blastx analysis, the extended sequence encodes is full-length at the C-terminus.

Human AA397553 (SEQ ID NO: 51, SEQ ID NO:171)

10        Since the initial filing of this application, the partial AA397553 sequence appeared in the public database as the full-length gene encoding CRK7 (AF227198), a novel CDC2-related protein kinase that colocalizes with interchromatin granule clusters.

Human AA789239 (SEQ ID NO: 52, SEQ ID NO:172)

15        Since the initial filing of this application, the partial AA789239 sequence appeared in the public database as the full-length gene encoding NKIAMRE (AF130372), a novel kinase deleted in human leukemia.

Human AA631990 (SEQ ID NO:55, SEQ ID NO:175)

20        Blastn analysis revealed an extension to encompass the full-length ORF for AA631990. The full ORF was reconstructed from 253847.5 and AA631990 and AA207220. Frame corrections: delete 1 C at 1380, delete 2N's at 2033/2034.

Human AA557536 (SEQ ID NO:56, SEQ ID NO:176)

25        Blastn analysis revealed an extension to encompass full-length ORF for AA557536. The full ORF was reconstructed from AA557536, celera 11000504061899 and the Incyte 097089.1 EST. An 85bp intron was removed from AA557536.

Human N34132 (SEQ ID NO: 63, SEQ ID NO:183)

Full sequencing of EST N34132 (1.3 kb) confirmed that this cDNA encodes a novel NEK-subfamily kinase. Blast analysis against the EST database showed that four

EST sequences (AA283140, AA283140, AA282911 and N53011) extended the sequence of N34132 at the 3' end to form a 2.31 kb contig. Blast analysis of the new contig against the nonredundant public database showed that the N34132 extended contig overlapped (100% identity) over 228 bp at its 3' end with human KIAA0344 (AB002342), a 5,787 bp cDNA encoding a 1246 aa polypeptide. The 5' 790 bp of the KIAA0344 cDNA (encoding the 58 N-terminal protein sequence) were found to be divergent with respect to the extended 2.32 kb N34132 contig. Evidence that the extended N34132 contig (2.31kb) and KIAA0344 (AB002342) belong to the same gene is the following. First, blast analysis of the nucleotide sequences for N34132 and KIAA0344 against the NR database confirmed that these cDNA's are transcribed from the same genomic locus defined by two overlapping BACs (AC004765 and AC004803) from chromosome 12p13.3. Second, full sequence determination of a PCR fragment amplified from single-stranded cDNA confirmed the junction between the extended N34132 contig and KIAA0344\_h (AB002342). The 462 PCR product was amplified with primers CTCCTCAACAGACAGTGCAG (5' primer) and GACATTCTACTACTCGGTCTC (3' primer) designed from the N34132 extended contig and KIAA0344 sequences, respectively. The region of N34132 containing the start Met was isolated by PCR from a testis cDNA library (Clontech).

Human 5R69-17-2 (SEQ ID NO:67, SEQ ID NO:187)

The full-length ORF for 5R69-17-2 was isolated by screening a cDNA library using a probe derived from 5R69-17-2.

Human H85811 (SEQ ID NO:68, SEQ ID NO:188)

Tblastn, Smith-Waterman and blastn analyses using cDNA databases revealed an extension to encompass full-length ORF for H85811. The full ORF was reconstructed from Incyte ESTs 202971.8, 034583.3 and 034583.1 and public ESTs H85811 and AI570599.

Human R43524 (SEQ ID NO:73, SEQ ID NO:192)

Blastn analysis revealed an extension to encompass the complete catalytic region and the C-terminus of R43524. Since the initial filing of this application, the partial R43524 sequence appeared in the public database as the full-length gene encoding the heme-regulated initiation factor 2-alpha kinase (HRI) (AF181071).

Human AA088547 (SEQ ID NO:78, SEQ ID NO:197)



Genewise and Genescan analyses of genomic databases revealed an extension to encompass the complete ORF for AA088547.

Human orthologue of AA139478\_m (SEQ ID NO:80, SEQ ID NO:199)

5 Tblastn identified the Incyte 211475.1 as the potential full-length human orthologue of murine AA139478

Human AA232253 (SEQ ID NO:82, SEQ ID NO:201)

10 The full-length ORF for AA232253 was isolated by screening a cDNA library using a probe derived from AA232253. Since the initial filing of this application, the AA232253 sequence appeared in the public database as the full-length gene encoding SLK (AB011422). SLK is a stress-regulated mixed lineage kinase-like protein that activation of Rac and induction of apoptosis. cDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

15 Table 9. Isoforms for AA232253

Kestrl Name	Kestrl AA Acc #	Isoform type	Description*
MLK4	AA232253	MLK4	Substitution of C for W at 346
		MLK4B	Different Cterm (332-800); seq in MLK4B is as shown in *

\* C-terminus specific to MLK4B

LPLAARMSEESYFESKTEESNSAEMSCQITATSNNGEGHGMNPSLQAMMLMGFGDI

FSMNKAGAVMHSGMQINMQAKQNSS

20 KTTSKRARGKKVNMALGFSDFDLSEGDDDDDDGEEEDNDMDNSE

Human H97685 (SEQ ID NO:84, SEQ ID NO:203)

25 Blastn analysis revealed an extension to encompass the full-length ORF for H97685. The full ORF was reconstructed from Incyte 474824.1 and the public ESTs H97685 and M62021.

Human AI052250 (SEQ ID NO:87, SEQ ID NO:206)

Blastn analysis revealed an extension to encompass the full-length ORF for AI052250. The full ORF was reconstructed from Incyte 396868.1, the public partial cDNA FLJ10074 (minus intron) and the public ESTs and the public ESTs AI052250 and H97685, AI499220 and M62021.

5 Human AA278842 (SEQ ID NO:88, SEQ ID NO:206)

A nearly full-length cDNA (FL4F12) for AA278842 was isolated by screening a cDNA library using a probe derived from AA278842. A full-length virtual ORF was generated using FL4F12 and AA278842.

Human AA599286 (SEQ ID NO:89, SEQ ID NO:208)

10 Since the initial filing of this application, the partial AA599286 sequence appeared in the public database as a full-length ORF (AK000342).

Human AA425725 (SEQ ID NO:90, SEQ ID NO:209)

Since the initial filing of this application, the partial AA425725 sequence appeared in the public database as MSSK1, a serine kinase gene located from human chromosome Xq28.

15 Human SGK022 orthologue of AA060026\_m (SEQ ID NO:91, SEQ ID NO:210)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed a potential human orthologue for murine AA060026. The full-length ORF for SGK022 was reconstructed from genomic locus AC022307.

20 Human AA399669 (SEQ ID NO:93, SEQ ID NO:212)

Blastn analysis revealed an extension to encompass the full-length ORF for AA399669. The full ORF was reconstructed as follows: sequence 1-1007 from AL136295.2; sequence1008-2319 from AA399669 and Incyte 428177.1.

Human AA883975 (SEQ ID NO:95, SEQ ID NO:214)

25 Genescan and Genewise analyses of the genomic databases revealed an extension for AA883975 to encompass the full-length ORF

Human AA905446 (SEQ ID NO:96, SEQ ID NO:215)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed an extension for AA905446 to encompass the full-length ORF. For the Smith-Waterman analysis murine STK22 ( NP\_033462) was used as the closest orthologue. Contig formation: range 162133-163687 from HGP\_h 6921333\_9; removed intron (146-893) predicted from blastx analysis.

Human H29974 (SEQ ID NO: 97 SEQ ID NO:216)

Blastn analysis revealed an extension to encompass a complete catalytic ORF for AA399669. The nearly full-length ORF was reconstructed using Incyte 213829.1 and H29974.

5 Human AA215311 (SEQ ID NO:99, SEQ ID NO:218)

Blastn analysis revealed an extension to encompass the full-length ORF for AA21531. The full ORF was reconstructed from Incyte 067584.1, 022456.1, AA215311 and the reverse complement of CPG\_043208.

Human AA018361 (SEQ ID NO:100, SEQ ID NO:219)

10 The full-length ORF for AA018361 was isolated by screening a cDNA library using a probe derived from AA018361. This yielded clone Sug4-30. Clone Sug4-30, like multiple, independent cDNA clones contained a 181bp intron. The existence of intron-less RNA's was confirmed by a PCR reaction that generated a product that upon sequence analysis skipped the intron region. The full-length virtual ORF for AA018361 was  
15 generated through a contig between AL117482 (seq 1-367) and the sequence for clone Sug4-30.

Human orthologue of AA396601\_m (SEQ ID NO:106, SEQ ID NO:225)

tBlastn and Smith-Waterman analyses of genomic sequence revealed an extension to encompass the full catalytic region for the human orthologue of AA396601. The ORF  
20 was reconstructed from Incyte 018653.9 (7261449H1, 6891740J1) and genomic sequence CPG\_040010.

Human orthologue of AA671275\_m (SEQ ID NO:108, SEQ ID NO:227)

Since the initial filing of this application, a potential human orthologue for murine AA671275 appeared in the public database as the full-length ORF for vaccinia related  
25 kinase 3 (BAA90769).

Human H05721 (SEQ ID NO:111, SEQ ID NO:230)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for H05721.

Human AI086865 (SEQ ID NO:112, SEQ ID NO:231)

30 Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AI086865. The full-length ORF was reconstructed from Celera 17000102901516, Incyte 243269.1 and public AL1377531.

Human AA836348 (SEQ ID NO:113, SEQ ID NO:232)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AA836348.

Human R86668 (SEQ ID NO:14, SEQ ID NO:233)

5 The full-length ORF for R86668 was isolated by screening a cDNA library using a probe derived from R86668. Since the initial filing of this application, the R8668 sequence appeared in the public database as the full-length gene mitogen-activated protein kinase kinase kinase 6 (MAP3K6) (NM\_00467).

Human 2R41-9-4 (SEQ ID NO: 16, SEQ ID NO:235)

10 The full-length virtual ORF for 2R41-9-4 was generated using genomic sequence to provide the Nterminus for the partial ORF predicted from clone 2R41-9-4

Table 10. Sequences deleted from the provisional patent due to duplication with other genes in the patent

Prov. SEQ ID NO: (na)	Prov. SEQ ID NO: (aa)
160	196
213	214
215	216
122	126
119	123
148	184
4	20
7	23
205	206
14	30
15	31
35	56
42	63
51	72
44	65
77	91

78	92
79	93
80	94
157	193

## Results

Table 1 documents the results from the analysis of the nucleic acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610)]. "ORF Start", "ORF End", "ORF Length" refer to the open reading frame range and length as calculated by standard nucleic acid translation programs such as MapDraw (DNASStar). "DNA Repeats" refers to regions of low complexity sequence or repetitive elements such as Alu, LINE, SINE, and LTR sequences. The chromosomal location (CHR localization) for 37 of the 110 novel protein kinases is shown on Table 1 (NA, not available). The methods for determining chromosomal position are outlined below, in Example 2.

Table 2 documents the results from the analysis of the amino acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610)]. "nraa Score", "ID match aa", "Identity", "Similar", "nraa Match Acc#", "Description" refer to the data obtained using a Smith-Waterman search of the amino acid sequence against the non-

redundant protein database (Matrix: Pam100; gap open/extension penalties 14/1). "Kinase Domain Start", "Kinase Domain End", "Profile Start" and "Profile End" refer to data obtained using a Hidden-Markov Model to define catalytic range boundaries. The profile has a length of 261 amino acids, corresponding to the complete protein kinase catalytic domain. Proteins in which the profile recognizes a full length catalytic domain have a "Profile Start" of 1 and a "Profile End" of 261. The boundaries of the catalytic domain within the overall protein are noted in the "Kinase Domain Start" and "Kinase Domain End" columns.

10 The following abbreviations were used for kinases:

ASK	Apoptosis signal-regulating kinase
CaMK	Ca <sup>2+</sup> /calmodulin-dependent protein kinase
CCRK	Cell cycle-related kinase
CDK	Cyclin-dependent kinase
CK	Casein kinase
DAPK	Death-associated protein kinase
DM	myotonic dystrophy kinase
Dyrk	dual-specificity-tyrosine phosphorylating-regulated kinase
GAK	Cyclin G-associated kinase
GRK	G-protein coupled receptor
GuC	Guanylate cyclase
HIPK	Homeodomain-interacting protein
IRAK	Interleukin-1 receptor-associated kin
MAPK	Mitogen activated protein kinase
MAST	Micotubule-associated STK
MLCK	Myosin-light chain kinase
MLK	Mixed lineage kinase
NIMA	NimA-related protein kinase
PKA	cAMP-dependent protein kinase
RSK	Ribosomal protein S6 kinase
RTK	Receptor tyrosine kinase

SGK	Serum and glucocorticoid-regulated kinase
STK	serine threonine kinase
ULK	UNC-51-like kinase

The following abbreviations were used for species

H	Human
M	Murine
R	Rat
FV	Fowlpox virus
MT	<i>M. thermoautotrophicum</i>
CE	<i>Caenorhabditis elegans</i>
DM	<i>Drosophila melanogaster</i>
OS	<i>Oryza sativa</i>
SP	<i>Schizosaccharomyces pombe</i>
TP	<i>Tetrahymena pyriformis</i>
PI	<i>Petunia inflata</i>
NC	<i>Neurospora crassa</i>
MSV	<i>Medicago sativa</i>
MSV	Moloney murine sarcoma virus
SA	<i>Squalus acanthias</i>
CS	<i>Cucumis sativus</i>
GM	<i>Glycine max</i>
LL	<i>Lilium longiflorum</i>
TV	<i>Trichomonas vaginalis</i>
MP	<i>Mycoplasma pneumoniae</i>
DD	<i>Dictyostelium discoideum</i>
SC	<i>Saccharomyces cerevisiae</i>
MT	<i>Methanobacterium thermoautotrophicum</i>

### Domain and Motif Identification

A Hidden Markov model (HMM) (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. (1994). Hidden Markov models in computational biology: Applications to protein modeling. J. Mol. Biol., 235:1501-1531) was used to identify, both catalytic and extracatalytic domains. Table 4 shows extra-catalytic domains that were identified using the HMM program. Other domains such as coiled-coil and pest motifs were identified as described next.

Potential coiled-coil domains were identified using the COILS program ([www.ch.embnet.org/software/COILS\\_form.html](http://www.ch.embnet.org/software/COILS_form.html)). The matrix used was MTIDK with windows of 14, 21, 28 amino acids. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region.

Protein sequences containing potential pest motifs were identified using the program PESTfind ([www.at.embnet.org/embnet/tools/bio/PESTfind/](http://www.at.embnet.org/embnet/tools/bio/PESTfind/)). PEST regions in proteins are by definition sequences that tend to be rich in proline, glutamic or aspartic acid, arginine and histidine; they have been associated with increased protein turnover rates (Rogers S. *et al.* (1986) Science 234, 364-368. The algorithm defines PEST sequences as hydrophilic stretches of amino acids greater than or equal to 12 residues in length. Such regions contain at least one P, one E or D and one S or T. They are flanked by lysine (K), arginine (R) or histidine (H) residues, but positively charged residues are disallowed within the PEST sequence. PESTfind produces a score ranging from about -50 to +50. By definition, a score above zero denotes a possible PEST region; a value greater than +5 defines a high probability that there is a PEST domain.

### **Identification of potential coiled-coil domains and PEST domains in N34132**

Potential coiled-coil domains were identified in N34132 (SEQ ID NO:183) using the COILS program. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region. The amino acid positions within N34231 scoring for potential coil-coil regions are shown below.



Table 11 coiled-coil domains predicted for N34132

Coiled-coil Region	Amino acid range	Length (aa)
1	124-147	24
2	437-451	15
3	495-526	32
4	1,723-1,749	27

Potential PEST domains were identified in N34132 using PESTfind, a value greater than +5 defines a high probability that there is a PEST domain. The amino acid positions within N34132 scoring for potential PEST regions are shown below.

Table 12 Potential Pest domains identified in N34132

PEST Region	Score	Amino acid range	Amino Acid Length
1	+ 4.91	54-95	42
2	+11.4	537-570	34
3	+31.08	1293-1304	12
4	+10.15	1543-1565	23
5	+ 6.17	1698-1732	35

## EXAMPLE 2. Chromosomal Localization of Novel Mammalian Protein Kinases

### Materials and Methods

Several sources were used to find information about the chromosomal localization of each of the genes described in this patent. First, the accession number for the nucleic acid sequence was used to query the Unigene database. The site containing the Unigene search engine is: <http://www.ncbi.nlm.nih.gov/UniGene/Hs.Home.html>. Information on map position within the Unigene database is imported from several sources, including the Online Mendelian Inheritance in Man (OMIM, <http://www.ncbi.nlm.nih.gov/Omim/searchomim.html>), The Genome Database (<http://gdb.infobiogen.fr/gdb/simpleSearch.html>), and the Whitehead Institute human physical map ([http://carbon.wi.mit.edu:8000/cgi-bin/contig/sts\\_info?database=release](http://carbon.wi.mit.edu:8000/cgi-bin/contig/sts_info?database=release)). For example, searching Unigene with W56561, an EST for a MAK-like kinase, the

following information is retrieved: Chr.14, D14S65-qTEL. The location of this gene on an "ideogram" of the cytogenetic map of chromosome 14 is also provided, showing that W56561 maps to the bottom of chromosome 14, between 14q31 and 14qTel. If Unigene has not mapped the EST, then the nucleic acid for the gene of interest is used as a query against databases, such as dbsts and htgs (described at

5 [http://www.ncbi.nlm.nih.gov/BLAST/blast\\_databases.html](http://www.ncbi.nlm.nih.gov/BLAST/blast_databases.html)) containing sequences that have been mapped already. The nucleic acid sequence is searched using BLAST-2 at NCBI (<http://www.ncbi.nlm.nih.gov/cgi-bin/BLAST/nph-newblast>) and is used to query either dbsts or htgs. In addition to the Whitehead and GDB sites mentioned above,

10 Stanford University maintains a useful site for chromosomal mapping from STS data (<http://www-shgc.stanford.edu/RH/rhserverformnew.html>). Matches in htgs are often resolved immediately because the genomic region hit is annotated in the htgs entry. If an exact match match is found (defined roughly as 99% identity over a region of about 100 base pairs or longer, excluding any repetitive sequence), then the mapped position of the

15 entry in the database is assigned to the original kinase query. Once a cytogenetic region has been identified by one of these approaches, disease association is established by searching OMIM (see above for URL) with the cytogenetic location. OMIM maintains a searchable catalog of cytogenetic map locations organized by disease. A thorough search of available literature for the cytogenetic region is also made using Medline

20 (<http://www.ncbi.nlm.nih.gov/PubMed/medline.html>). References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123.

### Results

25 The chromosomal location for 37 of the 110 novel protein kinases is shown on Table 1. Three of the novel protein kinases were mapped to regions associated with cancer amplicons, as shown on this table. The regions were also cross-checked with the Mendelian Inheritance in Man database, which tracks genetic information for many human diseases, including cancer. References for association of the mapped sites with

30 chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123. Association of these mapped regions with other diseases is

documented in the Online Mendelian Inheritance in Man (OMIM)  
(<http://www.ncbi.nlm.nih.gov/htbin-post/Omim>).

### EXAMPLE 3: Generation of Specific Immunoreagents

#### 5 Materials and Methods

Peptide sequences to extra-catalytic regions of novel kinases are chosen which are not homologous to other known kinases based on a Smith Waterman homology search against the non-redundant protein database and predicted to be antigenic based on the DNASTar Protean program. These peptides are conjugated to KLH using Glutaraldehyde.

10 Rabbits are immunized with the KLH-peptide conjugates by four injections three weeks apart. The rabbits are bled ten and fourteen days following the third injection and bled out ten days after the fourth. The serum is checked against the peptide by ELISA.

Table 13. Peptides to be used as immunogens for raising antibodies

Clone Name	SEQ ID NO (aa)	Peptide Sequence	Amino Location
AA8256850	124	KSRDNSRDSSQSEND	339-353
		TEKLKRSQDLPREPLP	372-386
		RGWRPYDIHS	223-232
5R79-46-1	126	FEGPRRNKEVMYK	224-236
		KDDYNETVHKKTE	451-463
		GTHPKDRNVEKLQ	541-553
		EVSKYQEYTNELQET	643-657
AA256100	129	IDDTSNFDDFPESDI	405-419
		TEPDYKSKDWVFL	427-439
		EEKKLRRSQHARKET	61-75
AA210825	130	SNKDTLRKRHYWRLD	507-521
		RHTTRKSSTTLRE	488-500
		FQNNTTNRYEYKEIPL	528-542
		GKHRKTGRDVAVK	668-680
		FPTKQESQLRNE	687-698

AA316804	132	ESHVHQEPSKRIPS	239-252
		HTKRKSSTMVKEGW	409-422
		PSDLDERDEEAVK	375-388
		SPGQGDHDKDLSTSI	543-557
R47805	143	EPVGRWDQDYDRAVL	44-58
		KPKGPGGKRGHKRLI	325-339
		PTDVAQLPSRVPRDA	219-233
AA234451	167	DPDFWEKTGNDGSLT	293-307
		HPRPQEKDVWEE	374-385
		RENTDEVFPDEQLSD	340-354
		RSEITQPDRDIPLVR	427-441
AA460132	180	LKSYSTSSKKARPVL	222-236
		KKLDEVRLRGRKRSM	237-251
		ETEKTAQGLSNLAKT	131-145
N34132	183	SGRRRRPTKSKGSKS	1848-1862
		PGTAPSKPPLTKAPV	1474-1488
		VSDTQPKAPGIDD	1365-1378
		AHSLDKTSHSSTTGL	1253-1267
5R69-17-2	187	GTTREKTDVRKST	178-190
		HSEAPELHGKIRSSN	138-152
		DETVTPPQFSIV	87-98
		QYDVKSEIYS	204-213
AA278842	206	TVDPEKSVRDQAFKA	515-529
		DSSTADRWDDWGS	637-651
		SVSEDPTQLEEVEKD	539-553
AA836348	232	NAPTKRPRSSTVTEA	323-337
		LDSEEDYYTPQKVDV	514-528
		GDKASYRQPKHVEKL	409-423

EXAMPLE 4. Expression analysis of Novel Mammalian Protein KinasesGENE EXPRESSION ANALYSISTissue Arrays

“cDNA libraries” derived from a variety of sources were immobilized onto nylon  
5 membranes and probed with <sup>32</sup>P-labeled cDNA fragments derived from the gene(s) of  
interest.

Total RNA or mRNA was used as template in a reverse transcription reaction to  
generate single-stranded cDNAs (ss cDNA) that were tagged with specific sequences at  
each end. An oligo dT primer containing a specific sequence (CDS:

10 AAGCAGTGGTAACAACGCAGAGTACT30VN (V=A,G,C N=A,G,C,T)) anneals at  
the polyA track at the 3' end of the mRNA and the reverse transcriptase (MMLV  
RnaseH-) transcribes the antisense strand until it reaches the end of the RNA strand when  
it adds additional C residues. If a primer (SMII:

AAGCAGTGGTAACAACGCAGAGTACGCGGG or ML2G:

15 AAGTGGCAACAGAGATAACGCGTACGCGGG) ending with 3 Gs is added, it anneals  
to the added Cs and the MMLV recognizes the rest of the primer sequence as template and  
continues transcription. As a result, the synthesized cDNAs contain specific sequence tags  
at both the 5' and the 3' end. When the 5' and the 3' ends are tagged with the same  
sequence (CDS and SMII) it is referred to as “symmetric.” When the 5' end is tagged

20 with a different sequence than the 3' end (CDS and ML2G) is referred to as “asymmetric”  
A double-stranded “cDNA library “ is then generated by PCR amplification using the  
3'PCR and ML2 primers (3' PCR: AAGCAGTGGTAACAACGCAGAGT and ML2:  
AAGTGGCAACAGAGATAACGCGT) that anneal to the added sequence tags.

The amplified “cDNA libraries” were manually arrayed onto nylon membranes  
25 with a 384 pin replicator. The DNA was denatured by alkali treatment, neutralized and  
cross-linked by UV light. The arrays were pre-hybridized with Express Hyb (Clontech)  
and hybridized with <sup>32</sup>P labeled probes generated by random hexamer priming of cDNA  
fragments corresponding to the genes of interest. After washing, the blots were exposed to  
phosphorimaging cassettes and the intensity of the signal was quantified. The amount of  
30 the DNA on the arrays was also quantified by treating non-denatured or denatured arrays  
with Syber Green I or Syber Green II respectively (1:100,000 in 50mM Tris, pH8.0) for 2  
minutes. After washing with 50mM Tris, pH8.0, the fluorescent emission was detected

with a phosphorimager (Molecular Dynamics) and quantified. The amount of the arrayed DNA was used to normalize the hybridization signal and the corrected values are tabulated in Table 3.

## 5 Results

The results of the microarray expression analysis of the protein kinases presented in this application is shown in Table 3. Data presentation from left to right is as follows: "Tissue": tissue type of the cDNA; "Tumor sym", indicates that the tissue is derived from a tumor, "sym" refers to the fact that the 5' and 3' primers used to make the sample are the same; "Normal Sym", indicates normal tissue was used to make the sample, with symmetric primers as described above; "Tumor 1o", indicates that primary tumor tissue was used to make the cDNA; "Tumor cells", indicates that these cDNA samples were made from cultured tumor cells; "Normal", indicates that these samples are derived from normal tissue or cell lines; "Endos", indicates that these samples are derived from endothelium-related tissue sources; "p53" refers to the status, mutant or wild-type, of the p53 gene in the source samples. Normalized expression values are presented for each gene referred to by its SEQ ID# on the subsequent columns. Genes represented in expression Table 3 are: SEQ ID NO:3 (AA826850), SEQ ID NO:5 (TBK1), SEQ ID NO:6 (AA305176), SEQ ID NO:8 (AA256100), SEQ ID NO:9 (CAB43292), SEQ ID NO:11 (EPK2), SEQ ID NO:12 (PKNbeta), SEQ ID NO:14 (H19102), SEQ ID NO:16 (RSK4), SEQ ID NO:17 (AAD30182), SEQ ID NO:20 (SGK2), SEQ ID NO:22 (PTK9L), SEQ ID NO:26 (AA383293), SEQ ID NO:29 (DRAK2), SEQ ID NO:31 (DRAK1), SEQ ID NO:032 (AA015726), SEQ ID NO:40 (MAK-V), SEQ ID NO:044 (TRAD), SEQ ID NO:044 (TRAD), SEQ ID NO:45 (AA454060), SEQ ID NO:47 (AA234451), SEQ ID NO:48 (AA436054), SEQ ID NO:49 (AA626859), SEQ ID NO:51 (KIAA0904), SEQ ID NO:52 (AA789239), SEQ ID NO:54 (CCRK), SEQ ID NO:55 (CLK4), SEQ ID NO:56 (AA557536), SEQ ID NO:57 (W56561), SEQ ID NO:60 (AA579641), SEQ ID NO:63 (NEK7), SEQ ID NO:66 (CAMKKB), SEQ ID NO:68 (HIPK2), SEQ ID NO:72 (R19609), SEQ ID NO:73 (HRI), SEQ ID NO:78 (AA088547), SEQ ID NO:79 (AA449542), SEQ ID NO:082a (MLK4), SEQ ID NO:82 (MLK4b), SEQ ID NO:84 (RIP4), SEQ ID NO:88 (AA278842), SEQ ID NO:89 (AA195964), SEQ ID NO:90 (MSSK1), SEQ ID NO:93 (TSK4), SEQ ID NO:94 (AI025291), SEQ ID NO:95

(AA948538), SEQ ID NO:96 (AA905446), SEQ ID NO:97 (H85389), SEQ ID NO:100 (AA018361), SEQ ID NO:101 (AA311714), SEQ ID NO:110 (AA452647), SEQ ID NO:111 (AA310219), SEQ ID NO:112 (AJ086865), SEQ ID NO:114 (MEKK6), and SEQ ID NO:116 (SuRTK106).

5

EXAMPLE 5. Kinase assays for Erk, JNK1 and p38 MAP kinases

293T cells were transiently transfected with HA- p38 or co-transfected with Flag-tagged wt MLK4A, kinase-dead MLK4A, wild-type MLK4B or kinase-dead MLK4B using Lipofectamine 2000 (Lifetech). Cells were lysed 36 hr post-transfection. Cell lysates normalized to contain equivalent amounts of HA-p38 were immunoprecipitated with anti-HA antibody (Mab HA-11, Babco). Immunoprecipitates were split in two portions, one portion was Western-blotted with anti- HA antibody and the other with a phospho-specific p38 antibody (Promega) to detect activated levels of p38. Activation of Erk1 and Jnk1 was measured similarly. (This example applies to AA232253 (SEQ ID NO:82, SEQ ID NO:201).)

15

Results:

In transient assays wild-type MLK4A and MLK4B (but not kinase-inactive MLK4A(K45M) or MLK4B(K45M)) activate Erk, JNK1 and p38 MAP kinases.

20 EXAMPLE 6. RAC1 guanine-exchange factor assay

293T cells were transiently transfected with HA-Rac1 or co-transfected with Flag-tagged Duet C, Duet E, Dbl and HA-Tiam-1. Cells were lysed 36 hour post-transfection. Cell lysates normalized to contain equivalent amounts of Rac1 were affinity precipitated with immobilized GST-PBD (p21-binding domain of Pak3). Bound proteins were Western blotted and probed with anti-HA antibody to detect levels of activated Rac1. ((This example applies to R199772 (Trad/Duet)(SEQ ID NO:44, SEQ ID NO:164).)

25

Results:

Duet C and Duet E both act as guanine nucleotide exchange factors on Rac1.

### CONCLUSION

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The molecular complexes and the methods, procedures, treatments, molecules, specific compounds described herein are presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention.

All patents and publications mentioned in the specification are indicative of the levels of those skilled in the art to which the invention pertains.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed.

In particular, although some formulations described herein have been identified by the excipients added to the formulations, the invention is meant to also cover the final formulation formed by the combination of these excipients. Specifically, the invention includes formulations in which one to all of the added excipients undergo a reaction during formulation and are no longer present in the final formulation, or are present in modified forms.

In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush



group. For example, if X is described as selected from the group consisting of bromine, chlorine, and iodine, claims for X being bromine and claims for X being bromine and chlorine are fully described.

Other embodiments are within the following claims.

What is claimed is:

CLAIMS

1. An isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

2. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises a nucleotide sequence that:

(a) encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) is the complement of the nucleotide sequence of (a);

(c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide;

(d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(e) is the complement of the nucleotide sequence of (d);

(f) encodes a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, wherein said domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(g) is the complement of the nucleotide sequence of (f);

(h) encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID

NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID  
NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID  
NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID  
NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID  
5 NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID  
NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID  
NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID  
NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID  
NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID  
10 NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID  
NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID  
NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID  
NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID  
NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID  
15 NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID  
NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID  
NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID  
NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID  
NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID  
20 NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID  
NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID  
NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID  
NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not  
all, of the domains selected from the group consisting of an N-terminal domain, a catalytic  
25 domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure  
region, and a C-terminal tail; or

(i) is the complement of the nucleotide sequence of (h).

3. The nucleic acid molecule of claim 1, further comprising a vector or  
promoter effective to initiate transcription in a host cell.

4. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is isolated, enriched, or purified from a mammal.

5. The nucleic acid molecule of claim 4, wherein said mammal is a human.

6. A nucleic acid probe for the detection of nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is selected from the group consisting of

5 SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146,

10 SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,

15 SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,

20 SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

30

7. The probe of claim 6, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.



8. A recombinant cell comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

9. The cell of claim 8, wherein said polypeptide is a fragment of a protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

10. An isolated, enriched, or purified kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, 5 SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, 10 SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, 15 SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, 20 SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, 25 SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

11. The polypeptide of claim 10, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

12. The polypeptide of claim 10, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ  
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ  
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ  
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ  
5 ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ  
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ  
ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ  
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ  
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ  
10 ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ  
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ  
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ  
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ  
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ  
15 ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ  
ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ  
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ  
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ  
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ  
20 ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ  
ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and  
SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ  
ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ  
25 ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ  
ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ  
ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ  
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ  
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ  
30 ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ  
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ  
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ

ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

13. The kinase polypeptide of claim 10, wherein said polypeptide is isolated, purified, or enriched from a mammal.

14. The kinase polypeptide of claim 13, wherein said mammal is a human.

15. The kinase polypeptide of claim 10, wherein said polypeptide is a AA144574, AA116841, AA256100, AA305176, AA210825, AA316804, AA980090, N42050, AA476563, AA626690, AA960957, H19102, AA045601, AA107515, AA109508 or AA887783 polypeptide.

16. The kinase polypeptide of claim 10, wherein said polypeptide is a H60215, AA197883, AA297313, W30246, AA172300, AA383293, AA542015, H01248, N23936, W44160, 2R22-5-11, 5R72-18-1, AA021445, AA207220, AA426580, AA544838, W90839, 5R79-54-1, AA839940, R19772 or 5R72-8-2 polypeptide.

17. The kinase polypeptide of claim 10, wherein said polypeptide is a AA234451 polypeptide.

18. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R65-16-1, AA061797, AA065538, AA124976, AA397553, AA435956, AA575635, AA626859, AA789239, AI086865, H17727, H29974, AA557536 or N28606 polypeptide.

19. The kinase polypeptide of claim 10, wherein said polypeptide is a AA631990 or W08549 polypeptide.

20. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R72-16-2, R19927 or R43524 polypeptide.

21. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R57-10-2 polypeptide.

5 22. The kinase polypeptide of claim 10, wherein said polypeptide is a AA232253 polypeptide.

23. The kinase polypeptide of claim 10, wherein said polypeptide is a AA430250, AA836348, R86668 or N34132 polypeptide.

10 24. The kinase polypeptide of claim 10, wherein said polypeptide is a AA098024 or SuRTK106 polypeptide.

25. The kinase polypeptide of claim 10, wherein said polypeptide is a R47805, AA099102, AA589241, H85811, AA013524, AA452647, AA840598, AA088547, AA139478, AA826850, R87679, W65887, H97685, W20810, AA599286, AA425725, AA103218, AA711829, AA060026, AA399669, AA758539, AA883975, AA948538, 15 AA018361, AA215311, AA311714, AA498104, 5R69-17-2, 5R69-23-3, 5R69-26-2, AA118352, AA396601, AA671275, AA278842, AA460132 or H05721 polypeptide.



26. An antibody or antibody fragment having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

27. The antibody or antibody fragment of claim 26, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ  
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ  
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ  
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ  
5 ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ  
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ  
ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ  
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ  
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ  
10 ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ  
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ  
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ  
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ  
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ  
15 ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ  
ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ  
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ  
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ  
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ  
20 ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ  
ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and  
SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ  
ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ  
25 ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ  
ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ  
ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ  
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ  
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ  
30 ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ  
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ  
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ

ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID  
NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID  
NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID  
NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID  
5 NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID  
NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID  
NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID  
NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID  
NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID  
10 NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID  
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID  
NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting  
of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a  
proline-rich region, a coiled-coil structure region, and a C-terminal tail.

28. A hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

29. A method for identifying a substance that modulates kinase activity comprising:

(a) contacting a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,

SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141,  
SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146,  
SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151,  
SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156,  
5 SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,  
SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166,  
SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,  
SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,  
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,  
10 SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,  
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,  
SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,  
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,  
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,  
15 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,  
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,  
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,  
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,  
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,  
20 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,  
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,  
and SEQ ID NO:242 with a test substance;

(b) measuring the activity of said polypeptide; and

(c) determining whether said substance modulates the activity of said  
25 polypeptide.

30. A method for identifying a substance that modulates kinase activity in a  
cell comprising:

(a) expressing a kinase polypeptide in a cell, wherein said polypeptide  
is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID  
30 NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID  
NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID  
NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID

NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID  
NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID  
NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID  
NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID  
5 NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID  
NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID  
NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID  
NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID  
NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID  
10 NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID  
NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID  
NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID  
NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID  
NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID  
15 NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID  
NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID  
NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID  
NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID  
NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID  
20 NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID  
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

- (b) adding a test substance to said cell; and
- (c) monitoring a change in cell phenotype or the interaction between  
said polypeptide and a natural binding partner.

31. A method for treating a disease or disorder by administering to a patient in need of such treatment a substance that modulates the activity of a kinase selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

32. The method of claim 31, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

33. The method of claim 31, wherein said substance modulates kinase activity *in vitro*.



34. The method of claim 33, wherein said substance is a kinase inhibitor.

35. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

- (a) contacting said sample with a nucleic acid probe which hybridizes  
5 under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,  
10 SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,  
15 SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,  
20 SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,  
25 SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,  
30 SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding said polypeptide, fragments thereof, or the complements of said sequences and fragments; and

(b) detecting the presence or amount of the probe:target region hybrid as an indication of said disease.

36. The method of claim 35, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease,  
5 neurodegenerative disorders, and cancer.

37. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) comparing a nucleic acid target region encoding said kinase polypeptide in a sample, wherein said kinase polypeptide is selected from the group  
10 consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ  
15 ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ  
20 ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ  
25 ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ  
30 ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ

ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding said kinase polypeptide, or one or more fragments thereof; and

5 (b) detecting differences in sequence or amount between said target region and said control target region, as an indication of said disease or disorder.

38. The method of claim 37, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

Table 1

Gene Name	SP	Prov	Seq	D	NA	Prov	Seq	D	NA	SEQ ID #	NA	SEQ ID #	NA	Family	Group	Length	NA	Length	AA	ORF Start	ORF End	ORF Length	DNA Repeats	CHR Localization	
XBP117 h BARQ2 h	M	1	1	1	1	1	1	1	1	127	1	127	1	AGC	GRK	2087	988	2087	988	1	2084	1134	2084	X	22q11
AA14457.4 m BARQ2 m	M	1	17	1	1	1	17	1	1	133	1	133	1	AGC	GRK	1398	378	1398	378	2	1135	1134	1134	X	22q11
AA26850 h	M	140	1	1	1	1	140	1	1	134	1	134	1	AGC	GRK	1788	419	1788	419	8	1287	1287	1287	285-304	NA
AA390957 h	M	11	37	1	1	1	37	1	1	135	1	135	1	AGC	M3C11.1.08	3724	414	3724	414	85	1306	1306	1306	X	4p18.1
5R19-06.1 h TBK1 h	M	207	206	1	1	1	207	206	1	135	1	135	1	AGC	M3C11.1.08	3013	328	3013	328	53	1030	1030	1030	X	NA
AA305176 h	M	4.2	19,30	1	1	1	4.2	19,30	1	137	1	137	1	AGC	NDR	1421	328	1421	328	53	1030	1030	1030	X	10p11.2
AA118841 m	M	4.2	19,30	1	1	1	4.2	19,30	1	138	1	138	1	AGC	NDR	582	88	582	88	3	208	208	208	X	NA
AA256100 h	M	3	1	1	1	1	3	1	1	138	1	138	1	AGC	NDR	4983	464	4983	464	86	1677	1677	1677	X	12p11
AA210425 h	M	5	21	1	1	1	5	21	1	139	1	139	1	AGC	PKC	3283	978	3283	978	117	3050	3050	3050	X	19p13-q13.3
AA127288 h	M	203	204	1	1	1	203	204	1	139	1	139	1	AGC	PKC	315	315	315	315	1	315	315	315	X	NA
AA317604 h EPK2	M	8	22	1	1	1	8	22	1	139	1	139	1	AGC	PKC	2673	890	2673	890	1	2670	2670	2670	X	2p21
NA2050 h PKNbeta	M	8	24	1	1	1	8	24	1	139	1	139	1	AGC	PKC	2673	890	2673	890	1	2670	2670	2670	X	2p21
A021023 m PKNbeta m	M	8	24	1	1	1	8	24	1	139	1	139	1	AGC	PKC	2673	890	2673	890	1	2670	2670	2670	X	2p21
H19102 h	M	12	28	1	1	1	12	28	1	134	1	134	1	AGC	PKC	929	205	929	205	2	616	615	615	X	CH17
AA476553 h RPS9KC1	M	9	25	1	1	1	9	25	1	136	1	136	1	AGC	SKK	1155	384	1155	384	1	1152	1152	1152	X	12p12-q13.1
AA276880 h RSK4	M	10	25	1	1	1	10	25	1	136	1	136	1	AGC	SKK	1410	490	1410	490	1	1407	1407	1407	X	12p12-q13.1
AA216880 h	M	227	228	1	1	1	227	228	1	137	1	137	1	AGC	SKK	2228	745	2228	745	1	2235	2235	2235	X	14q21.3
SGK h	M	2	1	1	1	1	2	1	1	138	1	138	1	AGC	SKK	1650	548	1650	548	1	1647	1647	1647	707-708	NA
AA107515 m	M	3	28	1	1	1	3	28	1	138	1	138	1	AGC	SKK	1288	431	1288	431	1	1285	1285	1285	459-468	NA
AA109508 m	M	3	28	1	1	1	3	28	1	138	1	138	1	AGC	SKK	2432	430	2432	430	75	1364	1364	1364	1804-1810	NA
AA397765 h SK3 SKKL	M	15	32	1	1	1	15	32	1	140	1	140	1	AGC	SKK	1348	244	1348	244	2	733	733	733	X	NA
RA71805 h PTK8L	M	16	32	1	1	1	16	32	1	141	1	141	1	AGC	SKK	1348	244	1348	244	2	733	733	733	X	NA
RA70212 h PTK8L	M	16	32	1	1	1	16	32	1	141	1	141	1	AGC	SKK	1348	244	1348	244	2	733	733	733	X	NA
SGK3 h	M	33	54	1	1	1	33	54	1	143	1	143	1	Atypical	SKK	1050	349	1050	349	1	1047	1047	1047	X	NA
1328248 m SK3324 m	M	33	54	1	1	1	33	54	1	143	1	143	1	Atypical	SKK	1050	349	1050	349	1	1047	1047	1047	X	NA
AA353543 h	M	36	57	1	1	1	36	57	1	144	1	144	1	CAK	AMPK	2310	440	2310	440	420	1738	1738	1738	X	3p14.3
AA197683 m	M	38	59	1	1	1	38	59	1	145	1	145	1	CAK	CAK	3240	682	3240	682	7	2082	2078	2078	208-227	NA
AA172900 h DRK2	M	34	55	1	1	1	34	55	1	145	1	145	1	CAK	CAK	1248	297	1248	297	1	891	891	891	X	NA
NA44150 m DRK2 m	M	37	59	1	1	1	37	59	1	146	1	146	1	CAK	CAK	2424	688	2424	688	1	2058	2058	2058	439-458	NA
H01248 h DRK1 h	M	40	61	1	1	1	40	61	1	149	1	149	1	CAK	DAPK	1628	373	1628	373	382	2418	2418	2418	X	NA
AA021445 h	M	45	60	1	1	1	45	60	1	150	1	150	1	CAK	DAPK	2671	372	2671	372	171	1288	1288	1288	X	NA
21222-5-11 h	M	43	64	1	1	1	43	64	1	152	1	152	1	CAK	DAPK	1245	414	1245	414	1	1242	1242	1242	91-110	7p11-q11
RA31237.1 h AAC33487	M	49	70	1	1	1	49	70	1	154	1	154	1	CAK	EMK	4321	1311	4321	1311	146	4078	4078	4078	91-2281, 1258-12	11p22.1-1q22.3
W00839 m	M	49	70	1	1	1	49	70	1	154	1	154	1	CAK	EMK	2100	728	2100	728	1	2178	2178	2178	X	NA
AA544838 m A06786 m	M	48	69	1	1	1	48	69	1	156	1	156	1	CAK	EMK	1584	520	1584	520	1	1580	1580	1580	X	NA
AA705735 h	M	48	69	1	1	1	48	69	1	156	1	156	1	CAK	EMK	1584	520	1584	520	1	1580	1580	1580	X	NA
AA207220 h	M	48	67	1	1	1	48	67	1	158	1	158	1	CAK	EMK	1250	230	1250	230	3	692	690	690	1002-1022	NA
AA426560 h MAK V h	M	47	68	1	1	1	47	68	1	159	1	159	1	CAK	EMK	2191	629	2191	629	103	2052	2052	2052	X	NA
238720 h	M	50	71	1	1	1	50	71	1	160	1	160	1	CAK	EMK	2148	714	2148	714	1	2142	2142	2142	X	NA
SGK088 h	M	39	60	1	1	1	39	60	1	162	1	162	1	CAK	EMK	2623	874	2623	874	1	2622	2622	2622	X	NA
AA542015 m SGK088 m	M	39	60	1	1	1	39	60	1	162	1	162	1	CAK	EMK	2623	874	2623	874	1	2622	2622	2622	X	NA
RI19772 h	M	52	73	1	1	1	52	73	1	164	1	164	1	CAK	EMK	1251	127	1251	127	1	391	391	391	X	NA
5R172.8.2 h	M	53	74	1	1	1	53	74	1	164	1	164	1	CAK	EMK	1251	127	1251	127	1	391	391	391	X	NA
SGK309 h	M	159	105	1	1	1	159	105	1	165	1	165	1	CAK	EMK	2584	1287	2584	1287	1	391	391	391	X	NA
AA234451 h	M	73	78	1	1	1	73	78	1	168	1	168	1	CAK	EMK	2584	1287	2584	1287	1	391	391	391	X	NA
AA435856 h	M	82	88	1	1	1	82	88	1	168	1	168	1	CAK	EMK	2584	1287	2584	1287	1	391	391	391	X	NA
AA628659 h	M	84	88	1	1	1	84	88	1	168	1	168	1	CAK	EMK	2584	1287	2584	1287	1	391	391	391	X	NA
AA061197 m	M	81	85	1	1	1	81	85	1	170	1	170	1	CAK	EMK	2584	1287	2584	1287	1	391	391	391	X	NA
AA397553 h CRK7	M	81	85	1	1	1	81	85	1	170	1	170	1	CAK	EMK	2584	1287	2584	1287	1	391	391	391	X	NA
AA789239 h	M	85	89	1	1	1	85	89	1	171	1	171	1	CAK	EMK	2584	1287	2584	1287	1	391	391	391	X	NA
AA124878 h	M	85	89	1	1	1	85	89	1	171	1	171	1	CAK	EMK	2584	1287	2584	1287	1	391	391	391	X	NA
AA575635 m CCRK m	M	85	89	1	1	1	85	89	1	171	1	171	1	CAK	EMK	2584	1287	2584	1287	1	391	391	391	X	NA
AA631980 h CLK4	M	105	107	1	1	1	105	107	1	174	1	174	1	CAK	EMK	2584	1287	2584	1287	1	391	391	391	X	NA
AA557536 h	M	86	90	1	1	1	86	90	1	175	1	175	1	CAK	EMK	2584	1287	2584	1287	1	391	391	391	X	NA
NA28606 h MOK	M	86	90	1	1	1	86	90	1	175	1	175	1	CAK	EMK	2584	1287	2584	1287	1	391	391	391	X	NA
AB023153 h ICX	M	86	90	1	1	1	86	90	1	175	1	175	1	CAK	EMK	2584	1287	2584	1287	1	391	391	391	X	NA
AA639840 h	M	86	90	1	1	1	86	90	1	175	1	175	1	CAK	EMK	2584	1287	2584	1287	1	391	391	391	X	NA
AA460132 h	M	195	201	1	1	1	195	201	1	178	1	178	1	CAK	EMK	1776	413	1776	413	1	1239	1239	1239	X	NA
SGK041 h	M	147	153	1	1	1	147	153	1	180	1	180	1	CAK	EMK	1428	253	1428	253	109	857	857	857	X	NA
AA103318 m SGK034 m	M	147	153	1	1	1	147	153	1	180	1	180	1	CAK	EMK	1428	253	1428	253	109	857	857	857	X	NA
AA103318 m SGK034 m	M	147	153	1	1	1	147	153	1	180	1	1													

Table 1 (cont'd)

Gene Name	SP	Prov	Seq ID	NA	Prov	Seq ID	NA	SEQ ID #	NA	SEQ ID #	NA	Family	Group	Length NA	Length AA	ORF Start	ORF End	ORF Length	DNA Repeats	C-HH Localization
BCON3 h	H							84		184		Other	CRC2 ca	2164	516	113	1717	1608	246-267	NA
AA111829 m	M							65		185		Other	CRC2 ca	1560	376	1	1134	1134		NA
AA08102 h CAMKKB	H							66		186		Other	CAMKKB	1587	388	1	1764	1764	95-84	12323-14
BRBP 17.2 h	H							67		187		Other	CTRI	3387	241	1850	2872	723	409-521	NA
TRB811 h	H							68		188		Other	DYRK	3993	1171	183	3695	3513	1335-1548	CHRT
AA02163 h DYRK3	H							69		189		Other	DYRK	2141	533	253	1911	1659		NA
AA35041 m DYRK3	M							70		190		Other	DYRK	741	166	3	508	504		NA
SR12 16.2 h R19827 h	H							71		191		Other	EFK	8153	1849	20	4968	4947		NA
AA3324 h HRI h R19809	H							72		192		Other	EFK	3932	930	1	1890	1890		7622-2223
1700057619467 h	H							73		193		Other	EFK	3055	759	219	877	759	2283-2385	NA
AA013528 m	M							74		194		Other	EFK	3055	759	219	877	759		NA
17000138801187 h IRAKM	H							75		195		Other	EFK	3055	759	219	877	759		NA
AA040599 m IRAKM	M							76		196		Other	EFK	3055	759	219	877	759		NA
AA089547 h	H							77		197		Other	EFK	3055	759	219	877	759		NA
HGP 0544468	H							78		198		Other	EFK	3055	759	219	877	759		NA
AA449542 m	M							79		199		Other	EFK	3055	759	219	877	759		NA
5557 10.2 m TESK2 m	M							80		200		Other	EFK	3055	759	219	877	759		NA
AA33253 h	H							81		201		Other	EFK	3055	759	219	877	759		NA
AI375137 h	H							82		202		Other	EFK	3055	759	219	877	759		NA
H97865 h	H							83		203		Other	EFK	3055	759	219	877	759		NA
W20810 m	M							84		204		Other	EFK	3055	759	219	877	759		NA
AA744235 h	H							85		205		Other	EFK	3055	759	219	877	759		NA
AI052250 h	H							86		206		Other	EFK	3055	759	219	877	759		NA
AA278642 h	H							87		207		Other	EFK	3055	759	219	877	759		NA
AA569286 h	H							88		208		Other	EFK	3055	759	219	877	759		NA
AA26725 h	H							89		209		Other	EFK	3055	759	219	877	759		NA
SGK022 h	H							90		210		Other	EFK	3055	759	219	877	759		NA
AA090026 m SGK022 m	M							91		211		Other	EFK	3055	759	219	877	759		NA
AA390869 h	H							92		212		Other	EFK	3055	759	219	877	759		NA
AA758339 h	H							93		213		Other	EFK	3055	759	219	877	759		NA
AA683975 h	H							94		214		Other	EFK	3055	759	219	877	759		NA
AA605446 h	H							95		215		Other	EFK	3055	759	219	877	759		NA
H28974 h	H							96		216		Other	EFK	3055	759	219	877	759		NA
AA488104 m H28974 m	M							97		217		Other	EFK	3055	759	219	877	759		NA
AA215311 h	H							98		218		Other	EFK	3055	759	219	877	759		NA
AA018391 h	H							99		219		Other	EFK	3055	759	219	877	759		NA
AA311714 h	H							100		220		Other	EFK	3055	759	219	877	759		NA
SGK384 h	H							101		221		Other	EFK	3055	759	219	877	759		NA
SGK384 h	H							102		222		Other	EFK	3055	759	219	877	759		NA
AA210451 m SGK384 m	M							103		223		Other	EFK	3055	759	219	877	759		NA
SGK071 2 h	H							104		224		Other	EFK	3055	759	219	877	759		NA
AA118353 m SGK071 m	M							105		225		Other	EFK	3055	759	219	877	759		NA
0186539 h	H							106		226		Other	EFK	3055	759	219	877	759		NA
AA390869 h	H							107		227		Other	EFK	3055	759	219	877	759		NA
AA390869 h	H							108		228		Other	EFK	3055	759	219	877	759		NA
AA71275 h VRK3	H							109		229		Other	VRK	1425	474	1	1422	1422		18q13
ST1575 m VRK3	M							110		230		Other	VRK	1425	474	1	1422	1422		18q13
AA452624 h MF-SK1	H							111		231		Other	VRK	1425	474	1	1422	1422		18q13
H3721 h	H							112		232		Other	VRK	1425	474	1	1422	1422		18q13
AI088655 h	H							113		233		Other	VRK	1425	474	1	1422	1422		18q13
AA039348 h	H							114		234		Other	VRK	1425	474	1	1422	1422		18q13
RR6868 h MOK6	H							115		235		Other	VRK	1425	474	1	1422	1422		18q13
PAK3 h 5585-20-11	H							116		236		Other	VRK	1425	474	1	1422	1422		18q13
SURTK106 h 2541-p-4 h	H							117		237		Other	VRK	1425	474	1	1422	1422		18q13
AA088024 m	M							118		238		Other	VRK	1425	474	1	1422	1422		18q13
SGK384 h	H							119		239		Other	VRK	1425	474	1	1422	1422		18q13
H09850 h CORK	H							120		240		Other	VRK	1425	474	1	1422	1422		18q13
NM 007170 h TESK2	H							121		241		Other	VRK	1425	474	1	1422	1422		18q13

Table 2

	Patent	Seq	Family	Group	nraa	Length	match	ID	%	Similar	nraa	Match	Description	Kinase Domain(s)	Kinase Domain(s)	Profile start	Profile end
SP ID#	na	seq	seq	seq	seq	seq	seq	seq	seq	seq	seq	seq	seq	seq	seq	seq	seq
H 1	122	AGC	GRK	2.7E-314	688	687	100	100	100	100	CAB45657.1	NP 037028.1	BARK2 [Homo sapiens]	191	453	1	281
M 2	123	AGC	GRK	1.30E-190	378	371	98	98	98	98	NP 037028.1	NP 037028.1	Adrenic receptor kinase, beta 2 (G-protein-linked receptor kin	3	143	121	281
H 3	124	AGC	GRK	5.80E-108	419	282	71	88	88	88	CAB78471.1	CAB78471.1	Serine/threonine protein kinase [Homo sapiens]	28	286	1	281
H 4	125	AGC	GRK	1.40E-137	414	414	100	100	100	100	CAB78471.1	CAB78471.1	Serine/threonine protein kinase [Homo sapiens]	23	283	1	281
H 5	126	AGC	GRK	0	729	729	100	100	100	100	NP 037386.1	NP 037386.1	TANK-binding kinase 1 [Homo sapiens]	9	304	1	281
H 6	127	AGC	NDR	1.20E-98	329	73	46	66	66	66	BAA76817.1	KIAA0973	protein [Homo sapiens]	35	310	1	281
M 7	128	AGC	NDR	1.30E-19	84	42	49	71	71	71	AAF55594.1	CG7719	gene product [Drosophila melanogaster]	24	44	242	281
H 8	129	AGC	NDR	6.10E-181	484	483	100	100	100	100	BAA76808.1	KIAA0885	protein [Homo sapiens]	90	383	1	281
H 9	130	AGC	PKC	8.90E-100	978	615	67	80	80	80	NP 002733.1	Protein kinase C, mu [Homo sapiens]	651	907	1	281	
H 10	131	AGC	PKC	1.10E-10	105	42	42	57	57	57	P05127	Protein kinase C, BETA-1 TYPE (PKC-BETA-2) [Homo sapiens]	19	24	256	281	
H 11	132	AGC	PKC	0	880	880	100	100	100	100	NP 005804.1	Protein kinase C, nu [Homo sapiens]	578	832	1	281	
H 12	133	AGC	PKC	9.4E-319	889	889	100	100	100	100	NP 037487.1	PKNbeta	[Homo sapiens]	559	818	1	281
M 13	134	AGC	PKC	1.20E-108	205	204	100	100	100	100	JC7083	Protein kinase N beta [Homo sapiens]	1	134	126	281	
H 14	135	AGC	PKC	3.80E-12	384	94	38	55	55	55	AA02485.1	Ribosomal protein S6 kinase 3 [Homo sapiens]	61	333	1	281	
H 15	136	AGC	SGK	2.80E-257	489	489	100	100	100	100	NP 036558.1	Ribosomal protein S6 kinase, 52kd, polypeptide 1 [Homo sapien	225	459	1	281	
H 16	137	AGC	SGK	7.00E-178	745	745	100	100	100	100	NP 036558.1	Ribosomal protein S6 kinase, 52kd, polypeptide 1 [Homo sapien	225	459	1	281	
H 17	138	AGC	SGK	9.80E-222	549	549	100	100	100	100	NP 036558.1	Ribosomal protein S6 kinase, 52kd, polypeptide 1 [Homo sapien	225	459	1	281	
H 18	139	AGC	SGK	9.20E-103	431	430	100	100	100	100	AA04109.1	SGK [Homo sapiens]	153	539	1	281	
M 19	140	AGC	SGK	2.80E-157	430	429	99	99	99	99	NP 035491.1	Serum/glucocorticoid regulated kinase [Mus musculus]	98	355	1	281	
M 20	141	AGC	SGK	2.00E-74	244	244	100	100	100	100	AAF12757.2	Protein kinase [Homo sapiens]	1	189	24	281	
H 21	142	AGC	SGK	4.10E-211	448	375	88	88	88	88	AAF27051.1	SGK-like protein SGK [Homo sapiens]	182	369	1	281	
H 22	143	AGC	SGK	5.80E-218	349	349	100	100	100	100	NP 009215.1	Protein tyrosine kinase 9-like (A6-related protein) [Homo sapiens]	10	17	253	281	
H 23	144	CAMK	AMPK	1.40E-19	440	88	39	61	61	61	CA04119.1	Protein tyrosine kinase 9-like (A6-related protein) [Homo sapiens]	40	333	1	281	
H 24	145	CAMK	AMPK	1.50E-165	899	468	65	77	77	77	Q15075	DCAMK1 (DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1) [Mus musculus]	398	625	1	281	
M 25	146	CAMK	AMPK	1.80E-62	297	199	67	83	83	83	AAF28875.1	CPG18 [Mus musculus]	59	297	1	281	
H 26	147	CAMK	AMPK	2.80E-48	708	181	44	60	60	60	Q15075	DCAMK1 (DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1) [Mus musculus]	415	673	1	281	
M 28	148	CAMK	AMPK	2.80E-31	806	147	55	73	73	73	AAF28875.1	CPG18 [Mus musculus]	514	771	1	281	
H 29	149	CAMK	DAPK	3.10E-121	372	372	100	100	100	100	NP 004217.1	Death-associated protein kinase-related 2	33	293	1	281	
M 30	150	CAMK	DAPK	7.90E-93	372	340	91	95	95	95	NP 004217.1	Death-associated protein kinase-related 2	32	293	1	281	
H 31	151	CAMK	DAPK	1.20E-113	414	414	100	100	100	100	NP 004751.1	Death-associated protein kinase-related 1	61	321	1	281	
H 32	152	CAMK	EMK	5.90E-165	1311	1053	80	80	80	80	BAA78443.1	KIAA0989	protein [Homo sapiens]	8	258	1	281
H 33	153	CAMK	EMK	1.20E-45	436	153	51	70	70	70	T22427	Hypothetical protein F40C5.4 - [Caenorhabditis elegans]	74	325	1	281	
H 34	154	CAMK	EMK	1.40E-32	436	122	48	65	65	65	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	56	307	1	281	
M 35	155	CAMK	EMK	1.30E-184	729	728	100	100	100	100	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	56	307	1	281	
H 36	156	CAMK	EMK	3.50E-128	462	462	100	100	100	100	AAC33487.1	R31237, 1, partial CDS [Homo sapiens]	59	340	1	281	
M 37	157	CAMK	EMK	0	1330	1235	100	100	100	100	BAA09484.1	KIAA0135	gene related to pim-1 oncogene, [Homo sapiens]	999	1258	1	281
M 38	158	CAMK	EMK	5.10E-59	230	183	79	85	85	85	BAA09484.1	KIAA0135	gene related to pim-1 oncogene, [Homo sapiens]	1	158	23	281
H 39	159	CAMK	EMK	3.00E-111	928	838	100	100	100	100	BAA34501.1	KIAA0781	protein [Homo sapiens]	20	271	1	281
H 40	160	CAMK	EMK	7.30E-80	628	367	57	69	69	69	NP 055655.1	KIAA0537	gene product [Homo sapiens]	53	304	1	281
H 41	161	CAMK	EMK	1.40E-244	714	714	100	100	100	100	NP 055655.1	KIAA0537	gene product [Homo sapiens]	61	320	1	281
H 42	162	CAMK	MLCK	8.20E-76	874	211	83	80	80	80	AAF73168.1	Homomally upregulated neuro-associated kinase [Homo sa	570	825	1	281	
H 43	163	CAMK	Tro	0	2268	2227	100	100	100	100	AAF73168.1	Skeletal muscle myosin light chain kinase [Homo sapiens]	820 & 1088	873 & 1356	1	281	
M 44	164	CAMK	Tro	7.80E-37	127	67	99	99	99	99	BAA92535.1	KIAA1297	protein [Homo sapiens]	3	78	186	281
H 45	165	CAMK	Tro	0	1287	1284	100	100	100	100	BAA92535.1	KIAA1297	protein [Homo sapiens]	985	1239	1	281
H 46	166	CKI	CKI	5.00E-20	514	114	41	63	63	63	NP 008995.1	STK with Dbl- and pleckstrin homology domains [Homo sapiens]	985	1239	1	281	
H 47	167	CKI	CKI	3.30E-89	508	181	53	65	65	65	P25323	MLCK [Dictyostelium discoideum]	116	381	1	281	
H 48	168	CMGC	CDK	8.80E-98	478	168	57	68	68	68	AAF59340.1	CG11533	gene product [Drosophila melanogaster]	34	313	1	281
H 49	169	CMGC	CDK	9.80E-39	268	138	62	79	79	79	NP 036527.1	PFTARE	protein kinase 1 [Homo sapiens]	21	471	1	281
H 49	169	CMGC	CDK	7.10E-48	247	146	59	75	75	75	NP 004187.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sa	1	191	23	281	

Table 2 (cont'd)

M 50	170	CMGC	CDK	2.90E-64	288	193	65	78	NP 004187.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	1	240	24	261
H 51	171	CMGC	CDK	1.10E-284	1490	1490	100	100	AAF38409.1	CDC2-related protein kinase 7 [Homo sapiens]	21	1020	1	261
H 52	172	CMGC	CDK	9.20E-101	534	377	82	82	AAF38508.1	NKIATRE [Homo sapiens]	4	385	1	261
M 53	173	CMGC	CDK	1.40E-128	337	225	92	92	AAF34871.1	NKIATRE alpha [Rattus norvegicus]	1	28	235	261
M 54	174	CMGC	CDK	3.00E-68	211	159	79	84	NP 038251.1	Cell cycle related kinase [Homo sapiens]	1	183	134	261
H 55	175	CMGC	CLK	1.50E-242	499	436	91	83	NP 031740.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	177	493	1	261
H 56	176	CMGC	RCK	9.10E-89	544	343	57	84	AAD127719.1	Extracellular signal-regulated kinase 7: ERK7 [Rattus norvegicus]	13	305	1	261
H 57	177	CMGC	RCK	2.30E-189	419	419	100	100	NP 056041.1	Renal tumor antigen [Homo sapiens]	4	285	1	261
H 58	178	CMGC	RCK	1.50E-180	832	832	100	100	AAF37272.1	Intestinal cell kinase [Homo sapiens]	4	284	1	261
H 59	179	CMGC	RCK	1.80E-79	413	198	60	77	P20969	MLCK [Rattus norvegicus]	109	364	1	261
H 60	180	Microb	PK	2.50E-45	253	102	46	67	AAF50799.1	CG10873 gene product [Drosophila melanogaster]	101	187	85	147
H 61	181	Other	C28C2	2.30E-158	509	258	100	100	CAB70864.1	Hypothetical protein [Homo sapiens]	2	287	1	261
M 62	182	Other	C28C2	1.60E-152	281	243	94	98	CAB70864.1	Hypothetical protein [Homo sapiens]	59	86	235	261
H 63	183	Other	C28C2	6.70E-300	1952	1193	99	99	NP 056638.1	KIAA0344 gene product [Homo sapiens]	221	479	1	261
H 64	184	Other	C28C2	1.10E-254	535	535	100	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	73	327	1	261
M 65	185	Other	C28C2	2.50E-208	378	372	98	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	1	170	85	261
H 66	186	Other	CAMKK	3.80E-148	588	588	100	100	AAD31507.1	Ca2+/calmodulin-dependent protein kinase beta [Homo sapiens]	165	448	1	261
H 67	187	Other	CTRI	9.90E-24	287	87	33	52	QJ1743	Hypothetical 33.5K protein - rab5b fibrona virus	24	285	1	261
H 68	188	Other	DYRK	0	1171	1137	97	98	AAD32668.1	Nuclear body associated kinase 1a [Mus musculus]	199	527	1	261
H 69	189	Other	DYRK	2.10E-280	563	553	100	100	NP 035773.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	174	467	1	261
M 70	190	Other	DYRK	2.30E-95	168	149	90	98	NP 035773.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	76	103	235	261
H 71	191	Other	EIFK	0	1649	1493	90	98	NP 038747.1	GCN2 eIF2alpha kinase [Mus musculus]	280 & 590	539 & 1001	1	261
H 72	192	Other	EIFK	1.50E-220	253	102	46	67	NP 056228.1	Heme-regulated initiation factor 2-alpha kinase [Homo sapiens]	167	583	1	261
H 73	193	Other	Endop	2.50E-45	216	100	45	94	AAF50799.1	CG10873 gene product [Drosophila melanogaster]	101	187	85	147
M 74	194	Other	Endop	3.70E-45	596	596	100	100	AAF50799.1	CG10873 gene product [Drosophila melanogaster]	116	150	116	147
M 75	195	Other	IRAK	0	596	596	100	100	NP 009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	185	443	1	261
M 76	196	Other	IRAK	1.20E-170	392	293	75	85	NP 009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	516	777	1	261
H 77	197	Other	IRE	1.5e-323	922	748	82	89	NP 038148.1	Ins1, insulin-requiring 1 gene [Mus musculus]	32	318	1	261
H 78	198	Other	KYK2	8.70E-40	225	102	45	62	AAF48758.1	CG8173 gene product [Drosophila melanogaster]	12	268	1	261
M 79	199	Other	KYK2	5.90E-32	280	108	32	90	NP 009101.1	Insulin-specific kinase 2 [Homo sapiens]	16	259	1	261
M 80	200	Other	LINK	2.90E-17	41	37	92	95	NP 009101.1	Mixed lineage kinase [Homo sapiens]	12	39	101	128
H 81	201	Other	MLK	2.50E-282	800	799	100	100	AAD63490.1	Puative protein-tyrosine kinase [Homo sapiens]	483	723	1	261
H 82	202	Other	MLK	8.60E-251	835	835	100	100	AAD29632.1	KIAA0472 protein [Homo sapiens]	357	620	1	261
H 83	203	Other	RIP	2.20E-158	634	395	100	100	BAA32317.1	Receptor interacting protein 3 [Mus musculus]	7	27	181	202
M 84	204	Other	RIP	5.30E-158	289	288	100	100	CAF55300.1	Hypothetical protein [Homo sapiens]	57	83	50	78
H 85	205	Other	SCY1	0	688	688	100	100	BAA92981.1	KIAA1360 protein [Homo sapiens]	32	327	1	261
H 86	206	Other	SCY1	1.70E-209	505	354	98	98	AAF58933.1	CG1973 gene product [Drosophila melanogaster]	85	131	47	116
H 87	207	Other	SCY1	2.20E-157	808	398	45	61	NP 055185.1	Unnamed protein product [Homo sapiens]	230	305	81	143
H 88	208	Other	SLOB7	7.40E-188	849	849	100	100	NP 033481.1	Serine/threonine kinase 22A [Homo sapiens]	10	285	1	261
H 89	209	Other	SRPK	5.80E-252	533	533	100	100	NP 033481.1	Serine/threonine kinase 22A (spemogenesis associated) [Mus musculus]	25	280	1	261
H 90	210	Other	STK22A	3.80E-53	268	122	46	70	NP 033462.1	Serine/threonine kinase 22A (spemogenesis associated) [Mus musculus]	12	272	1	261
H 91	211	Other	STK22	2.70E-52	268	127	48	68	NP 033462.1	Serine/threonine kinase 22B (spemogenesis associated) [Mus musculus]	1	213	7	261
M 92	212	Other	STK22A	4.80E-16	292	112	45	64	NP 033461.1	Serine/threonine kinase 22B (spemogenesis associated) [Mus musculus]	10	285	1	261
H 93	213	Other	STK22A	5.10E-123	358	322	90	96	NP 033461.1	Serine/threonine kinase 22B (spemogenesis associated) [Mus musculus]	25	280	1	261
H 94	214	Other	TSK	2.10E-33	273	122	46	62	NP 033461.1	Serine/threonine kinase 22A (spemogenesis associated) [Mus musculus]	12	272	1	261
H 95	215	Other	TSK	2.50E-32	216	93	41	58	NP 033461.1	Serine/threonine kinase 22A (spemogenesis associated) [Mus musculus]	1	213	7	261
H 96	216	Other	UNC	0.000082	333	57	36	56	AAD32787.1	Puative protein kinase [Arabidopsis thaliana]	1	329	1	261
H 97	217	Other	UNC	0.002492	412	53	37	52	BAA77341.1	UNC-51-like kinase (ULK) 2 [Mus musculus]	80	408	1	261
H 98	218	Other	UNC	0.001098	341	50	38	58	BAA77341.1	UNC-51-like kinase (ULK) 2 [Mus musculus]	8	340	1	261
H 99	219	Other	UNC	1.90E-68	480	247	100	100	T17265	Hypothetical protein DKF2p343C131.1 - human (fragment)	57	313	1	261
H 100	220	Other	UNC	1.80E-208	565	468	96	96	BAA81270.1	Unamed protein product [Homo sapiens]	4	265	1	261
H 101	221	Other	Unique	6.70E-10	39	27	59	80	AAD00575.1	Serum-inducible kinase [Homo sapiens]	1	39	84	124

Table 2 (cont'd)

M	103	222	Other	Unique	0.000322	349	38	30	50	CAA18118.1	Serine/threonine protein kinase like protein [Arabidopsis thaliana]	80	159	1	88
H	104	223	Other	Unique	0.00128	704	54	30	45	BAA8578.1	KIAA1284 protein [Homo sapiens]	1	248	25	261
M	105	224	Other	Unique	0.007385	640	25	42	81	AAF47518.1	The gene product [Drosophila melanogaster]	9	104	188	261
H	106	225	Other	Unique	0.31334	540	52	30	42	P10162	SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [Homo sapiens]	1	272	18	73
M	107	226	Other	Unique	0.022848	365	25	34	57	NP_006278.1	testis-specific kinase 1 [Homo sapiens]	68	66	42	71
H	108	227	Other	VRK	3.10E-263	474	474	100	100	BAA80769.1	Vaccinia related kinase 3 [Homo sapiens]	247	316	63	136
M	109	228	Other	VRK	1.20E-111	234	191	82	90	BAA90769.1	(AB031052) vaccinia related kinase 3 [Homo sapiens]	7	78	63	136
H	110	229	Other	YPL236.ac	7.40E-144	305	304	100	100	AAC28337.1	MPK [Homo sapiens]	20	290	1	261
H	111	230	Other	YQ09.c8	5.10E-46	581	135	43	83	AAF46188.1	CG4523 gene product [Drosophila melanogaster]	156	507	1	261
H	112	231	STE	NEK	3.30E-30	698	122	48	87	P01954	NEK1 (NIMA-RELATED PROTEIN KINASE 1) [Mus musculus]	4	261	1	261
H	113	232	STE	NEK	2.70E-119	836	357	88	86	AAD31839.1	(AC007055) unknown [Homo sapiens]	52	308	1	261
H	114	233	STE	STE11	1.10E-291	1011	1011	100	100	NP_004663.1	mitogen-activated protein kinase kinase kinase 6 [Homo sapiens]	376	629	6	261
H	115	234	STE	STE20-02	7.70E-177	719	719	100	100	BAA84194.1	(AB040812) protein kinase PAK5 [Homo sapiens]	449	700	1	261
H	116	235	TK	RTK-20	4.80E-24	495	77	38	56	AAA98465.1	(U40427) protein tyrosine kinase [Mus musculus]	187	453	1	261
M	117	236	TK	RTK-20	5.30E-18	183	53	39	57	NP_032036.1	fibroblast growth factor receptor 3 [Mus musculus]	8	143	123	261
H	118	237	AGC	SGK	6.30E-112	367	367	100	100	AAF12757.2	SGK2alpha protein kinase [Homo sapiens]	35	292	1	261
H	120	238	CMGC	CDK	2.80E-137	452	452	100	100	NP_039251.1	Cell cycle related kinase [Homo sapiens]	4	287	1	261
H	121	239	Other	LIMK	6.50E-233	555	555	100	100	NP_009101.1	Testis-specific kinase 2 [Homo sapiens]	62	293	5	261



164  
Table 3[illegible]

165  
Table 3 (cont'd)

[illegible]

167  
Table 3 (cont'd)

Tissue	Tumor-yes	Normal-yes	Tumor - to	Tumor calls	Normal	Ends	pos	SEQ 17 AM SEQ	20 SQ SEQ 23 PTSEQ	29 AM SEQ	29 SQ SEQ 31 PTSEQ	32 AM SEQ	32 SQ SEQ 34 PTSEQ	35 AM SEQ	35 SQ SEQ 37 PTSEQ	38 AM SEQ	38 SQ SEQ 40 PTSEQ	41 AM SEQ	41 SQ SEQ 43 PTSEQ	44 AM SEQ	44 SQ SEQ 46 PTSEQ	47 AM SEQ	47 SQ SEQ 49 PTSEQ	50 AM SEQ	50 SQ SEQ 52 PTSEQ	51 AM SEQ	51 SQ SEQ 53 PTSEQ	52 AM SEQ	52 SQ SEQ 54 PTSEQ	53 AM SEQ	53 SQ SEQ 55 PTSEQ	54 AM SEQ	54 SQ SEQ 56 PTSEQ	55 AM SEQ	55 SQ SEQ 57 PTSEQ	56 AM SEQ	56 SQ SEQ 58 PTSEQ	57 AM SEQ	57 SQ SEQ 59 PTSEQ	58 AM SEQ	58 SQ SEQ 60 PTSEQ	59 AM SEQ	59 SQ SEQ 61 PTSEQ	60 AM SEQ	60 SQ SEQ 62 PTSEQ	61 AM SEQ	61 SQ SEQ 63 PTSEQ	62 AM SEQ	62 SQ SEQ 64 PTSEQ	63 AM SEQ	63 SQ SEQ 65 PTSEQ	64 AM SEQ	64 SQ SEQ 66 PTSEQ	65 AM SEQ	65 SQ SEQ 67 PTSEQ	66 AM SEQ	66 SQ SEQ 68 PTSEQ	67 AM SEQ	67 SQ SEQ 69 PTSEQ	68 AM SEQ	68 SQ SEQ 70 PTSEQ	69 AM SEQ	69 SQ SEQ 71 PTSEQ	70 AM SEQ	70 SQ SEQ 72 PTSEQ	71 AM SEQ	71 SQ SEQ 73 PTSEQ	72 AM SEQ	72 SQ SEQ 74 PTSEQ	73 AM SEQ	73 SQ SEQ 75 PTSEQ	74 AM SEQ	74 SQ SEQ 76 PTSEQ	75 AM SEQ	75 SQ SEQ 77 PTSEQ	76 AM SEQ	76 SQ SEQ 78 PTSEQ	77 AM SEQ	77 SQ SEQ 79 PTSEQ	78 AM SEQ	78 SQ SEQ 80 PTSEQ	79 AM SEQ	79 SQ SEQ 81 PTSEQ	80 AM SEQ	80 SQ SEQ 82 PTSEQ	81 AM SEQ	81 SQ SEQ 83 PTSEQ	82 AM SEQ	82 SQ SEQ 84 PTSEQ	83 AM SEQ	83 SQ SEQ 85 PTSEQ	84 AM SEQ	84 SQ SEQ 86 PTSEQ	85 AM SEQ	85 SQ SEQ 87 PTSEQ	86 AM SEQ	86 SQ SEQ 88 PTSEQ	87 AM SEQ	87 SQ SEQ 89 PTSEQ	88 AM SEQ	88 SQ SEQ 90 PTSEQ	89 AM SEQ	89 SQ SEQ 91 PTSEQ	90 AM SEQ	90 SQ SEQ 92 PTSEQ	91 AM SEQ	91 SQ SEQ 93 PTSEQ	92 AM SEQ	92 SQ SEQ 94 PTSEQ	93 AM SEQ	93 SQ SEQ 95 PTSEQ	94 AM SEQ	94 SQ SEQ 96 PTSEQ	95 AM SEQ	95 SQ SEQ 97 PTSEQ	96 AM SEQ	96 SQ SEQ 98 PTSEQ	97 AM SEQ	97 SQ SEQ 99 PTSEQ	98 AM SEQ	98 SQ SEQ 100 PTSEQ	99 AM SEQ	99 SQ SEQ 101 PTSEQ	100 AM SEQ	100 SQ SEQ 102 PTSEQ	101 AM SEQ	101 SQ SEQ 103 PTSEQ	102 AM SEQ	102 SQ SEQ 104 PTSEQ	103 AM SEQ	103 SQ SEQ 105 PTSEQ	104 AM SEQ	104 SQ SEQ 106 PTSEQ	105 AM SEQ	105 SQ SEQ 107 PTSEQ	106 AM SEQ	106 SQ SEQ 108 PTSEQ	107 AM SEQ	107 SQ SEQ 109 PTSEQ	108 AM SEQ	108 SQ SEQ 110 PTSEQ	109 AM SEQ	109 SQ SEQ 111 PTSEQ	110 AM SEQ	110 SQ SEQ 112 PTSEQ	111 AM SEQ	111 SQ SEQ 113 PTSEQ	112 AM SEQ	112 SQ SEQ 114 PTSEQ	113 AM SEQ	113 SQ SEQ 115 PTSEQ	114 AM SEQ	114 SQ SEQ 116 PTSEQ	115 AM SEQ	115 SQ SEQ 117 PTSEQ	116 AM SEQ	116 SQ SEQ 118 PTSEQ	117 AM SEQ	117 SQ SEQ 119 PTSEQ	118 AM SEQ	118 SQ SEQ 120 PTSEQ	119 AM SEQ	119 SQ SEQ 121 PTSEQ	120 AM SEQ	120 SQ SEQ 122 PTSEQ	121 AM SEQ	121 SQ SEQ 123 PTSEQ	122 AM SEQ	122 SQ SEQ 124 PTSEQ	123 AM SEQ	123 SQ SEQ 125 PTSEQ	124 AM SEQ	124 SQ SEQ 126 PTSEQ	125 AM SEQ	125 SQ SEQ 127 PTSEQ	126 AM SEQ	126 SQ SEQ 128 PTSEQ	127 AM SEQ	127 SQ SEQ 129 PTSEQ	128 AM SEQ	128 SQ SEQ 130 PTSEQ	129 AM SEQ	129 SQ SEQ 131 PTSEQ	130 AM SEQ	130 SQ SEQ 132 PTSEQ	131 AM SEQ	131 SQ SEQ 133 PTSEQ	132 AM SEQ	132 SQ SEQ 134 PTSEQ	133 AM SEQ	133 SQ SEQ 135 PTSEQ	134 AM SEQ	134 SQ SEQ 136 PTSEQ	135 AM SEQ	135 SQ SEQ 137 PTSEQ	136 AM SEQ	136 SQ SEQ 138 PTSEQ	137 AM SEQ	137 SQ SEQ 139 PTSEQ	138 AM SEQ	138 SQ SEQ 140 PTSEQ	139 AM SEQ	139 SQ SEQ 141 PTSEQ	140 AM SEQ	140 SQ SEQ 142 PTSEQ	141 AM SEQ	141 SQ SEQ 143 PTSEQ	142 AM SEQ	142 SQ SEQ 144 PTSEQ	143 AM SEQ	143 SQ SEQ 145 PTSEQ	144 AM SEQ	144 SQ SEQ 146 PTSEQ	145 AM SEQ	145 SQ SEQ 147 PTSEQ	146 AM SEQ	146 SQ SEQ 148 PTSEQ	147 AM SEQ	147 SQ SEQ 149 PTSEQ	148 AM SEQ	148 SQ SEQ 150 PTSEQ	149 AM SEQ	149 SQ SEQ 151 PTSEQ	150 AM SEQ	150 SQ SEQ 152 PTSEQ	151 AM SEQ	151 SQ SEQ 153 PTSEQ	152 AM SEQ	152 SQ SEQ 154 PTSEQ	153 AM SEQ	153 SQ SEQ 155 PTSEQ	154 AM SEQ	154 SQ SEQ 156 PTSEQ	155 AM SEQ	155 SQ SEQ 157 PTSEQ	156 AM SEQ	156 SQ SEQ 158 PTSEQ	157 AM SEQ	157 SQ SEQ 159 PTSEQ	158 AM SEQ	158 SQ SEQ 160 PTSEQ	159 AM SEQ	159 SQ SEQ 161 PTSEQ	160 AM SEQ	160 SQ SEQ 162 PTSEQ	161 AM SEQ	161 SQ SEQ 163 PTSEQ	162 AM SEQ	162 SQ SEQ 164 PTSEQ	163 AM SEQ	163 SQ SEQ 165 PTSEQ	164 AM SEQ	164 SQ SEQ 166 PTSEQ	165 AM SEQ	165 SQ SEQ 167 PTSEQ	166 AM SEQ	166 SQ SEQ 168 PTSEQ	167 AM SEQ	167 SQ SEQ 169 PTSEQ	168 AM SEQ	168 SQ SEQ 170 PTSEQ	169 AM SEQ	169 SQ SEQ 171 PTSEQ	170 AM SEQ	170 SQ SEQ 172 PTSEQ	171 AM SEQ	171 SQ SEQ 173 PTSEQ	172 AM SEQ	172 SQ SEQ 174 PTSEQ	173 AM SEQ	173 SQ SEQ 175 PTSEQ	174 AM SEQ	174 SQ SEQ 176 PTSEQ	175 AM SEQ	175 SQ SEQ 177 PTSEQ	176 AM SEQ	176 SQ SEQ 178 PTSEQ	177 AM SEQ	177 SQ SEQ 179 PTSEQ	178 AM SEQ	178 SQ SEQ 180 PTSEQ	179 AM SEQ	179 SQ SEQ 181 PTSEQ	180 AM SEQ	180 SQ SEQ 182 PTSEQ	181 AM SEQ	181 SQ SEQ 183 PTSEQ	182 AM SEQ	182 SQ SEQ 184 PTSEQ	183 AM SEQ	183 SQ SEQ 185 PTSEQ	184 AM SEQ	184 SQ SEQ 186 PTSEQ	185 AM SEQ	185 SQ SEQ 187 PTSEQ	186 AM SEQ	186 SQ SEQ 188 PTSEQ	187 AM SEQ	187 SQ SEQ 189 PTSEQ	188 AM SEQ	188 SQ SEQ 190 PTSEQ	189 AM SEQ	189 SQ SEQ 191 PTSEQ	190 AM SEQ	190 SQ SEQ 192 PTSEQ	191 AM SEQ	191 SQ SEQ 193 PTSEQ	192 AM SEQ	192 SQ SEQ 194 PTSEQ	193 AM SEQ	193 SQ SEQ 195 PTSEQ	194 AM SEQ	194 SQ SEQ 196 PTSEQ	195 AM SEQ	195 SQ SEQ 197 PTSEQ	196 AM SEQ	196 SQ SEQ 198 PTSEQ	197 AM SEQ	197 SQ SEQ 199 PTSEQ	198 AM SEQ	198 SQ SEQ 200 PTSEQ	199 AM SEQ	199 SQ SEQ 201 PTSEQ	200 AM SEQ	200 SQ SEQ 202 PTSEQ	201 AM SEQ	201 SQ SEQ 203 PTSEQ	202 AM SEQ	202 SQ SEQ 204 PTSEQ	203 AM SEQ	203 SQ SEQ 205 PTSEQ	204 AM SEQ	204 SQ SEQ 206 PTSEQ	205 AM SEQ	205 SQ SEQ 207 PTSEQ	206 AM SEQ	206 SQ SEQ 208 PTSEQ	207 AM SEQ	207 SQ SEQ 209 PTSEQ	208 AM SEQ	208 SQ SEQ 210 PTSEQ	209 AM SEQ	209 SQ SEQ 211 PTSEQ	210 AM SEQ	210 SQ SEQ 212 PTSEQ	211 AM SEQ	211 SQ SEQ 213 PTSEQ	212 AM SEQ	212 SQ SEQ 214 PTSEQ	213 AM SEQ	213 SQ SEQ 215 PTSEQ	214 AM SEQ	214 SQ SEQ 216 PTSEQ	215 AM SEQ	215 SQ SEQ 217 PTSEQ	216 AM SEQ	216 SQ SEQ 218 PTSEQ	217 AM SEQ	217 SQ SEQ 219 PTSEQ	218 AM SEQ	218 SQ SEQ 220 PTSEQ	219 AM SEQ	219 SQ SEQ 221 PTSEQ	220 AM SEQ	220 SQ SEQ 222 PTSEQ	221 AM SEQ	221 SQ SEQ 223 PTSEQ	222 AM SEQ	222 SQ SEQ 224 PTSEQ	223 AM SEQ	223 SQ SEQ 225 PTSEQ	224 AM SEQ	224 SQ SEQ 226 PTSEQ	225 AM SEQ	225 SQ SEQ 227 PTSEQ	226 AM SEQ	226 SQ SEQ 228 PTSEQ	227 AM SEQ	227 SQ SEQ 229 PTSEQ	228 AM SEQ	228 SQ SEQ 230 PTSEQ	229 AM SEQ	229 SQ SEQ 231 PTSEQ	230 AM SEQ	230 SQ SEQ 232 PTSEQ	231 AM SEQ	231 SQ SEQ 233 PTSEQ	232 AM SEQ	232 SQ SEQ 234 PTSEQ	233 AM SEQ	233 SQ SEQ 235 PTSEQ	234 AM SEQ	234 SQ SEQ 236 PTSEQ	235 AM SEQ	235 SQ SEQ 237 PTSEQ	236 AM SEQ	236 SQ SEQ 238 PTSEQ	237 AM SEQ	237 SQ SEQ 239 PTSEQ	238 AM SEQ	238 SQ SEQ 240 PTSEQ	239 AM SEQ	239 SQ SEQ 241 PTSEQ	240 AM SEQ	240 SQ SEQ 242 PTSEQ	241 AM SEQ	241 SQ SEQ 243 PTSEQ	242 AM SEQ	242 SQ SEQ 244 PTSEQ	243 AM SEQ	243 SQ SEQ 245 PTSEQ	244 AM SEQ	244 SQ SEQ 246 PTSEQ	245 AM SEQ	245 SQ SEQ 247 PTSEQ	246 AM SEQ	246 SQ SEQ 248 PTSEQ	247 AM SEQ	247 SQ SEQ 249 PTSEQ	248 AM SEQ	248 SQ SEQ 250 PTSEQ	249 AM SEQ	249 SQ SEQ 251 PTSEQ	250 AM SEQ	250 SQ SEQ 252 PTSEQ	251 AM SEQ	251 SQ SEQ 253 PTSEQ	252 AM SEQ	252 SQ SEQ 254 PTSEQ	253 AM SEQ	253 SQ SEQ 255 PTSEQ	254 AM SEQ	254 SQ SEQ 256 PTSEQ	255 AM SEQ	255 SQ SEQ 257 PTSEQ	256 AM SEQ	256 SQ SEQ 258 PTSEQ	257 AM SEQ	257 SQ SEQ 259 PTSEQ	258 AM SEQ	258 SQ SEQ 260 PTSEQ	259 AM SEQ	259 SQ SEQ 261 PTSEQ	260 AM SEQ	260 SQ SEQ 262 PTSEQ	261 AM SEQ	261 SQ SEQ 263 PTSEQ	262 AM SEQ	262 SQ SEQ 264 PTSEQ	263 AM SEQ	263 SQ SEQ 265 PTSEQ	264 AM SEQ	264 SQ SEQ 266 PTSEQ	265 AM SEQ	265 SQ SEQ 267 PTSEQ	266 AM SEQ	266 SQ SEQ 268 PTSEQ	267 AM SEQ	267 SQ SEQ 269 PTSEQ	268 AM SEQ	268 SQ SEQ 270 PTSEQ	269 AM SEQ	269 SQ SEQ 271 PTSEQ	270 AM SEQ	270 SQ SEQ 272 PTSEQ	271 AM SEQ	271 SQ SEQ 273 PTSEQ	272 AM SEQ	272 SQ SEQ 274 PTSEQ	273 AM SEQ	273 SQ SEQ 275 PTSEQ	274 AM SEQ	274 SQ SEQ 276 PTSEQ	275 AM SEQ	275 SQ SEQ 277 PTSEQ	276 AM SEQ	276 SQ SEQ 278 PTSEQ	277 AM SEQ	277 SQ SEQ 279 PTSEQ	278 AM SEQ	278 SQ SEQ 280 PTSEQ	279 AM SEQ	279 SQ SEQ 281 PTSEQ	280 AM SEQ	280 SQ SEQ 282 PTSEQ	281 AM SEQ	281 SQ SEQ 283 PTSEQ	282 AM SEQ	282 SQ SEQ 284 PTSEQ	283 AM SEQ	283 SQ SEQ 285 PTSEQ	284 AM SEQ	284 SQ SEQ 286 PTSEQ	285 AM SEQ	285 SQ SEQ 287 PTSEQ	286 AM SEQ	286 SQ SEQ 288 PTSEQ	287 AM SEQ	287 SQ SEQ 289 PTSEQ	288 AM SEQ	288 SQ SEQ 290 PTSEQ	289 AM SEQ	289 SQ SEQ 291 PTSEQ	290 AM SEQ	290 SQ SEQ 292 PTSEQ	291 AM SEQ	291 SQ SEQ 293 PTSEQ	292 AM SEQ	292 SQ SEQ 294 PTSEQ	293 AM SEQ	293 SQ SEQ 295 PTSEQ	294 AM SEQ	294 SQ SEQ 296 PTSEQ	295 AM SEQ	295 SQ SEQ 297 PTSEQ	296 AM SEQ	296 SQ SEQ 298 PTSEQ	297 AM SEQ	297 SQ SEQ 299 PTSEQ	298 AM SEQ	298 SQ SEQ 300 PTSEQ	299 AM SEQ	299 SQ SEQ 301 PTSEQ	300 AM SEQ	300 SQ SEQ 302 PTSEQ	301 AM SEQ	301 SQ SEQ 303 PTSEQ	302 AM SEQ	302 SQ SEQ 304 PTSEQ	303 AM SEQ	303 SQ SEQ 305 PTSEQ	304 AM SEQ	304 SQ SEQ 306 PTSEQ	305 AM SEQ	305 SQ SEQ 307 PTSEQ	306 AM SEQ	306 SQ SEQ 308 PTSEQ	307 AM SEQ	307 SQ SEQ 309 PTSEQ	308 AM SEQ	308 SQ SEQ 310 PTSEQ	309 AM SEQ	309 SQ SEQ 311 PTSEQ	310 AM SEQ	310 SQ SEQ 312 PTSEQ	311 AM SEQ	311 SQ SEQ 313 PTSEQ	312 AM SEQ	312 SQ SEQ 314 PTSEQ	313 AM SEQ	313 SQ SEQ 315 PTSEQ	314 AM SEQ	314 SQ SEQ 316 PTSEQ	315 AM SEQ	315 SQ SEQ 317 PTSEQ	316 AM SEQ	316 SQ SEQ 318 PTSEQ	317 AM SEQ	317 SQ SEQ 319 PTSEQ	318 AM SEQ	318 SQ SEQ 320 PTSEQ	319 AM SEQ	319 SQ SEQ 321 PTSEQ	320 AM SEQ	320 SQ SEQ 322 PTSEQ	321 AM SEQ	321 SQ SEQ 323 PTSEQ	322 AM SEQ	322 SQ SEQ 324 PTSEQ	323 AM SEQ	323 SQ SEQ 325 PTSEQ	324 AM SEQ	324 SQ SEQ 326 PTSEQ	325 AM SEQ	325 SQ SEQ 327 PTSEQ	326 AM SEQ	326 SQ SEQ 328 PTSEQ	327 AM SEQ	327 SQ SEQ 329 PTSEQ	328 AM SEQ	328 SQ SEQ 330 PTSEQ	329 AM SEQ	329 SQ SEQ 331 PTSEQ	330 AM SEQ	330 SQ SEQ 332 PTSEQ	331 AM SEQ	331 SQ SEQ 333 PTSEQ	332 AM SEQ	332 SQ SEQ 334 PTSEQ	333 AM SEQ	333 SQ SEQ 335 PTSEQ	334 AM SEQ	334 SQ SEQ 336 PTSEQ	335 AM SEQ	335 SQ SEQ 337 PTSEQ	336 AM SEQ	336 SQ SEQ 338 PTSEQ	337 AM SEQ	337 SQ SEQ 339 PTSEQ	338 AM SEQ	338 SQ SEQ 340 PTSEQ	339 AM SEQ	339 SQ SEQ 341 PTSEQ	340 AM SEQ	340 SQ SEQ 342 PTSEQ	341 AM SEQ	341 SQ SEQ 343 PTSEQ	342 AM SEQ	342 SQ SEQ 344 PTSEQ	343 AM SEQ	343 SQ SEQ 345 PTSEQ	344 AM SEQ	344 SQ SEQ 346 PTSEQ	345 AM SEQ	345 SQ SEQ 347 PTSEQ	346 AM SEQ	346 SQ SEQ 348 PTSEQ	347 AM SEQ	347 SQ SEQ 349 PTSEQ	348 AM SEQ	348 SQ SEQ 350 PTSEQ	349 AM SEQ	349 SQ SEQ 351 PTSEQ	350 AM SEQ	350 SQ SEQ 352 PTSEQ	351 AM SEQ	351 SQ SEQ 353 PTSEQ	352 AM SEQ	352 SQ SEQ 354 PTSEQ	353 AM SEQ	353 SQ SEQ 355 PTSEQ	354 AM SEQ	354 SQ SEQ 356 PTSEQ	355 AM SEQ	355 SQ SEQ 357 PTSEQ	356 AM SEQ	356 SQ SEQ 358 PTSEQ	357 AM SEQ	357 SQ SEQ 359 PTSEQ	358 AM SEQ	358 SQ SEQ 360 PTSEQ	359 AM SEQ	359 SQ SEQ 361 PTSEQ	360 AM SEQ	360 SQ SEQ 362 PTSEQ	361 AM SEQ	361 SQ SEQ 363 PTSEQ	362 AM SEQ	362 SQ SEQ 364 PTSEQ	363 AM SEQ	363 SQ SEQ 365 PTSEQ	364 AM SEQ	364 SQ SEQ 366 PTSEQ	365 AM SEQ	365 SQ SEQ 367 PTSEQ	366 AM SEQ	366 SQ SEQ 368 PTSEQ	367 AM SEQ	367 SQ SEQ 369 PTSEQ	368 AM SEQ	368 SQ SEQ 370 PTSEQ	369 AM SEQ	369 SQ SEQ 371 PTSEQ	370 AM SEQ	370 SQ SEQ 372 PTSEQ	371 AM SEQ	371 SQ SEQ 373 PTSEQ	372 AM SEQ	372 SQ SEQ 374 PTSEQ	373 AM SEQ	373 SQ SEQ 375 PTSEQ	374 AM SEQ	374 SQ SEQ 376 PTSEQ	375 AM SEQ	375 SQ SEQ 377 PTSEQ	376 AM SEQ	376 SQ SEQ 378 PTSEQ	377 AM SEQ	377 SQ SEQ 379 PTSEQ	378 AM SEQ	378 SQ SEQ 380 PTSEQ	379 AM SEQ	379 SQ SEQ 381 PTSEQ	380 AM SEQ	380 SQ SEQ 382 PTSEQ	381 AM SEQ	381 SQ SEQ 383 PTSEQ	382 AM SEQ	382 SQ SEQ 384 PTSEQ	383 AM SEQ	383 SQ SEQ 385 PTSEQ	384 AM SEQ	384 SQ SEQ 386 PTSEQ	385 AM SEQ	385 SQ SEQ 387 PTSEQ	386 AM SEQ	386 SQ SEQ 388 PTSEQ	387 AM SEQ	387 SQ SEQ 389 PTSEQ	388 AM SEQ	388 SQ SEQ 390 PTSEQ	389 AM SEQ	389 SQ SEQ 391 PTSEQ	390 AM SEQ	390 SQ SEQ 392 PTSEQ	391 AM SEQ	391 SQ SEQ 393 PTSEQ	392 AM SEQ	392 SQ SEQ 394 PTSEQ	393 AM SEQ	393 SQ SEQ 395 PTSEQ	394 AM SEQ	394 SQ SEQ 396 PTSEQ	395 AM SEQ	395 SQ SEQ 397 PTSEQ	396 AM SEQ	396 SQ SEQ 398 PTSEQ	397 AM SEQ	397 SQ SEQ 399 PTSEQ	398 AM SEQ	398 SQ SEQ 400 PTSEQ	399 AM SEQ	399 SQ SEQ 401 PTSEQ	400 AM SEQ	400 SQ SEQ 402 PTSEQ	401 AM SEQ	401 SQ SEQ 403 PTSEQ	402 AM SEQ	402 SQ SEQ 404 PTSEQ	403 AM SEQ	403 SQ SEQ 405 PTSEQ	404 AM SEQ	404 SQ SEQ 406 PTSEQ	405 AM SEQ	405 SQ SEQ 407 PTSEQ	406 AM SEQ	406 SQ SEQ 408 PTSEQ	407 AM SEQ	407 SQ SEQ 409 PTSEQ	408 AM SEQ	408 SQ SEQ 410 PTSEQ	409 AM SEQ	409 SQ SEQ 411 PTSEQ	410 AM SEQ	410 SQ SEQ 412 PTSEQ	411 AM SEQ	411 SQ SEQ 413 PTSEQ	412 AM SEQ	412 SQ SEQ 414 PTSEQ	413 AM SEQ	413 SQ SEQ 415 PTSEQ	414 AM SEQ	414 SQ SEQ 416 PTSEQ	415 AM SEQ	415 SQ SEQ 417 PTSEQ	416 AM SEQ	416 SQ SEQ 418 PTSEQ	417 AM SEQ	417 SQ SEQ 419 PTSEQ	418 AM SEQ	418 SQ SEQ 420 PTSEQ	419 AM SEQ	419 SQ SEQ 421 PTSEQ	420 AM SEQ	420 SQ SEQ 422 PTSEQ	421 AM SEQ	421 SQ SEQ 423 PTSEQ	422 AM SEQ	422 SQ SEQ 424 PTSEQ	423 AM SEQ	423 SQ SEQ 425 PTSEQ	424 AM SEQ	424 SQ SEQ 426 PTSEQ	425 AM SEQ	425 SQ SEQ 427 PTSEQ	426 AM SEQ	426 SQ SEQ 428 PTSEQ	427 AM SEQ	427 SQ SEQ 429 PTSEQ	428 AM SEQ	428 SQ SEQ 430 PTSEQ	429 AM SEQ	429 SQ SEQ 431 PTSEQ	430 AM SEQ	430 SQ SEQ 432 PTSEQ	431 AM SEQ	431 SQ SEQ 433 PTSEQ	432 AM SEQ	432 SQ SEQ 434 PTSEQ	433 AM SEQ	433 SQ SEQ 435 PTSEQ	434 AM SEQ	434 SQ SEQ 436 PTSEQ	435 AM SEQ	435 SQ SEQ 437 PTSEQ	436 AM SEQ	436 SQ SEQ 438 PTSEQ	437 AM SEQ	437 SQ SEQ 439 PTSEQ	438 AM SEQ	438 SQ SEQ 440 PTSEQ	439 AM SEQ	439 SQ SEQ 441 PTSEQ	440 AM SEQ	440 SQ SEQ 442 PTSEQ	441 AM SEQ	441 SQ SEQ 443 PTSEQ	442 AM SEQ	442 SQ SEQ 444 PTSEQ	443 AM SEQ	443 SQ SEQ 445 PTSEQ	444 AM SEQ	444 SQ SEQ 446 PTSEQ	445 AM SEQ	445 SQ SEQ 447 PTSEQ	446 AM SEQ	446 SQ SEQ 448 PTSEQ	447 AM SEQ	447 SQ SEQ 449 PTSEQ	448 AM SEQ	448 SQ SEQ 450 PTSEQ	449 AM SEQ	449 SQ SEQ 451 PTSEQ	450 AM SEQ	450 SQ SEQ 452 PTSEQ	451 AM SEQ	451 SQ SEQ 453 PTSEQ	452 AM SEQ	452 SQ SEQ 454 PTSEQ	453 AM SEQ	453 SQ SEQ 455 PTSEQ	454 AM SEQ	454 SQ SEQ 456 PTSEQ	455 AM SEQ	455 SQ SEQ 457 PTSEQ	456 AM SEQ	456 SQ SEQ 458 PTSEQ	457 AM SEQ	457 SQ SEQ 459 PTSEQ	458 AM SEQ	458 SQ SEQ 460 PTSEQ	459 AM SEQ	459 SQ SEQ 461 PTSEQ	460 AM SEQ	460 SQ SEQ 462 PTSEQ	461 AM SEQ	461 SQ SEQ 463 PTSEQ	462 AM SEQ	462 SQ SEQ 464 PTSEQ	463 AM SEQ	463 SQ SEQ 465 PTSEQ	464 AM SEQ	464 SQ SEQ 466 PTSEQ	465 AM SEQ	465 SQ SEQ 467 PTSEQ	466 AM SEQ	466 SQ SEQ 468 PTSEQ	467 AM SEQ	467 SQ SEQ 469 PTSEQ	468 AM SEQ	468 SQ SEQ 470 PTSEQ	469 AM SEQ	469 SQ SEQ 471 PTSEQ	470 AM SEQ	470 SQ SEQ 472 PTSEQ	471 AM SEQ	471 SQ SEQ 473 PTSEQ	472 AM SEQ	472 SQ SEQ 474 PTSEQ	473 AM SEQ	473 SQ SEQ 475 PTSEQ	474 AM SEQ	474 SQ SEQ 476 PTSEQ	475 AM SEQ	475 SQ SEQ 477 PTSEQ	476 AM SEQ	476 SQ SEQ 478 PTSEQ	477 AM SEQ	477 SQ SEQ 479 PTSEQ	478 AM SEQ	478 SQ SEQ 480 PTSEQ	479 AM SEQ	479 SQ SEQ 481 PTSEQ	480 AM SEQ	480 SQ SEQ 482 PTSEQ	481 AM SEQ	481 SQ SEQ 483 PTSEQ	482 AM SEQ	482 SQ SEQ 484 PTSEQ	483 AM SEQ	483 SQ SEQ 485 PTSEQ	484 AM SEQ	484 SQ SEQ 486 PTSEQ	485 AM SEQ	485 SQ SEQ 487 PTSEQ	486 AM SEQ	486 SQ SEQ 488 PTSEQ	487 AM SEQ	487 SQ SEQ 489 PTSEQ	488 AM SEQ	488 SQ SEQ 490 PTSEQ	489 AM SEQ	489 SQ SEQ 491 PTSEQ	490 AM SEQ	490 SQ SEQ 492 PTSEQ	491 AM SEQ	491 SQ SEQ 493 PTSEQ	492 AM SEQ	492 SQ SEQ 494 PTSEQ	493 AM SEQ	493 SQ SEQ 495 PTSEQ	494 AM SEQ	494 SQ SEQ 496 PTSEQ	495 AM SEQ	495 SQ SEQ 497 PTSEQ	496 AM SEQ	496 SQ SEQ 498 PTSEQ	497 AM SEQ	497 SQ SEQ 499 PTSEQ	498 AM SEQ	498 SQ SEQ 500 PTSEQ	499 AM SEQ	499 SQ SEQ 501 PTSEQ	500 AM SEQ	500 SQ SEQ 502 PTSEQ	501 AM SEQ	501 SQ SEQ 503 PTSEQ	502 AM SEQ	502 SQ SEQ 504 PTSEQ	503 AM SEQ	503 SQ SEQ 505 PTSEQ	504 AM SEQ	504 SQ SEQ 506 PTSEQ	505 AM SEQ	505 SQ SEQ 507 PTSEQ	506 AM SEQ	506 SQ SEQ 508 PTSEQ	507 AM SEQ	507 SQ SEQ 509 PTSEQ	508 AM SEQ	508 SQ SEQ 510 PTSEQ	509 AM SEQ	509 SQ SEQ 511 PTSEQ	510 AM SEQ	510 SQ SEQ 512 PTSEQ	511 AM SEQ	511 SQ SEQ 513 PTSEQ	512 AM SEQ	512 SQ SEQ 514 PTSEQ	513 AM SEQ	513 SQ SEQ 515 PTSEQ	514 AM SEQ	514 SQ SEQ 516 PTSEQ	515 AM SEQ	515 SQ SEQ 517 PTSEQ	516 AM SEQ	516 SQ SEQ 518 PTSEQ	517 AM SEQ	517 SQ SEQ 519 PTSEQ	518 AM SEQ	518 SQ SEQ 520 PTSEQ	519 AM SEQ	519 SQ SEQ 521 PTSEQ	520 AM SEQ	520 SQ SEQ 522 PTSEQ	521 AM SEQ	521 SQ SEQ 523 PTSEQ	522 AM SEQ	52
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168  
Table 3 (cont'd)

Feature	Feature type	Material type	Feature - 1a	Feature code	Normal	Endos	p33	SEQ 17 AA	SEQ 20	SEQ 21	PTREQ 26 AA	SEQ 29	OR	SEQ 31	OR	SEQ 32	AREO 48	BASEO 64	T
646.3				25641				1	0	727	871	41121	0	0	0	0	0	0	0
756-0				43453				1415	1044	2482	2282	8374	1009	0	0	0	0	0	0
T-470				52705				0	4852	838	771	1518	1109	0	0	0	0	0	0
Mem-3				30045				47	216	500	0	0	0	0	0	0	0	0	0
CRIL 141 RPA 820				11952				0	486	1871	342	330	32	197	176	0	0	0	0
7811 Unstained - D1000				21215				0	0	0	0	0	0	0	0	0	0	0	0
808 poly A+				25643				194	0	1030	2000	1004	691	120	0	0	0	0	0
ACMY				38104				0	0	1156	2112	1092	265	0	0	0	0	0	0
LIACC-40				23910				0	1874	1090	823	874	750	371	120	0	0	0	0
MCCT 7400L RES				19352				0	80	1284	812	848	0	0	0	0	0	0	0
UTOS (BamHI) poly A+				12881				374	0	774	406	215	178	0	0	0	0	0	0
WISH (Colony) poly A+				8406				0	1204	572	149	0	0	0	0	0	0	0	0
45S module RPA				12880				0	0	14	0	82	0	0	0	0	0	0	0
COL 17 RPA 30108				12880				0	0	14	0	82	0	0	0	0	0	0	0
NA-36 726 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0				21190				0	563	0	1041	14092	411	0	0	0	0	0	0
CRIL 141 - TPA (200) 820				28088				0	0	0	3727	0	148	176	134	0	0	0	0
Mem-1				14725				0	133	0	0	355	862	0	0	0	0	0	0
Mem-2				29116				0	0	1485	358	447	157	381	0	0	0	0	0
Mem-3				33046				0	0	353	0	235	0	0	0	0	0	0	0
HOP-82				37330				43	804	154	0	22	0	887	0	0	0	0	0
MIOL-4				22249				0	88	726	740	82	0	0	0	0	0	0	0
EVZ				18708				0	12363	142	22	388	536	0	0	0	0	0	0
14-08				22457				387	303	1636	837	2757	371	0	0	0	0	0	0
MCCT-H2				30149				0	0	0	0	4264	2803	0	0	0	0	0	0
RPM 828				28852				886	901	305	387	958	1115	1134	1424	0	0	0	0
ASMBATCC				34425				0	0	209	567	184	134	222	160	0	0	0	0
SA				38616				0	0	645	0	0	153	812	403	0	0	0	0
OVCA-3				19506				0	1361	0	384	733	0	897	62	0	0	0	0
HCT-15				17443				30	289	899	1821	1417	284	3825	286	0	0	0	0
OVCA-2				10333				478	1077	0	157	587	0	718	0	0	0	0	0
UC-31				13456				0	415	0	242	737	0	0	116	0	0	0	0
OVCA-5				60297				0	3782	1752	584	7065	533	1024	271	0	0	0	0
SHLC				38550				119	3309	0	204	483	0	0	0	0	0	0	0
OVCA-8				16487				159	573	882	512	215	819	104	0	0	0	0	0
LOX MM				44886				0	18804	0	784	8133	0	279	899	0	0	0	0
IGROV-1				38128				121	289	180	373	1340	390	231	204	0	0	0	0
SK-CH-3				34735				737	259	1017	0	536	317	72	0	0	0	0	0
SK-MB-4				17172				282	0	0	312	884	0	157	118	0	0	0	0
SK-AC				13827				212	608	0	141	338	0	54	0	0	0	0	0
SK-MB-28				38531				866	1771	854	965	3468	0	9585	488	0	0	0	0
U-601				38485				0	337	617	1130	2325	0	262	0	0	0	0	0
LMCC-257				38125				198	11138	0	179	2892	588	55	336	0	0	0	0
MH1				25443				154	0	0	0	210	817	87	612	0	0	0	0
MCCT				19129				48	0	0	178	34	278	0	0	0	0	0	0
MDA-MB-435				88835				0	2892	486	807	1109	2558	448	583	0	0	0	0
MDA-MB-436				38815				0	578	815	40	563	5	0	0	0	0	0	0
MDA-MB-437				38488				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-438				37574				737	7063	0	737	0	182	2143	1472	278	0	0	0
MDA-MB-439				102505				872	2309	0	822	888	534	1356	545	0	0	0	0
MDA-MB-440				38883				48	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-441				48870				186	747	285	18826	0	5111	287	0	0	0	0	0
MDA-MB-442				47107				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-443				18800				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-444				52885				109	0	7188	17280	2781	1134	583	0	0	0	0	0
MDA-MB-445				48870				186	747	285	18826	0	5111	287	0	0	0	0	0
MDA-MB-446				47107				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-447				18800				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-448				52885				109	0	7188	17280	2781	1134	583	0	0	0	0	0
MDA-MB-449				48870				186	747	285	18826	0	5111	287	0	0	0	0	0
MDA-MB-450				47107				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-451				18800				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-452				52885				109	0	7188	17280	2781	1134	583	0	0	0	0	0
MDA-MB-453				48870				186	747	285	18826	0	5111	287	0	0	0	0	0
MDA-MB-454				47107				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-455				18800				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-456				52885				109	0	7188	17280	2781	1134	583	0	0	0	0	0
MDA-MB-457				48870				186	747	285	18826	0	5111	287	0	0	0	0	0
MDA-MB-458				47107				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-459				18800				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-460				52885				109	0	7188	17280	2781	1134	583	0	0	0	0	0
MDA-MB-461				48870				186	747	285	18826	0	5111	287	0	0	0	0	0
MDA-MB-462				47107				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-463				18800				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-464				52885				109	0	7188	17280	2781	1134	583	0	0	0	0	0
MDA-MB-465				48870				186	747	285	18826	0	5111	287	0	0	0	0	0
MDA-MB-466				47107				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-467				18800				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-468				52885				109	0	7188	17280	2781	1134	583	0	0	0	0	0
MDA-MB-469				48870				186	747	285	18826	0	5111	287	0	0	0	0	0
MDA-MB-470				47107				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-471				18800				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-472				52885				109	0	7188	17280	2781	1134	583	0	0	0	0	0
MDA-MB-473				48870				186	747	285	18826	0	5111	287	0	0	0	0	0
MDA-MB-474				47107				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-475				18800				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-476				52885				109	0	7188	17280	2781	1134	583	0	0	0	0	0
MDA-MB-477				48870				186	747	285	18826	0	5111	287	0	0	0	0	0
MDA-MB-478				47107				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-479				18800				0	0	0	0	0	0	0	0	0	0	0	0
MDA-MB-480				52885				109	0	7188	17280	2781	1134	583	0	0	0	0	0
MDA-MB-481				48870				186	747	285	18826	0	5111	287	0	0	0	0	0
MDA-MB-482																			





Table 3<sup>171</sup> (cont'd)[illegible]



Threat	Tumor-type	Normal-type	Tumor - Is	Tumor cells	Normal	Evoked	p33	SEQ 17	AN	SEQ 20	SEQ 22	P	SEQ 28	AN	SEQ 29	DN	SEQ 31	DN	SEQ 32	AN	SEQ 34	DN	SEQ 35	AN	SEQ 36	DN	SEQ 37	AN	SEQ 38	DN	SEQ 39	AN	SEQ 40	DN	SEQ 41	AN	SEQ 42	DN	SEQ 43	AN	SEQ 44	DN	SEQ 45	AN	SEQ 46	DN	SEQ 47	AN	SEQ 48	DN	SEQ 49	AN	SEQ 50	DN	SEQ 51	AN	SEQ 52	DN	SEQ 53	AN	SEQ 54	DN	SEQ 55	AN	SEQ 56	DN	SEQ 57	AN	SEQ 58	DN	SEQ 59	AN	SEQ 60	DN	SEQ 61	AN	SEQ 62	DN	SEQ 63	AN	SEQ 64	DN	SEQ 65	AN	SEQ 66	DN	SEQ 67	AN	SEQ 68	DN	SEQ 69	AN	SEQ 70	DN	SEQ 71	AN	SEQ 72	DN	SEQ 73	AN	SEQ 74	DN	SEQ 75	AN	SEQ 76	DN	SEQ 77	AN	SEQ 78	DN	SEQ 79	AN	SEQ 80	DN	SEQ 81	AN	SEQ 82	DN	SEQ 83	AN	SEQ 84	DN	SEQ 85	AN	SEQ 86	DN	SEQ 87	AN	SEQ 88	DN	SEQ 89	AN	SEQ 90	DN	SEQ 91	AN	SEQ 92	DN	SEQ 93	AN	SEQ 94	DN	SEQ 95	AN	SEQ 96	DN	SEQ 97	AN	SEQ 98	DN	SEQ 99	AN	SEQ 100	DN	SEQ 101	AN	SEQ 102	DN	SEQ 103	AN	SEQ 104	DN	SEQ 105	AN	SEQ 106	DN	SEQ 107	AN	SEQ 108	DN	SEQ 109	AN	SEQ 110	DN	SEQ 111	AN	SEQ 112	DN	SEQ 113	AN	SEQ 114	DN	SEQ 115	AN	SEQ 116	DN	SEQ 117	AN	SEQ 118	DN	SEQ 119	AN	SEQ 120	DN	SEQ 121	AN	SEQ 122	DN	SEQ 123	AN	SEQ 124	DN	SEQ 125	AN	SEQ 126	DN	SEQ 127	AN	SEQ 128	DN	SEQ 129	AN	SEQ 130	DN	SEQ 131	AN	SEQ 132	DN	SEQ 133	AN	SEQ 134	DN	SEQ 135	AN	SEQ 136	DN	SEQ 137	AN	SEQ 138	DN	SEQ 139	AN	SEQ 140	DN	SEQ 141	AN	SEQ 142	DN	SEQ 143	AN	SEQ 144	DN	SEQ 145	AN	SEQ 146	DN	SEQ 147	AN	SEQ 148	DN	SEQ 149	AN	SEQ 150	DN	SEQ 151	AN	SEQ 152	DN	SEQ 153	AN	SEQ 154	DN	SEQ 155	AN	SEQ 156	DN	SEQ 157	AN	SEQ 158	DN	SEQ 159	AN	SEQ 160	DN	SEQ 161	AN	SEQ 162	DN	SEQ 163	AN	SEQ 164	DN	SEQ 165	AN	SEQ 166	DN	SEQ 167	AN	SEQ 168	DN	SEQ 169	AN	SEQ 170	DN	SEQ 171	AN	SEQ 172	DN	SEQ 173	AN	SEQ 174	DN	SEQ 175	AN	SEQ 176	DN	SEQ 177	AN	SEQ 178	DN	SEQ 179	AN	SEQ 180	DN	SEQ 181	AN	SEQ 182	DN	SEQ 183	AN	SEQ 184	DN	SEQ 185	AN	SEQ 186	DN	SEQ 187	AN	SEQ 188	DN	SEQ 189	AN	SEQ 190	DN	SEQ 191	AN	SEQ 192	DN	SEQ 193	AN	SEQ 194	DN	SEQ 195	AN	SEQ 196	DN	SEQ 197	AN	SEQ 198	DN	SEQ 199	AN	SEQ 200	DN	SEQ 201	AN	SEQ 202	DN	SEQ 203	AN	SEQ 204	DN	SEQ 205	AN	SEQ 206	DN	SEQ 207	AN	SEQ 208	DN	SEQ 209	AN	SEQ 210	DN	SEQ 211	AN	SEQ 212	DN	SEQ 213	AN	SEQ 214	DN	SEQ 215	AN	SEQ 216	DN	SEQ 217	AN	SEQ 218	DN	SEQ 219	AN	SEQ 220	DN	SEQ 221	AN	SEQ 222	DN	SEQ 223	AN	SEQ 224	DN	SEQ 225	AN	SEQ 226	DN	SEQ 227	AN	SEQ 228	DN	SEQ 229	AN	SEQ 230	DN	SEQ 231	AN	SEQ 232	DN	SEQ 233	AN	SEQ 234	DN	SEQ 235	AN	SEQ 236	DN	SEQ 237	AN	SEQ 238	DN	SEQ 239	AN	SEQ 240	DN	SEQ 241	AN	SEQ 242	DN	SEQ 243	AN	SEQ 244	DN	SEQ 245	AN	SEQ 246	DN	SEQ 247	AN	SEQ 248	DN	SEQ 249	AN	SEQ 250	DN	SEQ 251	AN	SEQ 252	DN	SEQ 253	AN	SEQ 254	DN	SEQ 255	AN	SEQ 256	DN	SEQ 257	AN	SEQ 258	DN	SEQ 259	AN	SEQ 260	DN	SEQ 261	AN	SEQ 262	DN	SEQ 263	AN	SEQ 264	DN	SEQ 265	AN	SEQ 266	DN	SEQ 267	AN	SEQ 268	DN	SEQ 269	AN	SEQ 270	DN	SEQ 271	AN	SEQ 272	DN	SEQ 273	AN	SEQ 274	DN	SEQ 275	AN	SEQ 276	DN	SEQ 277	AN	SEQ 278	DN	SEQ 279	AN	SEQ 280	DN	SEQ 281	AN	SEQ 282	DN	SEQ 283	
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Table 3 (cont'd)

Tissue	Tumor-cys	Normal-cys	Tumor - vs	Tumor cells	Normal	Endon	p53	SEQ 44	SEQ 45	SEQ 46	SEQ 47	SEQ 48	SEQ 49	SEQ 50	SEQ 51	SEQ 52	SEQ 53	SEQ 54
Adipose gland - h	1	2518			1984	0	25	163	7015	2253	1792	2042	37991					
Brain cells - h	2	2518			267	0	267	8674	8574	7198	2170	7781	79730					
Brain marrow - h	3				1989	0	237	0	5963	3816	1261	1112	45217					
Esophagus gland - h	4	441			441	0	0	0	2795	1143	280	0	3070					
Heart - h	5	4981			4981	0	59	239	6405	809	897	11858	31126					
Intestine - h	6	368			368	0	0	344	7076	2343	888	8722	44206					
Intestine gland - h	7	8888			8888	0	70	7808	2838	3189	13789	83983						
Intestine gland - h	8	10870			10870	0	60	2311	8628	8997	332	32295	36020					
Intestine gland - h	9	32140			32140	0	267	89	7743	5814	3001	25437	41638					
Intestine gland - h	10	4434			4434	0	81	87	8183	2369	2312	41080	35006					
Intestine gland - h	11	2337			2337	0	253	0	8334	8433	1275	28344	72605					
Intestine gland - h	12	2093			2093	0	174	0	7873	2767	234	5651	21151					
Intestine gland - h	13	2879			2879	0	116	189	8968	1887	810	4385	41710					
Intestine gland - h	14	0			0	0	130	0	8905	3410	1128	5931	28823					
Intestine gland - h	15	8890			8890	0	219	345	10713	8378	1738	20842	64753					
Intestine gland - h	16	32499			32499	0	0	0	3708	9842	1183	2008	14912					
Intestine gland - h	17	8842			8842	0	10	191	8123	472	9022	2810	14787					
Intestine gland - h	18	2730			2730	0	16	144	7037	2846	443	4172	22590					
Intestine gland - h	19	0			0	0	181	225	8344	2842	781	7838	37845					
Intestine gland - h	20	0			0	0	126	0	8879	2846	588	1275	14331					
Intestine gland - h	21	8340			8340	0	0	0	4814	0	833	0	15780					
Intestine gland - h	22	2383			2383	0	0	188	8447	3308	831	887	18480					
Intestine gland - h	23	2011			2011	0	105	177	3888	2134	873	3438	24017					
Intestine gland - h	24	2882			2882	0	125	0	3888	812	281	1243	17857					
Intestine gland - h	25	20445			20445	0	1188	205	1838	8251	11884	32178	68577					
Intestine gland - h	26	1202			1202	0	47	23	8191	8825	1838	14408	85005					
Intestine gland - h	27	885			885	0	0	39	3398	0	0	0	1674					
Intestine gland - h	28	885			885	0	184	568	1880	568	8454	27850						
Intestine gland - h	29	108			108	0	19	98	18744	84	0	8460						
Intestine gland - h	30	3411			3411	0	79	0	8162	4182	1587	8588	34950					
Intestine gland - h	31	0			0	0	33	188	4488	19	383	9740						
Intestine gland - h	32	3081			3081	0	82	307	7287	7343	1364	7384	38840					
Intestine gland - h	33	194			194	0	25	70	5751	6835	218	681	6888					
Intestine gland - h	34	570			570	0	0	0	8288	0	0	17	21419					
Intestine gland - h	35	15118			15118	0	118	0	53737	3888	118	8887	25525					
Intestine gland - h	36	388			388	0	14	0	3412	388	31	0	243					
Intestine gland - h	37	8835			8835	0	0	0	88811	8072	134	0	22881					
Intestine gland - h	38	888			888	0	17	33	4086	10884	4	0	7201					
Intestine gland - h	39	888			888	0	87	8833	8751	0	0	0	28458					
Intestine gland - h	40	30			30	0	0	3090	0	0	0	0	2875					
Intestine gland - h	41	1182			1182	0	0	0	8889	8384	145	0	18626					
Intestine gland - h	42	0			0	0	403	0	9111	1427	0	0	16386					
Intestine gland - h	43	1732			1732	0	27	53	7444	18562	115	12733	22783					
Intestine gland - h	44	385			385	0	0	0	301	0	0	0	0					
Intestine gland - h	45	385			385	0	0	0	295	0	32	0	482					
Intestine gland - h	46	2188			2188	0	0	41	1387	387	21	0	8465					
Intestine gland - h	47	5180			5180	0	0	403	8850	2807	248	0	6825					
Intestine gland - h	48	354			354	0	46	0	6406	346	316	330	2534					
Intestine gland - h	49	244			244	0	71	0	1862	487	80	388	8788					
Intestine gland - h	50	343			343	0	0	1820	1178	0	0	0	7542					
Intestine gland - h	51	334			334	0	0	0	280	8049	117	0	0					
Intestine gland - h	52	332			332	0	6	0	4534	0	521	0	27818					
Intestine gland - h	53	332			332	0	0	0	47	0	0	0	361					
Intestine gland - h	54	332			332	0	280	10	7888	280	883	4389	15417					
Intestine gland - h	55	327			327	0	118	178	4837	0	0	42	488					
Intestine gland - h	56	326			326	0	0	250	8643	0	825	547	78037					
Intestine gland - h	57	343			343	0	0	0	2450	0	0	0	1482					
Intestine gland - h	58	320			320	0	0	0	3821	0	0	0	3857					
Intestine gland - h	59	218			218	0	313	0	8239	8643	0	0	68844					
Intestine gland - h	60	218			218	0	28	184	4057	2227	187	5651	22075					
Intestine gland - h	61	218			218	0	229	175	5272	443	383	588	88828					
Intestine gland - h	62	311			311	0	84	0	8050	810	27	0	17721					
Intestine gland - h	63	308			308	0	0	0	8486	708	0	0	11878					
Intestine gland - h	64	308			308	0	0	0	370	3428	0	86	285					
Intestine gland - h	65	308			308	0	34	228	5153	2282	68	822	22086					
Intestine gland - h	66	303			303	0	362	33	8370	4675	0	0	37188					
Intestine gland - h	67	302			302	0	370	304	8851	1873	145	1017	7889					
Intestine gland - h	68	298			298	0	223	64	8880	12811	684	2087	7818					
Intestine gland - h	69	297			297	0	8	474	4872	0	44	1983	38882					
Intestine gland - h	70	286			286	0	114	0	3815	3836	0	462	38438					
Intestine gland - h	71	286			286	0	84	0	3831	2045	304	843	38876					
Intestine gland - h	72	286			286	0	88	0	3832	682	178	134	18253					
Intestine gland - h	73	286			286	0	245	0	8280	831	88	824	48824					
Intestine gland - h	74	279			279	0	88	338	8448	118	0	385	8831					
Intestine gland - h	75	277			277	0	0	0	4734	1182	0	1385	18722					
Intestine gland - h	76	278			278	0	41	181	3784	874	83	0	0					
Intestine gland - h	77	289			289	0	7	0	3883	242	349	0	8229					
Intestine gland - h	78	289			289	0	0	118	3880	383	84	474	11174					
Intestine gland - h	79	238			238	0	0	188	7884	7888	0	1621	13790					
Intestine gland - h	80	236			236	0	83	154	8	4088	888	52	4582					
Intestine gland - h	81	234			234	0	0	0	8156	642	588	0	3487					
Intestine gland - h	82	233			233	0	875	0	47	0	8886	0	8721					
Intestine gland - h	83	231			231	0	0	0	4138	188	2221	118	417					
Intestine gland - h	84	229			229	0	80	189	3519	4888	152	0	8188					
Intestine gland - h	85	227			227	0	187	0	4186	717	0	0	4183					
Intestine gland - h	86	222			222	0	14	2	2450	0	53	0	8898					
Intestine gland - h	87	218			218	0	121	8847	0	0	454	12728						
Intestine gland - h	88	214			214	0	41	143	8834	1880	0	138	33840					
Intestine gland - h	89	213			213	0	90	78	3833	0	133	0	12882					
Intestine gland - h	90	212			212	0	0	77	1884	1884	188	77	18888					
Intestine gland - h	91	211			211	0	0	0	5286	241	0	0	848					
Intestine gland - h	92	210			210	0	173	0	8806	4184	188	681	18888					
Intestine gland - h	93	209			209	0	11	0	2834	2236	36	848	314					
Intestine gland - h	94	208			208	0	0	134	4247	0	0	0	384					

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Table 3 (cont'd)

Tissue	Tumor-type	Normal-type	Tumor - 10	Tumor cells	Normal	Endo	AS3	SEQ 841	TR50	AS	SEQ 47	ANSEQ 48	ANSEQ 49	ANSEQ 50	ANSEQ 51	ANSEQ 52	ANSEQ 53	ANSEQ 54	ANSEQ 55	CL
Cell-1				100				0	0	47	88	4012	0	164	258	5443				
T06-0				189				4917	0	0	912	7688	48	0	21583	20865				
T-47D				189				0	0	70	212	6456	73	206	6331	7187				
Mem-3				171				0	0	0	25	1546	278	8	0	261				
CRL 1441 RNA B30				181				0	0	0	662	1368	138	363	182	0				
7811 untreated + Q20mm				183				0	0	31	0	867	0	0	212	430				
MDA-MB-231				194				0	0	0	135	1053	24	52	211	7691				
MDA-MB-231				195				0	0	48	0	3437	0	84	84	2781				
ACHN				195				0	0	0	0	2832	258	171	8142	2184				
LMCC-42				200				385	0	38	131	1286	0	0	1277	1373				
MDA-MB-231				200				0	0	38	0	1357	700	0	1430	1039				
MDA-MB-231				200				0	0	171	22	0	0	0	0	2432				
MDA-MB-231				204				0	0	0	0	742	843	44	42	1191				
MDA-MB-231				205				5841	0	0	0	7137	0	0	0	8852				
MDA-MB-231				214				0	0	90	141	1194	3	100	0	527				
MDA-MB-231				219				0	0	0	0	2125	0	77	0	892				
CRL 1441 + TPA (24h) B30				220				0	0	0	224	126	50	0	0	0				
Mem-2				221				6889	0	0	0	16	1572	0	0	0	1757			
MDA-MB-231				225				738	0	172	0	2235	330	85	0	0	1881			
MDA-MB-231				241				128	0	0	3	1124	272	0	0	0	1758			
MDA-MB-231				242				1229	0	0	0	4188	1288	0	0	2452	1590			
MDA-MB-231				243				584	0	0	129	2740	138	217	3810	7440				
MDA-MB-231				244				0	0	0	0	3632	907	814	1488	10317				
MDA-MB-231				245				227	0	0	10	183	3528	1813	221	2042	8328			
MDA-MB-231				247				0	0	0	88	413	2887	7116	182	0	738			
MDA-MB-231				247				0	0	0	0	94	0	0	0	1084				
MDA-MB-231				249				0	0	0	0	2108	1910	33	28	1268				
MDA-MB-231				249				0	0	17	287	2481	0	45	163	644				
MDA-MB-231				250				1242	0	0	62	4698	1567	283	548	13841				
MDA-MB-231				251				63	0	83	15	552	0	7	480	817				
MDA-MB-231				252				347	0	0	66	814	0	0	463	947				
MDA-MB-231				253				0	0	89	722	8152	0	362	4788	6832				
MDA-MB-231				254				811	0	0	0	3554	2297	0	10455	1668				
MDA-MB-231				255				322	0	0	13	2681	812	0	2182	1742				
MDA-MB-231				256				0	0	77	343	6201	4800	383	2850	8100				
MDA-MB-231				257				0	0	94	0	3088	871	3	2387	3807				
MDA-MB-231				258				0	0	112	0	2243	481	338	1374	2894				
MDA-MB-231				259				0	0	0	0	1188	0	184	1450	1432				
MDA-MB-231				260				0	0	0	0	472	1228	198	0	198	1488			
MDA-MB-231				261				173	0	188	458	6873	2291	0	7414	2888				
MDA-MB-231				262				0	0	0	0	3230	841	0	2859	2883				
MDA-MB-231				263				157	0	85	31	8148	4336	216	2537	782				
MDA-MB-231				264				688	0	0	0	2891	0	42	0	1280				
MDA-MB-231				265				0	0	74	0	3278	151	181	0	1458				
MDA-MB-231				267				9820	0	0	20	8738	0	0	17484	28883				
MDA-MB-231				268				0	0	80	223	1824	0	0	744	1343				
MDA-MB-231				270				1742	0	0	0	1555	2883	67	0	2884				
MDA-MB-231				271				0	0	11	0	4127	0	283	1252	8025				
MDA-MB-231				272				8085	0	137	0	7232	1888	43	868	1872				
MDA-MB-231				273				2709	0	18	260	3086	32	264	879	8384				
MDA-MB-231				274				0	0	10	0	2952	848	171	98	8975				
MDA-MB-231				275				0	0	19	48	2177	843	24	0	18940				
MDA-MB-231				276				0	0	188	4154	686	578	773	4714					
MDA-MB-231				277				0	0	5	0	2448	3812	0	189	58382				
MDA-MB-231				278				0	0	35	0	3884	0	11	781	1101				
MDA-MB-231				279				0	0	0	0	2886	0	100	0	1148				
MDA-MB-231				280				0	0	357	2132	301	181	5222	2878					
MDA-MB-231				281				7880	0	22	0	8113	4555	0	8554	26831				
MDA-MB-231				282				7884	0	66	0	11688	19210	282	145893	38706				
MDA-MB-231				283				0	0	0	0	1886	0	0	2951	2885				
MDA-MB-231				284				0	0	227	3570	708	83	584	818					
MDA-MB-231				285				0	0	15	0	2189	0	139	0	1520				
MDA-MB-231				286				0	0	72	82	2072	0	165	0	0				
MDA-MB-231				287				0	0	60	25	4300	608	0	3475	18731				
MDA-MB-231				288				0	0	28	43	703	888	0	0	0				
MDA-MB-231				289				4211	0	0	0	1783	0	0	0	1095				
MDA-MB-231				290				0	0	44	137	1728	842	82	0	1130				
MDA-MB-231				291				0	0	30	262	3787	1580	288	0	8776				
MDA-MB-231				292				7948	0	0	184	1848	0	280	0	0				
MDA-MB-231				293				0	0	0	0	6281	0	0	0	18131				
MDA-MB-231				294				0	0	114	0	2870	0	0	0	18131				
MDA-MB-231				295				0	0	0	0	7888	2225	0	3008	17088				
MDA-MB-231				296				2845	0	0	0	28188	18870	313	37831	7453				
MDA-MB-231				297				0	0	0	0	1888	1275	37	386	1188				
MDA-MB-231				298				0	0	162	0	5482	437	0	438	88848				
MDA-MB-231				299				185	0	187	0	5811	0	0	0	2708				
MDA-MB-231				300				0	0	114	0	3851	8	0	0	12125				
MDA-MB-231				301				332	0	38	26	3238	588	0	0	348				
MDA-MB-231				302				0	0	29	0	8032	0	0	0	12860				
MDA-MB-231				303				0	0	0	0	4071	0	84	104	2302				
MDA-MB-231				304				1382	0	0	0	3071	1321	0	0	28149				
MDA-MB-231				305				0	0	0	0	3034	0	0	0	2891				
MDA-MB-231				306				1838	0	0	0	8175	1883	0	0	1773				
MDA-MB-231				307				0	0	73	0	4848	0	0	0	2834				
MDA-MB-231				308				0	0	0	0	884	24	45	243	1388				
MDA-MB-231				309				0	0	28	5	4362	0	440	0	3840				
MDA-MB-231				310				0	0	1178	2324	0	57	0	888					
MDA-MB-231				311				2888	0	872	0	4283	878	130	634	4445				
MDA-MB-231				312				280	0	0	0	5818	0	0	0	3888				
MDA-MB-231				313				0	0	30	114	4038	0	0	0	4727				
MDA-MB-231				314				430	0	0	132	8415	97	32	419	8154				
MDA-MB-231				315				0	0	0	0	47								

Table 3 (cont'd)

[illegible]

176  
Table 3 (cont'd)[illegible]

[illegible]

178.  
Table 3 (cont'd)

Thema	Tumor-xyz	Normal-xyz	Tumor -to	Tumor cells	Harvest	Embryo	p33	SEQ. 3A	SEQ. 3T	W1	SEQ. 4A	SEQ. 4B	SEQ. 4C	SEQ. 4D	SEQ. 4E	SEQ. 4F	SEQ. 4G	SEQ. 4H	SEQ. 4I	SEQ. 4J	SEQ. 4K	SEQ. 4L	SEQ. 4M	SEQ. 4N	SEQ. 4O	SEQ. 4P	SEQ. 4Q	SEQ. 4R	SEQ. 4S	SEQ. 4T	SEQ. 4U	SEQ. 4V	SEQ. 4W	SEQ. 4X	SEQ. 4Y	SEQ. 4Z	SEQ. 4AA	SEQ. 4AB	SEQ. 4AC	SEQ. 4AD	SEQ. 4AE	SEQ. 4AF	SEQ. 4AG	SEQ. 4AH	SEQ. 4AI	SEQ. 4AJ	SEQ. 4AK	SEQ. 4AL	SEQ. 4AM	SEQ. 4AN	SEQ. 4AO	SEQ. 4AP	SEQ. 4AQ	SEQ. 4AR	SEQ. 4AS	SEQ. 4AT	SEQ. 4AU	SEQ. 4AV	SEQ. 4AW	SEQ. 4AX	SEQ. 4AY	SEQ. 4AZ	SEQ. 4BA	SEQ. 4BB	SEQ. 4BC	SEQ. 4BD	SEQ. 4BE	SEQ. 4BF	SEQ. 4BG	SEQ. 4BH	SEQ. 4BI	SEQ. 4BJ	SEQ. 4BK	SEQ. 4BL	SEQ. 4BM	SEQ. 4BN	SEQ. 4BO	SEQ. 4BP	SEQ. 4BQ	SEQ. 4BR	SEQ. 4BS	SEQ. 4BT	SEQ. 4BU	SEQ. 4BV	SEQ. 4BW	SEQ. 4BX	SEQ. 4BY	SEQ. 4BZ	SEQ. 4CA	SEQ. 4CB	SEQ. 4CC	SEQ. 4CD	SEQ. 4CE	SEQ. 4CF	SEQ. 4CG	SEQ. 4CH	SEQ. 4CI	SEQ. 4CJ	SEQ. 4CK	SEQ. 4CL	SEQ. 4CM	SEQ. 4CN	SEQ. 4CO	SEQ. 4CP	SEQ. 4CQ	SEQ. 4CR	SEQ. 4CS	SEQ. 4CT	SEQ. 4CU	SEQ. 4CV	SEQ. 4CW	SEQ. 4CX	SEQ. 4CY	SEQ. 4CZ	SEQ. 4DA	SEQ. 4DB	SEQ. 4DC	SEQ. 4DD	SEQ. 4DE	SEQ. 4DF	SEQ. 4DG	SEQ. 4DH	SEQ. 4DI	SEQ. 4DJ	SEQ. 4DK	SEQ. 4DL	SEQ. 4DM	SEQ. 4DN	SEQ. 4DO	SEQ. 4DP	SEQ. 4DQ	SEQ. 4DR	SEQ. 4DS	SEQ. 4DT	SEQ. 4DU	SEQ. 4DV	SEQ. 4DW	SEQ. 4DX	SEQ. 4DY	SEQ. 4DZ	SEQ. 4EA	SEQ. 4EB	SEQ. 4EC	SEQ. 4ED	SEQ. 4EE	SEQ. 4EF	SEQ. 4EG	SEQ. 4EH	SEQ. 4EI	SEQ. 4EJ	SEQ. 4EK	SEQ. 4EL	SEQ. 4EM	SEQ. 4EN	SEQ. 4EO	SEQ. 4EP	SEQ. 4EQ	SEQ. 4ER	SEQ. 4ES	SEQ. 4ET	SEQ. 4EU	SEQ. 4EV	SEQ. 4EW	SEQ. 4EX	SEQ. 4EY	SEQ. 4EZ	SEQ. 4FA	SEQ. 4FB	SEQ. 4FC	SEQ. 4FD	SEQ. 4FE	SEQ. 4FF	SEQ. 4FG	SEQ. 4FH	SEQ. 4FI	SEQ. 4FJ	SEQ. 4FK	SEQ. 4FL	SEQ. 4FM	SEQ. 4FN	SEQ. 4FO	SEQ. 4FP	SEQ. 4FQ	SEQ. 4FR	SEQ. 4FS	SEQ. 4FT	SEQ. 4FU	SEQ. 4FV	SEQ. 4FW	SEQ. 4FX	SEQ. 4FY	SEQ. 4FZ	SEQ. 4GA	SEQ. 4GB	SEQ. 4GC	SEQ. 4GD	SEQ. 4GE	SEQ. 4GF	SEQ. 4GG	SEQ. 4GH	SEQ. 4GI	SEQ. 4GJ	SEQ. 4GK	SEQ. 4GL	SEQ. 4GM	SEQ. 4GN	SEQ. 4GO	SEQ. 4GP	SEQ. 4GQ	SEQ. 4GR	SEQ. 4GS	SEQ. 4GT	SEQ. 4GU	SEQ. 4GV	SEQ. 4GW	SEQ. 4GX	SEQ. 4GY	SEQ. 4GZ	SEQ. 4HA	SEQ. 4HB	SEQ. 4HC	SEQ. 4HD	SEQ. 4HE	SEQ. 4HF	SEQ. 4HG	SEQ. 4HH	SEQ. 4HI	SEQ. 4HJ	SEQ. 4HK	SEQ. 4HL	SEQ. 4HM	SEQ. 4HN	SEQ. 4HO	SEQ. 4HP	SEQ. 4HQ	SEQ. 4HR	SEQ. 4HS	SEQ. 4HT	SEQ. 4HU	SEQ. 4HV	SEQ. 4HW	SEQ. 4HX	SEQ. 4HY	SEQ. 4HZ	SEQ. 4IA	SEQ. 4IB	SEQ. 4IC	SEQ. 4ID	SEQ. 4IE	SEQ. 4IF	SEQ. 4IG	SEQ. 4IH	SEQ. 4II	SEQ. 4IJ	SEQ. 4IK	SEQ. 4IL	SEQ. 4IM	SEQ. 4IN	SEQ. 4IO	SEQ. 4IP	SEQ. 4IQ	SEQ. 4IR	SEQ. 4IS	SEQ. 4IT	SEQ. 4IU	SEQ. 4IV	SEQ. 4IW	SEQ. 4IX	SEQ. 4IY	SEQ. 4IZ	SEQ. 4JA	SEQ. 4JB	SEQ. 4JC	SEQ. 4JD	SEQ. 4JE	SEQ. 4JF	SEQ. 4JG	SEQ. 4JH	SEQ. 4JI	SEQ. 4JJ	SEQ. 4JK	SEQ. 4JL	SEQ. 4JM	SEQ. 4JN	SEQ. 4JO	SEQ. 4JP	SEQ. 4JQ	SEQ. 4JR	SEQ. 4JS	SEQ. 4JT	SEQ. 4JU	SEQ. 4JV	SEQ. 4JW	SEQ. 4JX	SEQ. 4JY	SEQ. 4JZ	SEQ. 4KA	SEQ. 4KB	SEQ. 4KC	SEQ. 4KD	SEQ. 4KE	SEQ. 4KF	SEQ. 4KG	SEQ. 4KH	SEQ. 4KI	SEQ. 4KJ	SEQ. 4KK	SEQ. 4KL	SEQ. 4KM	SEQ. 4KN	SEQ. 4KO	SEQ. 4KP	SEQ. 4KQ	SEQ. 4KR	SEQ. 4KS	SEQ. 4KT	SEQ. 4KU	SEQ. 4KV	SEQ. 4KW	SEQ. 4KX	SEQ. 4KY	SEQ. 4KZ	SEQ. 4LA	SEQ. 4LB	SEQ. 4LC	SEQ. 4LD	SEQ. 4LE	SEQ. 4LF	SEQ. 4LG	SEQ. 4LH	SEQ. 4LI	SEQ. 4LJ	SEQ. 4LK	SEQ. 4LL	SEQ. 4LM	SEQ. 4LN	SEQ. 4LO	SEQ. 4LP	SEQ. 4LQ	SEQ. 4LR	SEQ. 4LS	SEQ. 4LT	SEQ. 4LU	SEQ. 4LV	SEQ. 4LW	SEQ. 4LX	SEQ. 4LY	SEQ. 4LZ	SEQ. 4MA	SEQ. 4MB	SEQ. 4MC	SEQ. 4MD	SEQ. 4ME	SEQ. 4MF	SEQ. 4MG	SEQ. 4MH	SEQ. 4MI	SEQ. 4MJ	SEQ. 4MK	SEQ. 4ML	SEQ. 4MM	SEQ. 4MN	SEQ. 4MO	SEQ. 4MP	SEQ. 4MQ	SEQ. 4MR	SEQ. 4MS	SEQ. 4MT	SEQ. 4MU	SEQ. 4MV	SEQ. 4MW	SEQ. 4MX	SEQ. 4MY	SEQ. 4MZ	SEQ. 4NA	SEQ. 4NB	SEQ. 4NC	SEQ. 4ND	SEQ. 4NE	SEQ. 4NF	SEQ. 4NG	SEQ. 4NH	SEQ. 4NI	SEQ. 4NJ	SEQ. 4NK	SEQ. 4NL	SEQ. 4NM	SEQ. 4NN	SEQ. 4NO	SEQ. 4NP	SEQ. 4NQ	SEQ. 4NR	SEQ. 4NS	SEQ. 4NT	SEQ. 4NU	SEQ. 4NV	SEQ. 4NW	SEQ. 4NX	SEQ. 4NY	SEQ. 4NZ	SEQ. 4OA	SEQ. 4OB	SEQ. 4OC	SEQ. 4OD	SEQ. 4OE	SEQ. 4OF	SEQ. 4OG	SEQ. 4OH	SEQ. 4OI	SEQ. 4OJ	SEQ. 4OK	SEQ. 4OL	SEQ. 4OM	SEQ. 4ON	SEQ. 4OO	SEQ. 4OP	SEQ. 4OQ	SEQ. 4OR	SEQ. 4OS	SEQ. 4OT	SEQ. 4OU	SEQ. 4OV	SEQ. 4OW	SEQ. 4OX	SEQ. 4OY	SEQ. 4OZ	SEQ. 4PA	SEQ. 4PB	SEQ. 4PC	SEQ. 4PD	SEQ. 4PE	SEQ. 4PF	SEQ. 4PG	SEQ. 4PH	SEQ. 4PI	SEQ. 4PJ	SEQ. 4PK	SEQ. 4PL	SEQ. 4PM	SEQ. 4PN	SEQ. 4PO	SEQ. 4PP	SEQ. 4PQ	SEQ. 4PR	SEQ. 4PS	SEQ. 4PT	SEQ. 4PU	SEQ. 4PV	SEQ. 4PW	SEQ. 4PX	SEQ. 4PY	SEQ. 4PZ	SEQ. 4QA	SEQ. 4QB	SEQ. 4QC	SEQ. 4QD	SEQ. 4QE	SEQ. 4QF	SEQ. 4QG	SEQ. 4QH	SEQ. 4QI	SEQ. 4QJ	SEQ. 4QK	SEQ. 4QL	SEQ. 4QM	SEQ. 4QN	SEQ. 4QO	SEQ. 4QP	SEQ. 4QQ	SEQ. 4QR	SEQ. 4QS	SEQ. 4QT	SEQ. 4QU	SEQ. 4QV	SEQ. 4QW	SEQ. 4QX	SEQ. 4QY	SEQ. 4QZ	SEQ. 4RA	SEQ. 4RB	SEQ. 4RC	SEQ. 4RD	SEQ. 4RE	SEQ. 4RF	SEQ. 4RG	SEQ. 4RH	SEQ. 4RI	SEQ. 4RJ	SEQ. 4RK	SEQ. 4RL	SEQ. 4RM	SEQ. 4RN	SEQ. 4RO	SEQ. 4RP	SEQ. 4RQ	SEQ. 4RR	SEQ. 4RS	SEQ. 4RT	SEQ. 4RU	SEQ. 4RV	SEQ. 4RW	SEQ. 4RX	SEQ. 4RY	SEQ. 4RZ	SEQ. 4SA	SEQ. 4SB	SEQ. 4SC	SEQ. 4SD	SEQ. 4SE	SEQ. 4SF	SEQ. 4SG	SEQ. 4SH	SEQ. 4SI	SEQ. 4SJ	SEQ. 4SK	SEQ. 4SL	SEQ. 4SM	SEQ. 4SN	SEQ. 4SO	SEQ. 4SP	SEQ. 4SQ	SEQ. 4SR	SEQ. 4SS	SEQ. 4ST	SEQ. 4SU	SEQ. 4SV	SEQ. 4SW	SEQ. 4SX	SEQ. 4SY	SEQ. 4SZ	SEQ. 4TA	SEQ. 4TB	SEQ. 4TC	SEQ. 4TD	SEQ. 4TE	SEQ. 4TF	SEQ. 4TG	SEQ. 4TH	SEQ. 4TI	SEQ. 4TJ	SEQ. 4TK	SEQ. 4TL	SEQ. 4TM	SEQ. 4TN	SEQ. 4TO	SEQ. 4TP	SEQ. 4TQ	SEQ. 4TR	SEQ. 4TS	SEQ. 4TT	SEQ. 4TU	SEQ. 4TV	SEQ. 4TW	SEQ. 4TX	SEQ. 4TY	SEQ. 4TZ	SEQ. 4UA	SEQ. 4UB	SEQ. 4UC	SEQ. 4UD	SEQ. 4UE	SEQ. 4UF	SEQ. 4UG	SEQ. 4UH	SEQ. 4UI	SEQ. 4UJ	SEQ. 4UK	SEQ. 4UL	SEQ. 4UM	SEQ. 4UN	SEQ. 4UO	SEQ. 4UP	SEQ. 4UQ	SEQ. 4UR	SEQ. 4US	SEQ. 4UT	SEQ. 4UU	SEQ. 4UV	SEQ. 4UW	SEQ. 4UX	SEQ. 4UY	SEQ. 4UZ	SEQ. 4VA	SEQ. 4VB	SEQ. 4VC	SEQ. 4VD	SEQ. 4VE	SEQ. 4VF	SEQ. 4VG	SEQ. 4VH	SEQ. 4VI	SEQ. 4VJ	SEQ. 4VK	SEQ. 4VL	SEQ. 4VM	SEQ. 4VN	SEQ. 4VO	SEQ. 4VP	SEQ. 4VQ	SEQ. 4VR	SEQ. 4VS	SEQ. 4VT	SEQ. 4VU	SEQ. 4VV	SEQ. 4VW	SEQ. 4VX	SEQ. 4VY	SEQ. 4VZ	SEQ. 4WA	SEQ. 4WB	SEQ. 4WC	SEQ. 4WD	SEQ. 4WE	SEQ. 4WF	SEQ. 4WG	SEQ. 4WH	SEQ. 4WI	SEQ. 4WJ	SEQ. 4WK	SEQ. 4WL	SEQ. 4WM	SEQ. 4WN	SEQ. 4WO	SEQ. 4WP	SEQ. 4WQ	SEQ. 4WR	SEQ. 4WS	SEQ. 4WT	SEQ. 4WU	SEQ. 4WV	SEQ. 4WW	SEQ. 4WX	SEQ. 4WY	SEQ. 4WZ	SEQ. 4XA	SEQ. 4XB	SEQ. 4XC	SEQ. 4XD	SEQ. 4XE	SEQ. 4XF	SEQ. 4XG	SEQ. 4XH	SEQ. 4XI	SEQ. 4XJ	SEQ. 4XK	SEQ. 4XL	SEQ. 4XM	SEQ. 4XN	SEQ. 4XO	SEQ. 4XP	SEQ. 4XQ	SEQ. 4XR	SEQ. 4XS	SEQ. 4XT	SEQ. 4XU	SEQ. 4XV	SEQ. 4XW	SEQ. 4XX	SEQ. 4XY	SEQ. 4XZ	SEQ. 4YA	SEQ. 4YB	SEQ. 4YC	SEQ. 4YD	SEQ. 4YE	SEQ. 4YF	SEQ. 4YG	SEQ. 4YH	SEQ. 4YI	SEQ. 4YJ	SEQ. 4YK	SEQ. 4YL	SEQ. 4YM	SEQ. 4YN	SEQ. 4YO	SEQ. 4YP	SEQ. 4YQ	SEQ. 4YR	SEQ. 4YS	SEQ. 4YT	SEQ. 4YU	SEQ. 4YV	SEQ. 4YW	SEQ. 4YX	SEQ. 4YY	SEQ. 4YZ	SEQ. 4ZA	SEQ. 4ZB	SEQ. 4ZC	SEQ. 4ZD	SEQ. 4ZE	SEQ. 4ZF	SEQ. 4ZG	SEQ. 4ZH	SEQ. 4ZI	SEQ. 4ZJ	SEQ. 4ZK	SEQ. 4ZL	SEQ. 4ZM	SEQ. 4ZN	SEQ. 4ZO	SEQ. 4ZP	SEQ. 4ZQ	SEQ. 4ZR	SEQ. 4ZS	SEQ. 4ZT	SEQ. 4ZU	SEQ. 4ZV	SEQ. 4ZW	SEQ. 4ZX	SEQ. 4ZY	SEQ. 4ZZ
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180  
Table 3 (cont'd)[illegible]

181  
Table 3 (cont'd)[illegible]

182  
Table 3 (cont'd)

Gene	Tumor type	Normal type	Tumor - to	Tumor ratio	Normal	Endon	p33	SEQ 75	AA	SEQ 82	SEQ 83	SEQ 84	SEQ 85	AA	SEQ 86	AA	SEQ 87	SEQ 88	AA	SEQ 89	AA	SEQ 90	AA	SEQ 91	AA	SEQ 92	AA	SEQ 93	AA	SEQ 94	AA
DePang-7								0	1467	2281	94057	0	7232	0	238	1538															
DePang-8								0	2758	83	72626	0	8613	0	48	622															
DePang-9								0	2323	15	38655	0	14381	0	103	770															
DePang-11								0	11	2678	73695	0	8794	0	0	1245															
DePang-12								0	0	1063	1765	0	7699	0	0	1770															
DePang-10								0	34	0	23883	0	10777	0	0	915															
DePang-1								0	257	784	10021	0	2318	0	66	300															
DePang-2								0	488	285	148948	0	1211	0	48	383															
DePang-3								0	213	6567	105645	0	2713	0	384																
DePang-4								0	52	581	68193	0	559	0	354	801															
DePang-5								0	2855	0	45709	0	0	0	249	622															
DePang-6								0	1948	0	54536	0	58	0	15	492															
AS48 - 8							wt	0	29	4142	85151	0	2098	0	0	545															
BRVX - 8							mutant	0	164	4621	74530	0	7705	0	0	2322															
HCT-116 - 7							wt	0	173	836	22256	0	1578	0	72	1588															
HCT-116 - 8							wt	0	265	779	28245	0	2202	0	0	1781															
HT29 - 3							mutant	0	167	1301	47637	0	276	0	315	852															
HT29 - 7							mutant	0	0	80	14674	0	30	0	85	441															
HT29 - 8							mutant	0	45	663	36186	0	342	0	0	499															
SF338 - 7							wt	0	254	114	26838	0	1533	0	184	837															
SF338 - 8							wt	0	1007	176	36188	0	4118	0	0	1851															
SF-388 - 7							mutant	0	0	2013	52411	0	2540	0	167	1488															
SF-388 - 8							mutant	0	1395	1825	30182	0	4138	0	126	1271															
OVCA4-1 - 7							wt	0	899	0	34881	0	524	0	140	2425															
OVCA4-1 - 8							wt	0	0	2400	55206	0	6738	0	0	788															
OVCA4-1 - 7							mutant	0	1141	850	88880	0	2132	0	0	3745															
OVCA4-1 - 8							mutant	0	729	176	13631	0	0	0	571																
OVCA4-1 - 8							wt	0	204	0	46867	0	208	0	0	342															
ADR-RES - 8							wt	0	108	0	23503	0	101	0	323	1207															
HELA - 8							HPV IS	0	1303	1038	21952	0	384	0	269	651															
SW480 - 7							mutant	0	236	483	58435	0	1176	0	89	1435															
SW480 - 8							mutant	0	1123	0	27232	0	1972	0	330	879															
H1288 - 8							mutant	0	215	7288	20150	0	2881	0	53	774															
C3A - 7							mutant	0	1098	204	18811	0	8	0	0	650															
C3A - 8							mutant	0	1777	323	29434	0	3288	0	215	1863															
LUO6 - 7							mutant	0	720	1497	63571	0	3482	0	113	879															
LUO6 - 8							mutant	0	1325	826	33247	0	112	0	38	886															
HeLa - 7							wt	0	88	582	23298	0	8952	0	0	858															
HeLa - 8							wt	0	0	530	40810	0	1024	0	0	1105															
WI 38 - 8							wt	0	55	0	82606	0	142	0	0	800															
458 melanoma RNA								0	316	18713	14780	157513	855	80	0	2436															
COL 1572 371789								0	0	154	1378	83	21	0	2313																
Ren-4							wt	110	70	187	3788	916	805	254	0	12872															
HT308								0	33	0	4338	137	22	888	548	7832															
HT376								0	30	0	4642	18	0	44	0	3843															
HT308								160	115	354	5248	14188	1123	133	16827																
Ren-3								308	105	874	5379	0	287	258	0	6483															
Ren-3								173	105	0	1494	2459	0	0	0	4087															
Ren-5								175	45	113	220	154	44	0	0	2746															
Ren-9								177	0	0	1789	0	54	0	103	3483															
h. lamprocytes 2G2592 #19								10	0	0	2152	2734	0	81	80	5096															
Ren-10								237	87	90	0	4051	416	154	77	2480															
HT10								49	73	187	827	160	181	6	1021																
h. Neutrophils 391/88 #12								0	0	361	3570	0	518	0	111	1082															
Neutrophils h.								0	0	0	4530	0	0	0	0	474															
SAV90-C6 poly A+								236	87	4388	12803	205	495	373	11	22888															
SA-C6 (SAV90 poly A+)								332	0	2811	1281	8862	48	788	249	6785															
HEK poly A+								620	0	7825	1853	8563	271	1630	147	4771															
HCT-116 - 3							wt	0	0	817	28938	0	1747	0	0	0															
HCT-116 - 4							wt	0	213	234	32187	0	1460	0	52	307															
HCT-116 - 5							wt	0	7	37	34582	0	2413	0	0	1024															
HCT-116 - 6							wt	0	188	263	36888	0	1888	0	68	1304															
AS48 - 6							wt	0	6	0	21787	0	0	0	0	897															
HT29 - 3							mutant	0	203	1878	10879	0	143	0	159	888															
HT29 - 4							mutant	0	0	41	24371	0	167	0	92	1903															
HT29 - 5							mutant	0	133	0	26088	0	484	0	0	2538															
HT29 - 6							mutant	0	31	1363	78072	0	629	0	0	927															
HT29 - 8							mutant	0	470	0	62441	0	152	0	0	1389															
OVCA4-1 - 3							wt	0	238	338	29521	0	5217	0	0	879															
OVCA4-1 - 4																															

Table 3 (cont'd)

[illegible]

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Table 3 (cont'd)

[illegible]

Table 3 (cont'd)

[illegible]

Tissue	Tumor-arym	Normal-arym	Tumor - fe	Tumor calls	Hemost	Endos	p53	SEQ 96 ANSEQ 96 ANSEQ 97 HBBQX 180 ANSEQ 191 ANSEQ 110 ANSEQ 111 ANSEQ 112 ANSEQ 114					
DuPang-1	0	0	0	0	0	0	0	6153	258	0	1186	760	0
DuPang-2	0	0	0	0	0	0	0	1136	0	0	1136	264	0
DuPang-3	0	0	0	0	0	0	0	352	17	0	2407	903	0
DuPang-11	0	0	0	0	0	0	0	2810	477	0	1191	732	0
DuPang-12	0	0	0	0	0	0	0	0	50	0	5093	266	0
DuPang-18	0	0	0	0	0	0	0	11437	192	0	870	982	0
DuPang-1	0	0	0	0	0	0	0	0	80	0	120	636	0
DuPang-2	0	0	0	0	0	0	0	282	0	0	208	737	0
DuPang-3	0	0	0	0	0	0	0	5089	46	0	237	870	0
DuPang-4	0	0	0	0	0	0	0	3575	67	0	3069	794	0
DuPang-5	0	0	0	0	0	0	0	217	72	0	1090	645	0
DuPang-6	0	0	0	0	0	0	0	0	40	0	62	1987	0
MAB-8	0	0	0	0	0	0	0	1863	78	0	58	622	0
ERVX-8	0	0	0	0	0	0	0	6498	207	0	324	847	0
HCT-116-7	0	0	0	0	0	0	0	0	0	0	54	573	0
HCT-116-8	0	0	0	0	0	0	0	846	122	0	178	675	0
HT29-7	0	0	0	0	0	0	0	2091	0	0	856	844	0
HT29-7	0	0	0	0	0	0	0	2147	20	0	214	533	0
HT29-8	0	0	0	0	0	0	0	467	0	0	200	769	0
SF339-7	0	0	0	0	0	0	0	375	65	0	21	694	0
SF339-8	0	0	0	0	0	0	0	0	0	0	21	893	0
SF-298-7	0	0	0	0	0	0	0	646	164	0	706	829	0
SF-298-8	0	0	0	0	0	0	0	0	183	0	203	846	0
CNCAR-4-7	0	0	0	0	0	0	0	1395	526	0	0	0	0
CNCAR-4-8	0	0	0	0	0	0	0	527	328	0	2772	892	0
CNCAR-5-7	0	0	0	0	0	0	0	338	0	0	863	2184	0
CNCAR-5-8	0	0	0	0	0	0	0	0	0	0	911	550	0
UCS-7-8	0	0	0	0	0	0	0	740	164	0	646	898	0
AOR-HES-8	0	0	0	0	0	0	0	3013	0	0	826	1832	0
MAL-8	0	0	0	0	0	0	0	2243	117	0	130	675	0
BW480-7	0	0	0	0	0	0	0	1081	462	0	0	1025	0
BW480-8	0	0	0	0	0	0	0	7238	0	0	203	712	0
HT29-8	0	0	0	0	0	0	0	2283	0	0	0	737	0
CD3A-7	0	0	0	0	0	0	0	3129	0	0	163	760	0
CD3A-8	0	0	0	0	0	0	0	1813	0	0	588	1067	0
UCS-7-7	0	0	0	0	0	0	0	2184	0	0	13	811	0
UCS-8-8	0	0	0	0	0	0	0	0	167	0	668	868	0
HMB-7	0	0	0	0	0	0	0	4024	909	0	171	615	0
F468-7	0	0	0	0	0	0	0	4967	0	0	301	536	0
WI-38-8	0	0	0	0									

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Table 3 (cont'd)

Tissue	Tumor-type	Normal-type	Tumor-to	Tumor code	Normal	Endoc	p30	SEQ ID NO
adrenal gland - h	1							534
lymph node - h	2							822
thymus - h	3							2891
pancreas - h	4							236
coronary artery - h	5							685
pancreas - h	6							227
coronary artery - h	7							717
adrenal gland - h	8							762
adrenal gland - h	9							537
adrenal gland - h	10							548
adrenal gland - h	11							410
adrenal gland - h	12							0
adrenal gland - h	13							154
adrenal gland - h	14							514
adrenal gland - h	15							252
adrenal gland - h	16							259
adrenal gland - h	17							51
adrenal gland - h	18							167
adrenal gland - h	19							456
adrenal gland - h	20							594
adrenal gland - h	21							69
adrenal gland - h	22							141
adrenal gland - h	23							332
adrenal gland - h	24							0
adrenal gland - h	25							188
adrenal gland - h	26							3124
adrenal gland - h	27							91
adrenal gland - h	28							198
adrenal gland - h	29							189
adrenal gland - h	30							0
adrenal gland - h	31							179
adrenal gland - h	32							71
adrenal gland - h	33							1029
adrenal gland - h	34							102
adrenal gland - h	35							146
adrenal gland - h	36							123
adrenal gland - h	37							627
adrenal gland - h	38							140
adrenal gland - h	39							0
adrenal gland - h	40							0
adrenal gland - h	41							0
adrenal gland - h	42							365
adrenal gland - h	43							363
adrenal gland - h	44							251
adrenal gland - h	45							369
adrenal gland - h	46							354
adrenal gland - h	47							354
adrenal gland - h	48							354
adrenal gland - h	49							354
adrenal gland - h	50							354
adrenal gland - h	51							354
adrenal gland - h	52							354
adrenal gland - h	53							354
adrenal gland - h	54							354
adrenal gland - h	55							354
adrenal gland - h	56							354
adrenal gland - h	57							354
adrenal gland - h	58							354
adrenal gland - h	59							354
adrenal gland - h	60							354
adrenal gland - h	61							354
adrenal gland - h	62							354
adrenal gland - h	63							354
adrenal gland - h	64							354
adrenal gland - h	65							354
adrenal gland - h	66							354
adrenal gland - h	67							354
adrenal gland - h	68							354
adrenal gland - h	69							354
adrenal gland - h	70							354
adrenal gland - h	71							354
adrenal gland - h	72							354
adrenal gland - h	73							354
adrenal gland - h	74							354
adrenal gland - h	75							354
adrenal gland - h	76							354
adrenal gland - h	77							354
adrenal gland - h	78							354
adrenal gland - h	79							354
adrenal gland - h	80							354
adrenal gland - h	81							354
adrenal gland - h	82							354
adrenal gland - h	83							354
adrenal gland - h	84							354
adrenal gland - h	85							354
adrenal gland - h	86							354
adrenal gland - h	87							354
adrenal gland - h	88							354
adrenal gland - h	89							354
adrenal gland - h	90							354
adrenal gland - h	91							354
adrenal gland - h	92							354
adrenal gland - h	93							354
adrenal gland - h	94							354
adrenal gland - h	95							354
adrenal gland - h	96							354
adrenal gland - h	97							354
adrenal gland - h	98							354
adrenal gland - h	99							354
adrenal gland - h	100							354
adrenal gland - h	101							354
adrenal gland - h	102							354
adrenal gland - h	103							354
adrenal gland - h	104							354
adrenal gland - h	105							354
adrenal gland - h	106							354
adrenal gland - h	107							354
adrenal gland - h	108							354
adrenal gland - h	109							354
adrenal gland - h	110							354
adrenal gland - h	111							354
adrenal gland - h	112							354
adrenal gland - h	113							354
adrenal gland - h	114							354
adrenal gland - h	115							354
adrenal gland - h	116							354
adrenal gland - h	117							354
adrenal gland - h	118							354
adrenal gland - h	119							354
adrenal gland - h	120							354
adrenal gland - h	121							354
adrenal gland - h	122							354
adrenal gland - h	123							354
adrenal gland - h	124							354
adrenal gland - h	125							354
adrenal gland - h	126							354
adrenal gland - h	127							354
adrenal gland - h	128							354
adrenal gland - h	129							354
adrenal gland - h	130							354
adrenal gland - h	131							354
adrenal gland - h	132							354
adrenal gland - h	133							354
adrenal gland - h	134							354
adrenal gland - h	135							354
adrenal gland - h	136							354
adrenal gland - h	137							354
adrenal gland - h	138							354
adrenal gland - h	139							354
adrenal gland - h	140							354
adrenal gland - h	141							354
adrenal gland - h	142							354
adrenal gland - h	143							354
adrenal gland - h	144							354
adrenal gland - h	145							354
adrenal gland - h	146							354
adrenal gland - h	147							354
adrenal gland - h	148							354
adrenal gland - h	149							354
adrenal gland - h	150							354
adrenal gland - h	151							354
adrenal gland - h	152							354
adrenal gland - h	153							354
adrenal gland - h	154							354
adrenal gland - h	155							354
adrenal gland - h	156							354
adrenal gland - h	157							354
adrenal gland - h	158							354
adrenal gland - h	159							354
adrenal gland - h	160							354
adrenal gland - h	161							354
adrenal gland - h	162							354
adrenal gland - h	163							354
adrenal gland - h	164							354



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Table 3 (cont'd)

Therapy	Tumor-yes	Normal-yes	Tumor - No	Tumor only	Normal	Endone	p33	SEQ 116.3
TRAIL				188				0
TRAIL				188				0
T-47D				177				75
Kan-3				181				0
CRL 1451 RML 870				183				188
HT11 untreated + DMSO				184				47
KB poly A+				188				0
HES poly A+				188				0
ACR4				188				53
UACC-82				200				0
MCF-7ADR-RES				202				58
UTCM (Normal) poly A+				204				0
W1261 (Colony) poly A+				205				34
488 multiple RNA				208				280
COL 127 RMA 32198				218				0
W1-30 T2n 8.9APBS, 201 10% PBS				219				0
CRL 1451 + TPA (DMSO, 82)				220				242
Kan-1				221				84
Kan-2				222				79
Kan				222				0
HT29-2				241				0
MCF-7				242				0
BRVX				243				0
PL-40				244				0
MDA-MB-23				245				0
HPM 8226				248				60
AS48ATCC				247				241
SK				248				0
OVCA9-3				248				85
HCT-15				250				0
OVCA9-4				251				0
MDA-3				252				0
OVCA9-5				253				240
SN12C				254				0
OVCA9-6				255				0
LOX NBT				256				0
HURV1				257				0
SK-MEL-2				258				153
SK-OV-3				259				0
SK-MEL-5				260				0
BP-539				261				0
SK-MEL-28				262				0
K-562				263				22
UACC-257				264				33
814				265				0
BUC-7				267				48
MDA-MB-435				268				188
HT276				276				0
MDA-N				271				0
T29 poly A+				272				0
MDA-MB-231				280				26
HT298 2nd TPA RMA 922				308				147
HES-A-EXP-01885				313				83
HT298 on RNA				320				0
HT247				323				0
488 multiple RNA				324				126
MDA-MB-231				328				0
MDA-MB-231				328				51
U251				338				0
HT 188 poly A+				340				0
PC-3				341				0
HCC-2998				343				0
SW-620				345				0
HT 102				346				148
COL O 305				347				0
HT218				348				0
MDA-12				349				0
HT151				360				20
LA88				361				0
HT363				362				480
MDA-MB-231				363				0
TK-10				365				363
MDA-MB-3A				367				241
Pe 576T				368				0
HT213			50					312
HT286			52					0
HT232			54					0
HT155			56					0
HT163			58					185
HT176			60					81
HT172			62					137
HT138			62					0
HT178			64					32
HT194			65					19
HT180			66					40
HT189			67					140
HT189			68					0
HT143			69					0
HT190			70					0
HT145			71					130
HT222			72					181
HT302			73					0
HT214			74					0
HT171			76					0
MDA-MB-231 118			77					0
HT323			78					21
HT327			80					137
HT135			82					0
HT146			85					88
HT348			87					29
HT211			170					18
HT208			185					0
HT140			187					0
HT281			189					205
HT212			191					75
TC6P			207					40
HT180			216					48
HT207			217					62
HT208			224					250
HT220			226					0
HT211			228					114
HT277			230					155
HT282			236					112
MDA-MB-231 RNA			281					480
HT334			298					231
HT338			301					0
HT302			315					83
HT304			317					0
HT212			319					0
HT142			325					0
HT208			358					86
HT187			360					13
T-47D	183							63
MDA-N	181							0
MDA-MB-435	159							0
MDA-MB-231	157							30

Table 3 (cont'd)

Tissue	Tissue type	Normal type	Tumor - Is	Tumor cells	Normal	Endoth	p33	SE0 118 5
HA-ERT	154							0
MC-F-TIAOL-RES	153							0
MC-F-7	151							0
HA-4	149							7
LIACC-257	147							22
LIACC-62	145							0
SK-MEL-28	144							33
LI-O-31	143							0
SK-MEL-5	142							91
KOA-12	141							4
SK-MEL-2	140							263
MC-T-15	139							328
Melan-3M	138							181
CCLO-304	137							259
LOX-BM1	136							0
SR-428	135							0
TK-18	134							0
MC-T-116	133							0
786-S	132							56
PC-2008	131							78
ACHN	130							276
PC-3	129							0
RF-383	128							338
DA-145	127							89
Calu-1	126							276
SR	125							0
A498	124							127
RPM-8228	123							8
SW-62	122							128
HE-46	121							118
MC-T-4	120							0
OVCA-5	119							0
K-562	118							38
OVCA-4	117							542
CCRF-CEM	116							888
OVCA-3	115							191
SP-439	114							87
HPV-32	113							0
SK-295	112							161
ASIMATCC	111							110
BF-288	110							133
NCI-H22	109							5
U251	108							204
NCI-H460	107							0
SW-63	106							35
NCI-H222M	105							439
SW-63	104							70
NCI-H228	103							62
SK-OV-3	102							6
NCI-H20	101							777
SKOV-1	100							0
SKOV-3	99							54
OVCA-8	98							8
NCI-H2	97							43
h. keratinocyte 30182 #12	48							148
h. keratinocyte 3021492 #17	47							210
h. keratinocyte 302482 #19	46							125
TCOP	38							0
ASB-1						wt		5
ASB-2						wt		379
ASB-4						wt		458
ASB-5						wt		347
ASB-7						wt		72
ERVX-1						mutant		91
ERVX-4						mutant		250
ERVX-3						mutant		0
ERVX-5						mutant		481
ERVX-7						mutant		877
MC-F-7-1						wt		0
MC-F-7-3						wt		565
MC-F-7-4						wt		215
MC-F-7-5						wt		0
MC-F-7-7						wt		0
ADR-RES-1						mutant		3049
ADR-RES-3						mutant		159
ADR-RES-4						mutant		79
ADR-RES-5						mutant		18
ADR-RES-7						mutant		36
WI-38-1						wt		0
WI-38-3						wt		263
WI-38-4						wt		589
WI-38-5						wt		589
WI-38-7						wt		0
hPa-1						HPV E5		0
hPa-2						HPV E5		58
hPa-4						HPV E5		585
hPa-5						HPV E5		304
hPa-7						HPV E5		105
H1298-1						mutant		0
H1298-2						mutant		0
H1298-4						mutant		0
H1298-5						mutant		0
H1298-7						mutant		0
ASB-2						wt		293
ERVX-2						mutant		9
MC-T-116-1						wt		0
MC-T-116-2						wt		830
HT29-2						mutant		86
SP-339-1						wt		0
SP-339-2						wt		3
SP-339-3						mutant		202
SP-339-5						mutant		531
OVCA-4-1						wt		0
OVCA-4-2						wt		0
OVCA-5-1						mutant		532
OVCA-5-2						mutant		259
MC-F-7-2						wt		86
ADR-RES-2						mutant		221
hPa-3						HPV E5		172
SW-630-1						mutant		0
SW-630-2						mutant		191
H1298-3						mutant		1003
CCSA-1						mutant		0
CCSA-2						mutant		0
LRCS-1						mutant		271
LRCS-2						mutant		877
hPa-1						wt		0
hPa-2						wt		24
WI-38-2						wt		298
hPa-3						wt		5
hPa-4						wt		0
hPa-5						wt		0
hPa-6						wt		14529
hPa-7						wt		562
hPa-8						wt		0
hPa-9						wt		0

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Table 3 (cont'd)

Tissue	Tumor-type	Normal-type	Tumor - to	Tumor ratio	Normal	Endoc	p33	SEQ 118
DefPanc-2								1882
DefPanc-4								2891
DefPanc-8								8823
DefPanc-11								25923
DefPanc-12								515
DefPanc-20								358
DefPanc-3								474
DefPanc-2								0
DefPanc-3								222
DefPanc-4								0
DefPanc-5								0
DefPanc-6								0
AS49 - 5						wt		0
SKVX - 5						mutant		56
HCT-116 - 7						wt		0
HCT-116 - 9						wt		0
HT29 - 1						mutant		316
HT29 - 7						mutant		89
HT29 - 8						mutant		0
SF538 - 7						wt		155
SF538 - 8						wt		229
SF-268-7						mutant		215
SF-268-8						mutant		563
OVCAR-4 - 7						wt		450
OVCAR-4 - 8						wt		0
OVCAR-5 - 7						mutant		831
OVCAR-5 - 8						mutant		707
HCT-7 - 5						wt		36
ADR-RES - 8						mutant		857
Hela - 5						HPV ES		0
SW640 - 7						mutant		0
SW640 - 8						mutant		0
H1258 - 8						mutant		0
C33A - 7						mutant		0
C33A - 8						mutant		0
LUO5 - 7						mutant		729
LUO5 - 8						mutant		27
Hs578 - 7						wt		0
Hs578 - 8						wt		0
WI 38 - 5						wt		0
Hs578 (Hs578)						wt		0
QRL1572 21789						84		221
HT558								80
HT378								151
HT386								89
HT390								0
Res-2						173		487
Res-5						175		117
Res-8						177		481
A. tumefaciens 30540 870								0
Res-10						237		0
HTB10								0
A. tumefaciens 30540 872								0
resonance h								0
ARHGAP28 874 A+								35
SA-OS (Raman) 874 A+								0
Res 874 A+								0
HCT-116 - 3						wt		284
HCT-116 - 4						wt		0
HCT-116 - 5						wt		0
HCT-116 - 6						wt		0
AS49 - 6						wt		0
HT29 - 3						mutant		974
SKVX - 6						mutant		121
HT29 - 4						mutant		640
HT29 - 5						mutant		0
HT29 - 6						mutant		177
HT29 - 8						mutant		238
OVCAR-4 - 3						wt		0
OVCAR-4 - 4						wt		0
OVCAR-4 - 5						wt		96
OVCAR-4 - 6						wt		0
SF538 - 3						wt		726
SF538 - 4						wt		83
SF538 - 5						wt		0
SF538 - 6						wt		0
OVCAR-5 - 3						mutant		2219
OVCAR-5 - 4						mutant		286
OVCAR-5 - 5						mutant		0
ADR-RES - 5						mutant		0
HCT-7 - 6						wt		279
Hela - 6						HPV ES		271
HT29 - 8						mutant		0
SW640 - 3						mutant		51
SW640 - 4						mutant		0
SW640 - 5						mutant		203
SW640 - 6						mutant		225
C33A - 3						mutant		173
C33A - 4						mutant		162
C33A - 5						mutant		0
C33A - 6						mutant		35
Hs578 - 6						wt		0
LUO5 - 3						mutant		620
LUO5 - 4						mutant		581
LUO5 - 5						mutant		544
LUO5 - 6						mutant		0
WI 38 - 6						wt		0
SW640 - 3						wt		288
SW640 - 4						wt		521
SF-268-3						mutant		277
SF-268-4						mutant		0
SF-268-5						mutant		156
SF-268-6						mutant		33
DefPanc-13								21
Res-1 - 30								268
Res-1 - 31								0
Res-1 - 32								0
OVCAR-5 - 6						mutant		811
Res-1 - 10								86
Res-1 - 11								280
Res-1 - 12								884
Res-1 - 13								209
Res-1 - 14								150
Res-1 - 15								333
Res-1 - 16								0
Res-1 - 17								125
Res-1 - 18								0
Res-1 - 19								172

Table 4

Gene Name	SPID#	nalID#	aa	Family	Group	Length_AA	Extra-Catalytic Domains (Amino acid positions)
X69117_h_beta_adrenergic	H	1	122	AGC	GRK	688	Regulator of G protein signaling domain 54-175; PH domain 559-652
AA144574_m	M	2	123	AGC	GRK	378	PH domain 249-337
AA210925_h	H	9	130	AGC	PKC	978	Phorbol esters/diacylglycerol binding domain (C1 domain) 238-287; PH domain 497-577
AA318604_h	H	11	132	AGC	PKC	890	Phorbol esters/diacylglycerol binding domain (C1 domain) 155-204 and 272-321; PH domain 417-532
AA887783_h	H	21	142	AGC	SGK	448	PX domain 13-120
AA021445_h3	H	32	152	CAMK	EMK	1311	Vitamin K-dependent carboxylation/gamma-carboxyglutamic (GLA) domain 1072-1113
R31237_1_h_AAC3348	H	34	154	CAMK	EMK	728	UBA domain 327-365
408786.5_h	H	36	156	CAMK	EMK	1330	PAS domain 133-186, 247-280, 354-388
Z36720_h	H	41	161	CAMK	MLCK	874	WD domain, G-beta repeat 674-711
SGK088_h	H	42	162	CAMK	Trk	2287	Immunoglobulin domain 1-52, 97-153, 221-277, 518-578, 1817-1878; Fibronectin type III domain 301-390, 1897-1779
R19772_h	H	44	164	CAMK	Trk	1287	RhoGEF domain 235-405; Fibronectin type III domain 870-955; Immunoglobulin domain 788-851; PH domain 419-528
17000139801197_h_IRA	H	76	195	Other	IRAK	598	Death domain 28-108
AA088547_h	H	78	197	Other	IRE	922	PQQ enzyme repeat 39-76
AA232253_h	H	82	201	Other	MLK	800	SAM domain (Sterile alpha motif) 337-408
AA589286_h	H	89	208	Other	SLOB	649	PX domain 15-122
AA836348_h	H	113	232	STE	NEK	836	Regulator of chromosome condensation (RCC1) 387-427, 427-480, 483-532, 588-650
PAK6_h	H	115	234	STE	STE20-02	719	P21-Rho-binding domain 11-89

## FIGURE 1A

SEQ ID NO: 122\_X69117\_H BARK2\_H  
MADLEAVLADVSYLMAMEKSKATPAARASKRIVLPEPSIRSVMQKYLAERNEITFDKIFN  
QKIGFLLFKDFCLNEINEAVPQVKFYEEIKEYEKL DNEEDRLCRSRQIYDAYIMKELLSC  
SHPFSKQAVEHVQSHLSKKQVTSTL FQPYIEEICESLRGDI FQKFMESDKFTRFCQWKNV  
ELNIHLTMNEFSVHRIIGRGGFGEVYGC RKADTGKMYAMKCLDKKRIKMKQGETLALNER  
IMLSLVSTGDCPFIVCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSEKEMRFYATE  
IILGLEHVHNRFFVYRDLKPANILLDEHGHARISDLGLACDFS KKKPHASVGTHGYMAPE  
VLQKGTAYDSSADWFSLGCM LFKLLRGHSPFRQHKT KDKEIDRMTLT VNVELPDTFSPE  
LKSLLLEGLLQRDVSKRLGCHGGGSQEVKEHSFFKGVDWQH VYLQKYPPPLIPPRGEVNAA  
DAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERWQQEVTETVYEAVNADTDKIEARK  
RAKNKQLGHEEDYALGKDCIMHGYMLKLG NPF LTQWQRRYFYLF PNRLEWRGEGESRQNL  
LTMEQILSVEETQIKDKKCILFRIKGGKQFVLQCESDPEFVQWKKE LNETFKEAQRLLRR  
APKFLNKPRSGTVELPKPSLCHRSNGL

SEQ ID NO: 123\_AA144574\_M BARK2\_M  
CFVVYRDLKPANILLDEYGHVRI SDLG LACDFS KKKPHASVGTHGYMAPEVLQKGT CYDS  
SADWFSLGCM LFKLLRGHSPFRQHKT KDKEIDRMTLT VNVELPDTFSPELRSLLLEGLLQ  
RDVSQRLGCGGGGARELKEHIFFKGIDWQH VYL RKYPPPLIPPRGEVNAA DAFDIGSFDE  
EDTKGIKLLDCDQDLYKNFPLVISERWQQE VVETIYDAVNADTDKIEARKKAKNKQLGQE  
EDYAMGKDCIMHGYMLKLG NPF LTQWQRRYFYLF PNRLEWRGEGESRQSLLTMEQIMSVE  
ETQIKDRKCILLRIKGGKQFVLQCESDPEFAQWLKELTCTFNEAQRLLRRAPKFLNKPR  
AILEFSKPPLCHRNSSGL

SEQ ID NO: 124\_AA826850\_H  
MGSSMSAATARRPVFDDKEDVNFDFH QILRAIGKGSFGKVCIVQKRDT EKMYAMKYM NQK  
QCIERDEVNRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQ  
FSEDTVRLYICEMALALDYL RGQHIIHRDVKPDNILLDERGHAHLTDFNIATIIKDG ERA  
TALAGTKPYMAPEIFXS FVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSSNAVESLV  
QLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVE  
PGFVPNGRLHCDPTFELEEMILES RPLHKKKKRLAKNKS RDNSRDSSQSENDYLQDCLD  
AIQQDFVIFNREKLKRSQDLPREPLPAPE SRDAAEPVEDEAERSALPMCGPICPSAGSG

SEQ ID NO: 125\_AA960957\_H  
MGGNHSKPPVFDENEEVNFDFH QILRAIGKGSFGKVCIVQKRDT KKMYAMKYM NQKCI  
ERDEVNRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFTE  
GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATVVKG AERASSM  
AGTKPYMAPEVFQVYMDRGP GYSYPVDWWSLGITAYELLRGWRPYEIH SVTPIDEILNMF  
KVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWD AVFKKALMPGF  
VPNGRLNCDPTFELEEMILES KPLHKKKKRLAKNRSRDGT KDSCPLNGHLQHCL ETVRE  
EFIIFNREKLRRQQGQGSQLLDTSRGGGQAQSKLQDGCNNNLLTHTCTRGCSS

SEQ ID NO: 126\_TBK1\_H  
MQSTSNHLWLLSDILGQGANVFRGRHKKTGDLFAIKVFNNISFLRPVDVQMREFEVLK  
KLNHNKIVKLFAIEEETTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDVV  
GGMNHLRENGIVHRDIKPGNIMRVIGEDGQSVYKLTDFGAARELEDDEQFVSLYGT E EYL  
HPDMYERAVLRKD HQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV MYKIITG  
KPSGAISGVQKAENGPIDWSGDMPVSCSLSRGLQVLLTPVLANILEADQEK CWGFDQFFA  
ETSDILHRMVIHVFSLQOMTAHKIYIHSYNTATIFHEL VYKQTKIIS SNQELIYEGRRIV  
LEPGRLAQHF PKTTEENPIFVVSREPLNTIGLIYEKISLPKVHPRYDLDGDASMAKAITG  
VVCYACRIASTLLLYQELMRKGIRWLI ELIKDDYNETVHKKTEVVITLDFCIRNIEKTVK

## FIGURE 1B

VYEKLMKINLEAAELGEISDIHTKLLRLSSSQGTIETSLQDIDSRLSPGGSLADAWAHQE  
GTHPKDRNVEKLQVLLNCMTEIYYQFKKDKAERRLAYNEEQIHKFDKQKLYYHATKAMTH  
FTDECVKKYEAFLNKSEEWIRKMLHLRKQLLSLTNQCFDIEEEVSKYQEYTNELQETLPQ  
KMFTASSGIKHTMTPIYPSSNTLVEMTLGMKKLKEEMEGVVKELAENNHILERFGSLTMD  
GGLRNVDCL

SEQ ID NO: 127\_AA305176\_H

MDPTAGSKKEPGGGAATEEGVNRIAVPKPPSIEEFSIVKPISRGAFGKVYLQKGKGLYA  
VKVVKKADMINKNMTHQVQAERDALALSKSPFIVHLYYSLQSANNVYLVMEYLIGDVK  
LLHIYGYFDEEMAVKYISEVALALDYLRHGI IHRDLKPDNMLI SNEGHI KLTD FGLSKV  
TLNRDINMMDILTTSPMAKPRQDYSRTPGQVLSLISSLGFNTPIAEKNQDPANILSACLS  
ETSQLSQGLVCPMSVDQKDTTPYSSKLLKSCLETVASNPGMPVKCLTSNLLQSRKRLATS  
SASSQSHTFISSVESECHSSPKWEKDCQV

SEQ ID NO: 128\_AA116841\_M

TRPIWPPEGEEKLSDNAQSAMDMLLTIDDSKRAGMRELKQHPLFSEVDWENLQHQTMPFV  
PQPDETDTSYFEARNNAQHLTVSGFSL

SEQ ID NO: 129\_AA256100\_H

MAMTAGTTTTFPMSNHTRERVTVAKLTLENFYSNLILQHEERETRQKKLEVAMEEEGLAD  
EEKLRRSQHARKETEFRLRLKTRLGLDDFESLKVIGRGAFGEVRLVQKKTGHIYAMKI  
LRKSDMLEKEQVAHIRAERDILVEADGAWVVKMFYSFQDKRNLYLIMEFLPGGDMMTLLM  
KKDTLTTEEETQFYISETVLAIDAIHQLGFIHRDIKPDNLLDAGHVKLSDFGLCTGLKK  
AHRTEFYRNLTHNPPSDFSQNMNSKRKAETWKKNRRLAYSTVGTPDYIAPEVFMQTGY  
NKLCDWWSLGVIMYEMLI GYPFCSETPQETYRKVMNWKETLVFPPEVPISEKAKDLILR  
FCIDSENRI GNSGV EEEKGHPFFEGVDWEHIRERPAAPIEIKSIDDTSNFD DFPESDIL  
QPVPNTTEPDYKSKDWVFLNYTYKRFEGLTQRGSIPTYMKAGKL

SEQ ID NO: 130\_AA210825\_H

DSLLPTPALGTPLPIWPVGLRTPLSLESTRSPTQRLLPSTPKDPAILRSPPPARSFLG  
SPLSHLLTRSRGSRTOGPPGPPGGSRVGSRRVAVPGLPPWPPPPHYAGLPSPGPGSP  
PPGGLELQSPPLLPQIPAPGSGVSFHIQIGLTREFVLLPAASELAHVQQLACSIVDQKF  
PECGFYGLYDKILLFKHDPTSANLLQLVRSSGDIQEGDLVEVLSASATFEDFQIRPHAL  
TVHSYRAPAFCDHCGEMLFGLVRQGLKCDGCLNYHKRCAFSIPNNCSGARKRRLSSTSL  
ASGHSVRLGTSES LPTAEELSRSTTELLPRRPSSSSSSSSASSYTGRPIELDKMLLSKV  
KVPHTFLIHSYTRPTVCQACKLLKGLFRQGLQCKDCKFNCHKRCATRVPNDCLEALIN  
GDVPMEEATDFSEADKSALMDESEDSGVI PGSHSENALHASEEEEEGEGGKAQSSLGYIPL  
MRVVQSVRHTTRKSS TTLREGWVVHYSNKD TLRKRHYWRLDCKCITLFQNN TTNRYYKEI  
PLSEILTVE SAQNFSLVPPGTNPHCFEIVTANATYFVGEMPGGT PGGPSGQGA EAARGLX  
ETAIRQALMPVILQDAPSAPGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSG  
QFGVVYGGKHKRKTGRDVAVKVIDKLRFP TKQESQLRNEVAILQSLRHPGIVNLECMFETP  
EKV FVMEK LHGDMLEMILSSEKGR LPERLT KFLITQILVALRHLHFKNIVHCDLK PENV  
LLASADFPFQVKLCDFGFARI IGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVGVI  
MYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAG AIDLINLLQVKMRKRYSVDK  
SLSHPWLQEYQTWLDLRELEGKMGERYITHESSDARWEQFAAEHPLPGSGLPTDRDLGGA  
CPPQDHDMQGLAERISVL

SEQ ID NO: 131\_AA127299\_H

IQFIIVGAKDLLAMDSNGLSDPYIKITNLSQKTKVKKTLTPTWNETFFVHFPEKTTLEL  
ECWDHDTFSDDFIGKASISLAEIPALAEVDMWIDMKTKKGEFAGK

## FIGURE 1C

SEQ ID NO: 132\_AA316804\_H

MSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSARLSNGSFSAPSILTNSRGSVHTV  
SFLQIGLTRESVTIEAQELSLSAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSEN  
ILQLITSADIEHGEDLVEVLSALATVEDFQIRPHTLYVHSYKAPTFCDYCGEMLWGLVR  
QGLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSNVSLPGPGLSVPRPLQPEYVALPSEES  
HVHQEPSKRIPSWSGRPIWMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGM  
QCKDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDIPMDIDNNDINSOSSRGLDDT  
EESPSPEDKMFFLDPSDLDERDEEAVKTISPSTSNIPLMRVQSIKHTKRKSSTMVKE  
GWMVHYTSRDNLRKRHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNISQG  
SNPHCFEIIITDMVYFVGENNGDSSHNPLAATGVGLDVAQSWEKAIRQALMPVTPQASV  
CTSPGQGDHDKDLSTSISVSNCQIQENVDISTVYQIFADEVLGSGQFGIVYGGKHKRTGR  
DVAIKVIDKMRFPKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVMEKLHGDML  
EMILSSEKSRLEPERITKFMVTQILVALRNLHFKNIVHCDLKPENVLLASAEFPQVKLCD  
FGFARIIGEKSFRRSVVGTPAYLAPEVLRSGYNRSLDMWSVGVIYVSLSGTFPFNEDE  
DINDQIQNAAFMYPNPWREISGEAIDLINLLQVKMRKRYSDKSLSHPWLQDYQTWLD  
LREFETRIGERYITHESDDARWEIHAYTHNLVYPKHFIMAPNPDDMEEDP

SEQ ID NO: 133\_PKNBETA\_H

MEEGAPRQPGPSQWPPPEDEKEVIRRAIQKELKIKEGVENLRRVATDRRHLLGHVQQLLRSS  
NRRLEQLHGELRELHARILLPGPGPGPAEPVASGPRPWAEQLRARHLEALRRQLHVELKV  
KQGAENMTHTCASGTPKERKLLAAQOQMLRDSQLKVALLRMKISSLEASGSPEPGPELLA  
EELQHRHLHVEAAVAEGAKNVVKLLSSRRTQDRKALAEQAQLQESSQKLDLLRLALEQLL  
EQLPPAHLRSRVTRRELRAAVPGYPQPSGTPVKPTALTGTQLQVRLGCEQLLTAVPGRSP  
AAALASSPSEGWLRTKAKHQGRGELASEVLAVLKVDNRVVGQTGWGQVAEQSWDQTFVI  
PLERARELEIGVHWRDWRQLCGVAFLRLDFLDNACHQLSLSLVPQGLLFAQVTFCDPVI  
ERRPRLQRQERIFSKRRGQDFLRRSQMNLGMAAWGRLVMNLLPPCSPSTISPPKGCPR  
PTTLREASDPATPSNFLPKKTPLGEEMTPPPKPPRLYLPQEPTSEETPRTRKPHMEPRTR  
RGPSPPASPTRKPPRLQDFRCLAVLGRGHFGKVLVQFKGTGKYAIAKALKKQEVLSRDE  
IESLYCEKRILEAVGCTGHPFLLSLLVCFQTSSSHARFVTEFVPGDLMMQIHEDVFPEPQ  
ARFYVACVVLGLQFLHEKKIYRDLKLDNLLLDAAQGFLKIADFGLCKEGIGFGDRTSTFC  
GTPEFLAPEVLTQEAYTQAVDWWALGVLLYEMLVGECPPFGDTEEEVFDCIVNMDAPYPG  
FLSVQGLEFIQKLLQKCPEKRLGAGEQDAEEIKVQPPFRITTNWQALLARTIQPPFVPTLC  
GPADLRYFEGEFTGLPPALTPPAPHSLLTARQQAARDFDFVSERFLEP

SEQ ID NO: 134\_AI021023\_M\_PKNBETA\_M

LKWDNLLLDAAQGFLKIADFGLCKEGIGFGDRTSTFCGTPEFLAPEVLTQEAYTRAVDWWG  
LGVLLYEMLVGECPPFGDTEEEVFDCIVNMDAPYPGFLSVQGLEFIQKLLQKCPEKRLGA  
GEQDAEEIKVQPPFRITTNWQALLARTIQPPFVPTLCGPADLRYFEGEFTGLPPALTPPAP  
HSLLTARQQAARDFDFVSERFLEP

SEQ ID NO: 135\_H19102\_H

GGNIRGPWARGWKSLSWTGLGTIRSDLEELWELRGHHYHQLHESLKPAFVLVEKPLPEWFPV  
QFINLFLPEFPPIRPIRGQQQLKILGLVAKGSFGTVLKVLDCTQKAVFAVKVPKVKVLQR  
DTVROCKEEVSIQRQINHPFVHSLGDSWQGRHLFIMCSYCSTDLYSLWSAVGCFPEASI  
RLFAAELVLVLCYLHDLGIMHRDVKMENILLDERGHLKLTDFGLSRHVPQGAQAYTICGT  
LQYMAPEVLSGGPYNHAADWWSLGVLLFSLATGKFPVAAERDHSVAMLASVTHSDSEIPAS  
LNQGLSLLLHELLCQNPLHRLRYLHHFQVHPFFRGVAFDPELLQKQPVNFVTETQATQPS  
SAETMPFDDFDCDLESFLLYPIPA

## FIGURE 1D

SEQ ID NO: 136\_AA476563\_H

MEFFRIDSKDSASELLGLDFGEKLYSLKSEPLKPFFTLPDGDSASRSFNTSESKVEFKAQ  
DTISRGSDSVFVIFSKDAAFDDVSGTDEGRPDLLVNLPGELESTREAAAMGPTKFTQTN  
IGIIEINKLLEAPDVLCLRLSTEQCOAHEEKGIEELSDPSGPKSYSITEKHQAQEDPRMLF  
VAAVDHSSSGDMSLLPSSDPKFQGLGVVESAVTANNTESLFRICSPLSGANEYIASTDT  
LKTEEVLLFTDQTDLLAKEEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALAS  
RFYIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHIQLTYFSRWSEVEDS  
CDSDAIERMYCAPEVGAITEETEACDWWSLGAVLFELLTGKTLVECHPAGINTHTTLNMP  
ECVSEEARSLIQQLLQFNPLERLGAGVAGVEDIKSHPFFTPVDWAEELMR

SEQ ID NO: 137\_AA626690\_H

MLPFAPQDEPDREMEVFSGGGASSGEVNLKMWDEPMEEGEADSCHDEGVVKEIPITHH  
VKEGYEKADPAQFELLKVLGQGSFGKVFLVRKKTGPDAGQLYAMKVLKKASLKVRDRVRT  
KMERDILVEVNHPFIVKLHYAFQTEGKLYLILDFLRGGDVFTRLSKEVLFTEEDVKFYLA  
ELALALDHLHLQGLIVYRDLKPENILLDEIGHIKLTDGFLSKESVDQEKKAYSFCGTVEYM  
APEVVNRRGHSQSADWWSYGVLMFEMLTGTLPFQKDRNETMNMILKAKLGMPQFLSAEA  
QSLRLMLFKRNPANRLGSEGVVEIKRHLFFANIDWDKLYKREVQPPFKPASGKPDFTFCF  
DPEFTAKTPKDSPLPASANAHQLFKGFSFVATSIAEYKITPITSANVLPVQINGNAA  
QFGEVYELKEDIGVGSYSVCKRCIHATTNMEFAVKIIDKSKRDPSEEIEILMRYGQHPNI  
ITLKDVFDDGRYVYLVTDLMKGGELLDRILKQKCFEREASDILYVISKTVDYLHCQGVV  
HRDLKPSNILYMDESASADSIRICDFGFAKQLRGENGILLTPCYTANFVAPEVLMQQGYD  
AACDIWSLGVLFYTMLAGYTPFANGPNDTPEEILLRIGNGKFSLSGGNWDNISDGAKDLL  
SHMLHMDPHQRYTAEQILKHSWITHRDQLPNDQPKRNDVSHVVKGAMVATYSALTHKTFQ  
PVLEPVAASSLAQRRSMKKRTSTGL

SEQ ID NO: 138\_AA215680\_H

MSLVACECLPSPGLEPEPCSRARSQAHVYLEQIRNRVALGVPDMTKRDYLVDAATQIRLA  
LERDVSEDYEAFFNHQNGVDVLLRGIHVDPNKKERREAVKLKITKYLRRAEEIFNCHLQR  
PLSSGASPSAGFSSRLRLPIRTLSSAVEQLRGCRVVGVIKVLQVQDPATGGTFVVKSLP  
RCHMVSRERLTIIPHGVPMYTKLLRYFVSEDSIFLHLEHVQGGTLWSHLLSQAHSRHSGL  
SSGSTQERMKAQLNPHLNLTPARLPSGHAPGQDRIALEPPRTSPNLLLAGEAPSTRPQR  
EAEGEPTARTSTSGSSDLPKAPGGHLHLQARRAGQNSDAGPPRGLTWVPEGAGPVLGGCG  
RGMDQSCLSADGAGRGCGRATWSVREEQVKQWAAEMLVALEALHEQGVLCRDLHPGNLLL  
DQAGHIRLTYFGQWSEVEPQCCGEAVDNLISAPEVGGISELTEACDWWFSGSLLYELLTG  
MALSQSHPSGIAHTQLQLPEWLSRPAASLLTELLQFEPTRRLGMGEGGVSKLKSHPFFS  
TIQWSKLVG

SEQ ID NO: 139\_SGK\_H

MTVKTEAAKGTLYSRMRGMVAILIAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKI  
SQPQPELMNANPSPPPSPSQQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKA  
EVFYAVKVLQKAILKKKEEKHIMSERVLLKNVKHPFLVGLHFSFQTADKLYFVLDYIN  
GGELFYHLQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD  
FGLCKENIEHNSTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSR  
NTAEMYDNILNKPLQLKPNITNSARHLLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINW  
DDLINKKITPPFNPVSGPNELRHFDPEFTEEPVPNSIGKSPDSVLVTASVKEAAEAFLG  
FSYAPPTDSFL

SEQ ID NO: 140\_AA107515\_M

MTVKAEAAARSTLYSRMRGMVAILIAFMKQRRMGLNDFIQKIASNTYACKHAEVQSILKM  
SHPQPELMNANPSPPPSPSQQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKA



## FIGURE 1E

EVFYAVKVLQKKAILKKKEEKHIMSERNVLLKNVKHPFLVGLHFSFQTADKLYFVLDYIN  
GGELFYHLQRRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD  
XFQLRRIEHNGTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSRN  
TAEMYDNILNKPLQLKPNITNSARHLLLEGLLQKDRTKRLGAKDDFMEIKSHIFFSLINWD  
DLINKKITPPFNPVSGPSDLRHFDPFTEEPVPSSIGRSPDSILVTASVKEAAEAFLGF  
SYAPPVDSFL

SEQ ID NO: 141\_AA109508\_M

HLQRRERFLEPRARFYAAEVASAIIGYLHSLNIIYRDLKPENILLDCQGHVVLTDFGLCKE  
GVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSDVSQMY  
ENILHQPLQIPGGRTVAACDLLQSLHKKQQRQLGSKADFLEIKNHVFFSPINWDDLYHK  
RLTPPFNPVNTGPADLKHFDPEFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPEDDD  
ILDC

SEQ ID NO: 142\_AA887783\_H

MQRDHTMDYKESCPVXIPSSDEHREKKKRFTVYKVLVSVGRSEWFVFRRYAEFDKLYNT  
LKKQFPAXALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHDPDVRFLQMD  
SPKHQSDPSEDEDERSSQKLHSTSONINLGPSPHAKPTDFDFLKVIGKGSFGKVLLAK  
RKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKHPFLVGLHYSFQTTEKLYFVL  
DFVNGGEGHVLTDFGLCKEGIAISDTTTFCTGTPEYLAPEVIRKQPYDNTVDWWCLGAV  
LYEMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSIIEELLEKDRQNRLGAKEDF  
LEIQNHPPFESLSWADLVQKKIPPPFNPVAGPDDIRNFDTAFTEETVPYSVCVSSDYSI  
VNASVLEADDAFVGFSYAPPSDLFL

SEQ ID NO: 143\_R47805\_H

MAHQGTGIHATEELKEFFAKARAGSVRLIKVVIEDEQLVLGASQEPVGRWDQDYDRAVLPL  
LDAQQPCYLLYRLDSQNAQGFELFLAWSPDNSPVRLKMLYAATRATVKKEFGGGHIKDE  
LFGTVKDDLSFAGYQKHLSSCAAPAPLTSARERLQQIRINEVKTEISVESKHQTLQGLAF  
PLQPEAQRALQQLKQKMVNYIQMKDLERETIELVHTEPTDVAQLPSRVPRDAARYHFFL  
YKHTHEGDPLESVVFIYSMPGYKCSIKERMLYSSCKSRLLDSVEQDFHLEIAKKIEIGDG  
AELTAEFLYDEVHPKQHAFKQAFAPKPGGKRGHKRLIRGPGENGDDS

SEQ ID NO: 144\_H60215\_H

MSKLRMKRRASDRGAGETSARAKALGSGISGNNAKRAGPFILGPRLGNSPVPVSIQCLAR  
KDGTDDFYQLKILTLEERGQDQIESQEERQGMILLHTEYSLLSLLHTQDGVVHHHGLFQD  
RTCEIVEDTESSRMVKKMKKRICLVLDCLCAHDFSDKTADLINLQHYVIKEKRLSERETV  
VIFYDVVRVVEALHQKNIVHRDLKLGNMVLNKRTHRITITNFCGLKHLVSEGDLLKDQRG  
SPAYISPDVLSGRPYRGKPSDMWALGVVLTMLYGGFPFYDSIPQELFRKIKAAEYTIPE  
DGRVSENTVCLIRKLLVLDPQQRLLAAADVLEALSAIASWQSLSSLSGPLQVVPDIDDQM  
SNADSSQEAKVTEECQYEFENYMRQQLLLAEKSSIHDTRSWVPKRQFGSAPPVRLGH  
DAQPMTSLDTAILAQRYLRK

SEQ ID NO: 145\_SGK324\_H

MASTRSIELEHFEERDKRPRPGSRRGAPSSSGSSSGPKGNGLIPSPAHSAHCSFYRTR  
TLQALSSEKKAKKARFYRNGDRYFKGLVFAISSDRFRSFDALLIELTRSLSDNVNLPQGV  
RTIYTIDGSRKVTSLDELLEGESYVCASNEPFRKVDYTKNINPNWSVNIKGGTSRALAAA  
SSVKSEVKESKDFIKPKLVTVIRSGVKPRKAVRILLNKKTAHSFEQVLTIDITEAIKXASG  
VVKRLCTLDGKQVRVTCVHLPDFFGDDDVFIACGPEKFRYAQDDFVLDHSECRVLKSSYS  
RSSAVKYSGSKSPGSRSSQISAHGRSSSNVNGGPELDRCSIEGVNGNRCSESSTLLEK  
YKIGKVIKVDGNFAVVKECIDRSTGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNII

## FIGURE 1F

MLVEEMETATELFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHGLSIVH  
RDIKPENLLVCEYDPDGTSLKLGDFGLATVVEGPLYTVCGTPTYVAPXIIAETGYGLKVD  
IWAAGVITYILLCGFPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSAKELISQMLQ  
VNVEARCTAGQILSHPWVSDDASQENMQAEVTGKLKQHFNNALPKQNSTTTGVSVIMVS  
GRRQVWPDCGAGLEVFEFGSRELPSHGSWCLP

SEQ ID NO: 146\_W30246\_M SGK324\_M

TKSSSSSPTSPGSFRGLKISAQGRSSSNVNGGPELDRCLSPGVNGNRCSESFPILLEKYR  
IGKVI GDGNFAVVKECVDRTYGKEFALKI IDKAKCCGKEHLIENEVSILRRVKHPNIIML  
VEEMETATD LFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHSLSIVHRD  
IKPENLLVCEYDPDGTSLKLGDFGLATVVEGPLYTVCGTPTYVAPEIIAETGYGLKVDVW  
AAGVITYILLCGFPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSPCVCFRKCL

SEQ ID NO: 147\_AA383293\_H

PAAKRVVYRNGDPFFPGSQLVVTQRRFPTMEAFCEVTSAVQAPLAVRALYTPCHGHPV  
TNLADLKNRGQYVAAGFERFHKLPYQAFCLSVFRNGDLVSPFSLKLSQAASQDWETVL  
KLLTEKVKLQSGAVRLCTLEGLPLSAGKELVTGHYYVAVGEDEFKDLPPALSTRGLLAA  
GNEAHLRSGVGTVAGSPKPLGRKAKKETCLIVTLTLKYQQSETSRDQSFPSGVI GYGA  
PHRRKETAGALEVADDEDTQTEEPDQRAAQIVEQVTCLODFGDDDDVFIACGPEKFRYA  
QDDFVL DHSRRLLREHQAGFEKLRRTRGEEKEAEKEKKPCMSGRRMTLRDDQPAKLEK  
EPKTRPEENKPERPSGRKPRPMGI IANVEKHYETGRVIGDGNFAVVKECRHRRETRQAYA  
MKIIDKSRLKGKEDMVDSEILIIQSLSHPNIVKLHEVYETDMEIYLILEYVQGGDLFDAI  
IESVKFPEPDAALMIMDLCKALVHMHDKSIVHRDLKPENLLVQRNEDKSTTLKLADFGLA  
KHVVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPFRSPXXGDQDE  
LFNIIQLGHFEFLPPYWDNISDAKDLVSRLLVDPKKRYTAHQVLQHPWIETAGKTNTV  
KRQKQVSPSSDGHFRSQHKRVVEQVS

SEQ ID NO: 148\_AA197883\_M

MPTAPVLRPPPPATPAPPAPSRPAPP I PGHRGPCDHSCLKLSSKISERKLPGPWLPAGR  
GPLEKPV LGPRGAVMPLFSPQSSLHVSRAEHSPLKPRVTVVKLGQPLRKATLLNRRS  
VQTFEQLLSDISEALGFPRWKNDVRKLF TLKGREVKSVSDFFREGDAFIAMGKEPLTLK  
SIQLAMEELYPKNRALALAPHSRVPSRLRSRLPSKLLKGSHRCGEAGSYSAEMESKAVS  
RHQGKTSTVLAPEDKARAQKWVRGKQSESEPGGPPSPGAATQEETHASGEKHLGVEIEKTS  
GEIVRCEKCKRERELQLGLQREPCPLGTSELDLGRAQKRDSEKLVRTKSCRPSKAKFTD  
GEEGWKGD SHRGSPRDPPQEMRRPNSNSDKKEIRGSESQDSYPQGAQKDFVEGPPAV  
EEGPIDMRREDRHTCRSKHAAWLRREQQAEPPLPRTRGEEKQAEHEKKPGGLGERRAPE  
KESKRKLEEKPERPSGRKPRPKGI ISADVEKHYDIGGVI GDGNFATVKECRHRETKQAY  
AMKMIDKSQKLGKEDIVDSEILIIQSLSHPNIVKLHEVYETEAEIYLIMEYVQGGDLFDA  
IVENVKFPEPEAAVMITDLCKAFVHMHDKNIVHRDVKPENLLVQRNEDKSITLKLADFG  
AKYVVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPFRSPERDQDE  
LFNIIQVQGFEFLSPYWDNISDAKDLVRNLLVDPKKRYTAEQVLQHPWIEMVGHNTG  
NSQKEESPNSLGHFQSQHKKVAEQMP

SEQ ID NO: 149\_DRAK2\_H

MSRRRFDCRSISGLLTTPQIPIKMFNNFYILTSKELGRGKFAVVRQCI SKSTGQEYA  
AKFLKKRRRGQDCRAEILHEIAVLELAKSCPRVINLHEVYENTSEIILILEYAAGGEIFS  
LCLPELAEMVSENDVIRLIKQILEGVYYLHQNNIVHLDLKPQNILLSSIYPLGDIKIVDF  
GMSRKIGHACELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN  
QETYLNISQVNDYSEETFSSVSQLATDFIQSLLVKNPEKRPTAEICLSHSLWQQWDFEN

## FIGURE 1G

LFHPEETSSSSQTQDHSVRSSSEDKTSKSSCNGTCGDREDKENIPEDSSMVSKRFRFDDSL  
PNPHELVSDDLCC

SEQ ID NO: 150\_W44160\_M DRAK2\_M  
MSRRRFDRCRSVSGLLTTTPQTPIKTENFNNFYTLTPKELGRGKFAVVRQCISKSTGQEYA  
AKSLKKRRRGQDCRAEILHEIAVLELARSCPHVINLHEVYENATEIILVLEYAAGGEIFN  
LCLPELAEMVSENDVIRLIKQILEGVHYLHQNNIVHLDLKPQNILLSSIIYPLGDIKIVDF  
GMSRKIGNASELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN  
QETYLNISQVNVYDSEEMFSSVSQLATDFIQSLLVKNPEKRPTAESCLSHSWLQQWDFGS  
LFHPEETSGSSQIQDLTLRSSEKTSKSSCNGSCGAREDKENIPEDGSLVSKRFRFDDSL  
PSPHELVPDLFC

SEQ ID NO: 151\_H01248\_H, DRAK1\_H  
MIPLEKPGSGGSSPGATSGSGRAGRGLSGPCRPPPPQARGLLTEIRAVVRTEPFQDGYS  
LCPGRELGRGKFAVVRKCIKKDSGKEFAAKFMRKRRKGQDCRMEIIEIAVLELAQDNPW  
VINLHEVYETASEMILVLEYAAGGEIFDQCVADREEAFKEKDVQRLMRQILEGVHFLHTR  
DVVHLDLKPQNILLTSESPGDIKIVDFGLSRILKNSEELREIMGTPEYVAPEILSYDPI  
SMATDMWSIGVLTYYMLTGISPFLGNDKQETFLNISQMNLSYSEEEFDVLSSESAVDFIRT  
LLVKKPEDRATAEECLKHPWLTQSSIQEPSFRMEKALEEANALQEGHSVPEINSDDTKSE  
TEESIVTEELIVVTSYTLGQCRQSEKEKMEQKAIKSRFKFEEPLLQEIPEGFIY

SEQ ID NO: 152\_AA021445\_H  
MPARIGYYEIDRTIGKGNFAVVRATHLVTKAKVAIKIIDKTQLDEENLKKIFREVQIMK  
MLCHPHIIRLYQVMETERMIYLVTEYASGGEIFDHLVAHGRMAEKEARRKFKQIVTAVYF  
CHCRNIVHRDLKAENLLLDANLNIAKIDFGFSNLFTPGQLLKTWCGSPPYAAPELFEGKE  
YDGPVKDIWSLGVVLYVLVCGALPFDGSTLQNLRARVLSGKFRI PFFMSTECEHLIRHML  
VLDPNKRLSMEQICKHKWMKLGADPNFDRLIAECQQLKEERQVDPLNEDVLLAMEDMGL  
DKEQTLQSLRSDAYDHYSAIYSLLCDRHKRHKTLRLGALPSMPRALAFQAPVNIQAEQAG  
TAMNISVPQVQLINPENQIVEPDGTLNLDSDGEPEPSPEALVRYLSMRRTVGVADPRTE  
VMEDLQKLLPGFPGVNPQAPFLQVAPNVNFMHNLPMQNLQPTGQLEYKEQSLQPPPTLQ  
LLNGMGPLGRRASDGGANIQLHAQQLLKRPRGPSPLVTMTPAVPAVTPVDEESSDGEPOQ  
EAVQRYLANRSKRHTLAMTNPTAEIPPDQRLQGLQPPFRSRVWPPHLPDQHRSTYKDSN  
TLHLPTERFSPVRRFSDGAASIQAFKAHLEKMGNNSSIKQLQCECEQLQKMYGGQIDERT  
LEKTQQQHMLYQQEQHHQILQQQIQDSICPPQPSPLQAACENQALLTHQLRLRIQPS  
SPPNHPNNHLFRQPSNSPPPMSSAMIQPHGAASSSQFQGLPSRSAIFQQQPENCSSPPN  
VALTCLGMQPPAQSQQVTIQVQEPVDMLSNMPGTAAGSSGRGISISPSAGQMOMQHRTNL  
MATLSYGHRPLSKQLSADSAEAHSLNVNRFSPANYDQAHLPPLFSDQSRGSPSSYSPST  
GVGFSPTQALKVPPLDQFPTFPFSAHQPPHYTTSALQQALLSPTPPDYTRHQQVPHILQ  
GLLSRPHSLTGHSDIRLPPTFEFAQLIKRRQQQORQQQQQQQQQEQEYQELFRHMNQGDAGSL  
APSLGGQSMTERQALSQYQADSYHHHTSPQHLLQIRAEQCVSQASSPTPPHGYAHQPALM  
HSESMEEDCSCEGAKDGFQDSKSSSTLTGCHDSPLLLSTGGPGDPESLLGTVSHAQELG  
IHPYGHQPTAAFSKNKVPSREPVIGNCMDRSSPGQAVELPDHNLGYPARPSVHEHHRPR  
ALQRHHTIQNSDDAYVQLDNLPGMSLVAGKALSSARMSDAVLSQSSLMGSQQFQDGENEE  
CGASLGGHEHPDLSGDSQHLNSSCYPSTCITDILLSYKHPEVSFSMEQAGV

SEQ ID NO: 153\_2R22-5-11\_H  
MTAVYMNGGGLVNPHYARWDRRDSVESGCQTESSKEGEGQPRQLTPFEKLTQDMSQDEK  
VVREITLTKRIGFYRIRGEIGSGNFSQVKLGIHSLTKEKVAIKILDKTCLDQKTQRLLSR  
EISSMEKLHHPNIIRLYEVVETLSKLHLVMEYAGGELFGKISTEGKLSEPESEKLIQSQI  
VSAVKHMHENQIHRDLKAENVFYTSNTCVKVGDFGFSTVSKKGEMLNTFCGSPPYAAPE

## FIGURE 1H

LFRDEHYIGIYVDI WALGVLLYFMVTGTMPFRAETVAKLKKSILEGTYSVPPHVSEPCHR  
 LIRGVLLQQIPTERYGIDCIMNDEWMQGVYPTPLEPFQLDPKHLSETSTLKEEENEVKST  
 LEHLGITEEHIRNNQGRDARSSITGVYRIILHRVQRKKALESVPVMMLPDPKERDLKKGS  
 RYVRGIRHTSKFCSIL

SEQ ID NO: 154\_R31237\_1\_H, AAC33487

MSTRTPLPVTNERDTENHTSHGDGRQEVTSRTSRSGARCRNSIASCADQPHIGNYRLLK  
 TIGKGNFAKVKLARHILTGREVAIKIIDKTQLNPTSLQKLFREVRIMKILNHPNIVKLFE  
 VIETEKTLYLIMEYASGGEVFDYLVAHGRMKEKEARSKFRQIVSAVQYCHQKRIVHRDLK  
 AENLLLDADMNIKIADFGFSNEFTVGGKLDTF CGSPPYAAPELFGKKYDGP EVDVWSLG  
 VILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKRFLVLNPIKRGTL EQ  
 IMKDRWINAGHEEDELKPFVEPELDISDQKRIDIMVGMGYSQEEIQESLSKMKYDEITAT  
 YLLLGRKSSSELDASDSSSSSNLSLAKVRPSSDLNNSTGQSPHHKVQRSVSSSQKQRRYSD  
 HAGPAIPSVVAYPKRSQTSTADGLKEDGISSRKSSGSAVGGKGIAPASPMLGNASPNK  
 ADIPERKKSSTVPSSNTASGGMTRRNTYVCERTTADRHSVIQNGKENSTIPDQRTPVAS  
 THSISSAATPDRI RFPRTASRSTFHGQPRERRTATYNGPPASPSLSHEATPLSQTRSRG  
 STNLF SKLTSKLT SRNVSAEQDENKEAKPRSLRFTWSMKTTSMDPGDMMREIRKVL D  
 ANNC DYEQRERFLFCVHGDGHAENLVQWEMEVC KLPRLSLNGVRFKRISGTSIAFNIA  
 SKIANELKL

SEQ ID NO: 155\_W90839\_M

KGPSWSSRSLGARCRNSIASCPEEQPHVGNRYLLRTIGKGNFAKVKLARHILTGREVAIK  
 IIDKTQLNPSSLQKLFREVRIMKGLNHPNIVKLFEVIETEKTLYLMYASAGEVFDYLV  
 SHGRMKEKEARAKFRQIVSAVHYCHQKNIVHRDLKAENLLD AEANI KIADFGFSNEFTL  
 GSKLDTF CGSPPYAAPELFGKKYDGP EVDIWSLG VILYTLVSGSLPFDGHNKELRERV  
 LRGKYRVPFYMSTDCESILRRFLVLNPAKRCTLEQIMKDKWINIGYEGEELKPDTELKEE  
 RMPGRKASCSAVGSGSRGLPSSPMVSSAHNPNAEIPERRKDSTSTPNNLPPSMMTRRN  
 TYVCTERPGSERPSLLPNGKENS SGT SRVPPASPSHSLAPPSGERSRLARGSTIRSTFH  
 GGQVRDRRAGSGSGGVQNGPPASPTLAHEAAPLPSGRPRPTTNLFTKLTSKLTTRVTDE  
 PERIGGPEVTSCHLPWDKTETAPRLLRFPWSVKLTSSRPS

SEQ ID NO: 156\_406786.5\_H

MEVGGLTVFEEDQRCLSQLPLPVSAEGPAAQTAEPSRSFSSAHRHLSRRNGLSRLCQS  
 RTALSEDRWSSYCLSSLAQNICTSKLHCPAAPEHTDPSEPRGSVSCCSLLRGLSSGWSS  
 PLLPAPVCNPNKAIFTVDAKTTEILVANDKACGLLGYSQDLIGQKLTQFFLRSDSDVVE  
 ALSEEHMEADGHA AVVFGTVVDIITRSGEKI PVSVMKMRMRQERRLCCVVVLEPVERVST  
 WVAFAQSDGTITSCDSLFAHLHGYSGEDVAGQHITDLIPSVQLPPSGQHIPPKNLKIQRSV  
 GRARDGTTTFPLSLKLKSQPSSEEATTGEAAPVSGYRASVWVFCTISGLITLLPDGTIHGI  
 NHSFALTFLGYGKTELLGKNITFLIPGFYSYMDLAYNSSQLQPLDASCLDVGNESGCGER  
 TLDPWQGDPAEGGQDPRINVVLAGGHVVP RDEIRKLME SQDIFTGTQTELIAGGQLLSC  
 LSPQPAPGVDNVPESGLPVHGEQALPKDQQTALGREEPVAIESPGQDLLGESRSEPVDV  
 KPFASCEDSEAPVPAEDGSDAGMCGLCQKAQLERMGVSGPSGSDLWAGAAVAKPQAKGQ  
 LAGGSLLMHCPCYGSEWGLWWSQDLAPSPSGMAGLSFGTPTLDEPWLGVENDREELQTC  
 LIKEQLSQLSLAGALDVPHAE LVPTECQAVTAPVSSCDLGGRDLCGGCTGSSSACYALAT  
 DLPGGLEAVEAQEVDVNSFSWNKELFFSDQTDQTSSNCS CATSELRETPSSLAVGSDPD  
 VGS LQE QGSCVLDRELLLLTGTCVDLGQGRFRFRES CVGHDPTEPLEVCLVSSEHYAASD  
 RESPGHVPSTLDAGPEDTCPSAEPRNLNVQVTSTPVI VMRGAAGLQREIQEGAYS GSCYH  
 RDGLRLSIQFEVRRVELQGPTPLFCCWL VKDLLHSQRDSAARTRFLASLPGSTHSTAAE  
 LTGPSLVEVLRARPWFEPPKAVELEGLAACGEYSQKYSTMSPLGSGAFGFVWTAVDKG  
 KNKEVVVKFIKKEKVLEDCWIEDPKLGKVTLEIAILSRVEHANI KVLDIFENQGFQQLV

## FIGURE 11

MEKHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAGQSRLVSAVGYLRLKDI IHRDIKDEN  
 IVIAEDFTIKLIDFGSAAYLERGKLFYTFCGTIEYCAPEVLMGNPYRGPELEMWSLGVTL  
 YTLVFEENPFCELEETVEAAIHPPYLVSKEMLSVSGLLQPVPERRTTLEKLVTDWPVTO  
 PVNLADYTWEVFRVKNPESGVLASASLEMGNRSLSDVAQAQELCGGPVPGEAPNGQGCL  
 HPGDPRLLTS

SEQ ID NO: 157\_AA544838\_M 406786\_M

TRPHPCLEPLASFIHQRLVSAVGYLHSGGIIHRDIKDENIVIAEDFTIKLIDFGSAAYL  
 ERGKLFYTFCGTIEYCAPEVLIGNPYRGPELEMWSLGVTLTYTLIFEENPFCEVEETMEAV  
 IHPPFLVSQELMSLLSGLLQPCPEQRTTLEKLRDPWVTQPVNLASYTWEVCRTNQPS  
 GLLSASLEIGSRSPSEMAQREGLCGPPAPRETRGDQHCLHLKDPPLPVS

SEQ ID NO: 158\_AA785735\_H

MVMADGPRHLQRGVVRVGFYDIEGTLGKGNFAVVKLGRHRITKTEVAIKI IDKSQLDVN  
 LEKIYREVQIMKMLDHPHI IKLYQVMETKSMYLVTEYAKNGEIFDYLANHGRLNESEAR  
 RKFQWILSAVDYCHGRKIVHRDLKAENLLLDNNMNIIADFGFGNFFKSGELLATWCGSP  
 PYAAPEVFEGQQYEGPQLDIWSMGVVLVYLVCGALPFDGPTLPILRQRVLEGRFRIPYFM  
 SEDCEHLIRRMVLDPKRLTIAQIKEHKWMLIEVPVQRPVLYPQEQENEPSIGEFNEQV  
 LRLMHSGLIDQKXIESLQNKSYNHFAAIYFLLVERLKSRRSSFPVEQRLDGRQRRPSTI  
 AEQTVAKAQTVGLPVTMHSNPMRLLRSALLPQASNVEAFSFPASGCQAEAAFMEEECVDT  
 PKVNGCLLDPPVPLVRKGCQSLPSNMETSIDEGLETEGEAEEDPAHAFAEFQSTRSGQ  
 RRHTLSEVTNQLVMPGAGKIFSMNDSPSLSDVSEYDMGSVQRDNLNLEDNPSLKDIML  
 ANQPSPRMTSPFISLRPTNPAMQALSSQKREVNHRSPVSFREGRRASDTSLTQGI VAFRQ  
 HLQNLARTKGILELNKVQLLYEQIGPEADPNLAPAAPQLQDLASSCPQEEVSQQQESVST  
 LPASVHPQLSPQSLETQYLQHRLOKPSLLSKAQNTCQLYCKEPPRSLEQQLOEHRLOOK  
 RLFLQKQSQLQAYFNQMQUIAESYQPSQQLPLPRQETPPPSQQAPPFSLTQPLSPVLEP  
 SSEQMYSFPLSQYQEMQLQPLPSTSGPRAAPPLPTQLQQQQPPPPPPPPRQPGAAPA  
 PLQFSYQTCELPSAASPAPDYPTPCQYPVDGAQQSDLTGPDPCRSPGLQEAPSSYDPLAL  
 SELPGLFDCEMLDAVDPQHNGYVLVN

SEQ ID NO: 159\_AA207220\_H

MESLVFARRSGPTPSAAELARPLAEGLIKSPKPLMKKQAVKRHHKHNLRHRYEFLETGL  
 KGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHIIAIEHVEFE  
 NSSKIVIMEYASRGDLYDIISERQQLSEREARHFFRQIVSAVHYCHQNRVVRDLKLEN  
 ILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVDSWSLGVLL  
 YILVHGTMPFDGHDHKLIVKQISNGAYREPPKPSDCLXGLIRWLLMVNPTRRATLEDVAS  
 HWWVNWGYATRVGEQEPHEGGHPGSDSARASMAWDLRRSSRPLENGAKVCSFFKQHAP  
 GGGSTTPGLERQHSLLKSRKENDMAQSLHSDTADDTAHRPGKSNLKLPKGILKKKVSASA  
 EGVQEDPPELSPIPASPGQAAPLLPKKGILKKPRQRESGYYSPEPSESSELDDAGDVVF  
 SGDPKEQKPPQASGLLLHRKGILKLNKFSQTALELAAPTTFGSLDELAPRPLARASRP  
 SGAVSEDSILSSESFDQLDLPERLPEPPLRGCVSDNLTGLEPPSEGPGSCLRRWRQDP  
 LGDSCFSLTDCQEVATATYRQALRVCSKLT

SEQ ID NO: 160\_AA426580\_H, MAK\_V\_H

MPAAAGDGLLEGAAPGGGGGAEDAAPAAACEGSFLPAWVSGVPRERLRDFQHHKRVGN  
 YLIGSRKLGEESFAKVRGLHVLTKGEKVAIKVIDKKRAKDTYVTKNLRREGQIQQMIRH  
 PNITQLLDILETENSYYLMELCPGGNLMHKIYEKKRLEESEARRYIRQLISAVEHLHRA  
 GVVRDLKIEENLLDEDNNIKLIDFGLSNCAGILGYSDPFSTQCGSPAYAAPELLARKKY  
 GPKIDVWSIGVNMAMLTGTLPTVEPFSRLALYQKMVDKEMNPLPTQLSTGAISFLRSL  
 LEPDPVKRPNIQQALANRWLNENYTGKVP CNVTYPNRISLEDLSPSVVLHMTKLGKNS

## FIGURE 1J

DVINTVLSNRACHILAIYFLLNKKLERYLSGKSDIQDSLCKYKTRLYQIEKYRAPKESYEA  
 SLDTWTRDLEFHAVQDKPKKEQEKRGDFLHRPFSKKLDKNLPSHKQPSGSLMTQIQNTKA  
 LLKDRKASKSSFPDKDSFGCRNIFRKTSDSNCVASSSMEFIPVPPRTPRIVKKPEPHQP  
 GPGSTGIPHKEDPLMLDMVRSFESVDRDDHVEVLSPSHHYRILNSPVSLARRNSSERTLS  
 PGLPSGMSPLHTPLHPTLVSFHEDKNSPKKEGLCCPPVPVPSNGPMQPLGSPNCVKSR  
 GRFPMMGIGQMLRKRHQSLOPSADRPLEASLPPLQPLAPVNLAFDMADGVKTQC

SEQ ID NO: 161\_Z36720\_H

MDTKLNMLNEKVDQLLHFQEDVTEKLQSMCRDMGHLEGLHRLEASRAPGPGGADGVPHI  
 DTQAGWPEVLELVRAMQQDAAQHGARLEALFRMVAAVDRAIALVGATFQKSKVADFLMQG  
 RVPWRRGSPGDSPEEWVKEEEVCFMPPVPPAPGAAGQSLQKDKGELSAEQGIWATLMTLV  
 IMVTAANKERVEEEGGKPKHVLSTSGVQSDAREPGEESQKADVLEGTAERLPPIRASGLG  
 ADPAQAVVSPGQGDGVPGPAPPAFPGHLPLPTKVEAKAPETPSENLRGTGLELAPAPGRVNV  
 VSPSLEVAPGAGQGASSSRPDPEPLEEGTRLTGPGPGPQCPGPPGLPAQARATHSGGETPP  
 RAALLKGAVAPGFSRRDLVFPISIFCACLGISIHQEMDTPGEMLMTGRGSLGPTLTTEAP  
 AAAQPGKQGPPTGRCLQAPGTEPGEQTPEGARELSPLQESSSPGGVKAEEEEQRAGAEPG  
 TRPSLARSDDNDHEVGALGLQQKSPGAGNPEPEQDCAARAPVRAEAVRRMPPGAEGSV  
 VLDDSPAPPAPFEHRVSVKETSISAGYEVQCQHEVLGGGRFGQVHRCTEKSTGLPLAAKI  
 IKVKSADREDVKNEINIMNQLSHVNLILQLYDAFESKHSCTLMMEYVDGGELFDRITDEK  
 YHLTELDVVLFTTRQICEGVHYLHQHYILHLDLKPENILCVNQTGHQIKIIDFGLARRYKP  
 REKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVIITYMLLSGLSPFLGETDAETMNFIV  
 NCSWDFDADTFEGLSEEAKDFVSRLLVKEKSCRMSATQCLKHEWLNNLPAKASRSKTRLK  
 SQLLLQKYIAQRKWKKHFYVVTAAANRLRKFTSP

SEQ ID NO: 162\_SGK088\_H

GEMALFECLVAGPTDVEVDWLCRGRLLQPALLKCKMHFDGRKCKLLLTSVHEDDSGVYTC  
 KLSTAKDELTC SARLTVRPSLAPLFTRLLEDVEVLEGRAARFDCKISGTPPPVVTWTHFG  
 CPMEESENLRLRQDGGHLHSLHIAHVGSEDEGLYAVSAVNTHGQAHCSAQLYVEEPRTAAS  
 GPSSKLEKMPISIPPEPEQGELERLSIPDFLRPLQDLEVLAKELAMLECQVTGLPYPTISW  
 FHNGHRIQSSDDRRMTQYRDVHRLVFPVAVGPQHAGVYKSVIANKLGAACYAHLYVTDVV  
 PGPPDGAPQVAVTGRMVTLTWNPPRSLDMAIDPDSLTYTVQHQLVGLSDQWTALVTGLRE  
 PGWAATGLRKGQVQHIFRVLSTTVKSSSKPSPSEPVLLEHGPTLEEAPAMLDPDIDVYV  
 VEGQPASVTVTFNHVEAQVWRSCRGALLEARAGVYELSOPDDQYCLRICRVSRDMDGA  
 LTCTARNRHGTQTC SVTLELAEAPRFESIMEDVEVGAGETARFAVVVEGKPLPDIMWYKD  
 EVLLTSSHVSFVYEENECSLVVLSTGAQDGGVYTCTAQNLAGEVSCKAELAVHSAQTAM  
 EVEGVGEDEDHRGRRLSDFYDIHQEIGRGAFSYLRRIVERSSGLEFAAKFIPSOAKPKAS  
 ARREARLLARLQHDCLVLYFHEAFERRRGLVITELCTEELLER IARKPTVCESEIRAYMR  
 QVLEGIHYLHQSHVLHLDVKPENLLVWDGAAGEQQVRICDFGNAQELTPGEPQYCQYGT  
 EFVAPEIVNQSPVSGVTDIWPVGVAFLCLTGISPFGVENDRTTLMNIRNYNVAFEETTF  
 LSLSREARGFLIKVLVQDRLRPTAEETLEHPWFKTQAKGAEVSTDHLKFLSRRRWQRSQ  
 ISYKCHLVLRPIPELLRAPPERVWVTMPRRPPPSGGLSSSSDSEEELEELPSVPRPLQP  
 EFGSGRVSLTDIPTEDALGTPETGAATPMDWQEQGRAPSQDQEAPSPEALPSPGQEPAA  
 GASPRRGELRRGSSAESALPRAGPRELGRGLHKAASVELPQRRSPGPGATRLARGGLGEG  
 EYAQRLLQALRQLLRGGPEDGKVSGLRGPLLES LGGRARDPRMARAASSEAPHHQPPE  
 NRGLOKSSSFSGEAEPRGRHRRAGAPLEIPVARLGARRLQESPSLSALSEAQPSSPARP  
 SAPKPSTPKSAEPSATTPSDAPQPPAPQPAQDKAPEPRPEPVRASKPAPPPQALQTLALP  
 LTPYAQIIQSLQLSGHAQGPSQGAAPPSEPKPHA AVFARVASPPPGAPEKRVPSAGGPP  
 VLA EKARVPTVPPRPGSSLSSSIENLESEAVFEAKFKRSRESPLSLGLRLLSRSRSEERG  
 PFRGAEEDGIYRPSAGTPLELVRRPERSRSVQDLRAVGEPGLVRRLSLSLSQRLRRT  
 PAQRHPAWEARGGDGESSEGGSSARGSPVLAMRRRLSFTLERLSSRLQRSSESSEDSSGAS

## FIGURE 1K

GRSTPLFGRLRRATSEGESLRRRLGLPHNQLAAQAGATTPSAESLGSEASATSGSSAPGES  
 RSRLRWGFSRPRKDKGLSPPNLSASVQEELGHQYVRSESDFPFVFIKLDQVLLGEAA  
 TLLCLPAACPAPHISWMKDKKSLRSEPSVIIVSCKDGRQLLSIPRAGKRHAGLYECSATN  
 VLGSITSSCTVAVARVPGKLAPPEVTQTYQDTALVLWKPGDSRAPCTYTLERRVDGESVW  
 HPVSSGIPDCYINVTHLPVGVTVRFRVACANRAGQGPFSSNSSEKVFVRGTQDSSAVPSAA  
 HQEAPVTSRPARARPPDSPTSLAPPLAPAAPTPPSVTVSPSSPPTPPSQALSSLKAVGPP  
 PQTTPRRHRGLQAARPAEPTLPSTHVTTPSEPKPFVLDGTGPIIPASTPQGVKPVSSSTPVY  
 VVTSFVSAPPAPPEPPAPEPPPEPTKVTVQSLSPAKEVSSPGSSPRSSPRPEGTTLRQGP  
 PQKPYTFLEEKARGRFGVVRACRENATGRTFVAKIVPYAAEGKPRVLQEYEVLRTHHER  
 IMSLHEAYITPRYLVLIAESCGNRELLCGLSDRFRYSEDDVATYMVQLLOGLDYLHGHV  
 LHLDIKPDNLLLAPDNALKIVDFGSAQYPNPQALRPLGHRTGTLEFMAPEMVKGEPISGA  
 TDIWGAGVLTYYIMLSGRSPFYEPDPQETEARIVGGRFADFQLYPNTSQSATLFLRKVLSV  
 HPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRRAEAATRHKVLLR  
 SYPGGP

SEQ ID NO: 163\_AA542015\_M SGK088\_M  
 ATDIWGAGVLTYYIMLSGYSPFYEPDPQETEARIVGGRFADFQLYPNTSQSATLFLRKVLS  
 VHPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRRAEAATRHKVLL  
 RSYPGSP

SEQ ID NO: 164\_R19772\_H  
 MKGGDRAYTRGPSLGWLFKCCCCFPCRDAYSHSSSENGGKSESVANLQAQPSLNFIHSS  
 PGPKRSTNTLKKWLTSPVRRNLNSGKADGNIKKQKKVRDGRKSF DLGSPKPGDETTPQGDS  
 ADESKKGWGEDEPDEESHTPLPPPMKIFDNDPTQDEMSSSLAARQASTEVP TAADLVNA  
 IEKLVKNKLSLEGSSYRGS LKDPAGCLNEGMAPPTPPKNPEEEQKAKALRGRMFVLNELV  
 QTEKDYVKDLGIVVEGFMKRIEEKGVPEDMRGKDKIVFGNIHQIYDWHKDFFLAELEKCI  
 QEQDRLAQLFIKHERKLHIYVWYCQNKPRSEYIVA EYDAYFEEVKQEINQRLTSLDFLIK  
 PIQRITKYQLLLKDFLYSEKAGLECS DIEKAVELMCLVPKRCNDMMNLGR LQGFEGTLT  
 AQGKLLQQDTFYVIELDAGMQSRTKERRVFLFEQIVIFSELLRKGS LTPGYMFKR SIKMN  
 YLVLEENVNDNDPCKFALMNRETSE RVVLQAA NADIQQAWVQDINQVLETQRDFLNALQSP  
 IEYQRKERSTAVMRSQPARLPQASPRPYSSVPAGSEKPPKGSSYNPPLPPLKISTSN GSP  
 GFEYHQPGDKFEASKNDLGCGNTSSMAVIKDYYALKENEICVSQGEVVQVLAVNQQNM C  
 LVYQPASDHSPAAEGWVPGSILAPLT KATAAESDGS IKKSCSWHTLRMRKRAEVENTG K  
 NEATGPRKPKDILGNKVS VKETNSSESECDLDPNTSMEILNPNFIQEVAP EFLVPLVD  
 VTCLLGDTVILQCKVCGRPKPTITWKGP DQNI LDTDNSSATYTVSSCDSGEITLKI CNLM  
 PQDSGIYTCIATNDHGT TSTSATVKVQGVPAAPNRPIAQERSCTSVILRWLPSSSTGNCT  
 ISGYTVEYREEGSQIWQQSVASTLDTYL VIEDLSPGCPYQFRVSASN PWGISLPSESEF  
 VRLPEYDAAADGATISWKENFDSAYTELNEIGRGRFSIVKKCIHKATRKDVAVK FVNKKM  
 KKKEQAAHEAALLQHLQHPQYITLHD TYESPTSYILILELMDDGRLLDYL MNHDELMEEK  
 VAFYIRDIMEALQYLHNCRV AHLDIKPENLLIDLRIPVPRVKLIDLEDAVQISGHFHIHH  
 LLGNPEFAAPEVIQGI PVSLGTDIWSIGVLT YVMLSGVSPFLDESKEETCINVC RVDFSF  
 PHEYFCGVSNAA RDFINVLQEDFRRRPTAATCLQHPWLQPHNGSYSKIPLDTSRLACFI  
 ERRKHQNDVRPIPNVKSYIVNRVNQGT

SEQ ID NO: 165\_5R72\_8\_2\_H  
 MADSGLDKKSTKCPDCSSASQKDVLCVCSSKTRVPPVLV VEMSQTSSIGSAESLISLERK  
 KEKNINRDITSRKDLPSRTSNVERKASQQQWGRGNFTEGKVPHIRIENGAAIEE IYTFGR  
 ILGKGSFGIVIEATDKETETKWA IKKVNKEKAGSSAVKLLEREVNILKSVKHEHI IHLEQ  
 VFETPKMYLVMELCEDGELKEILDRKGHFSENETRWI IQSLASAIAYLHNNDIVHRDLK  
 LENIMVKSSLIDNNEINLNIKV TDFGLAVKKQSRSEAMLQATCGTPIYMAPEVISAHDY

## FIGURE 1L

SQQCDIWSIGVVMYMLLRGEPFPLASSEAKLFELIRKGE LHFENAVWNSISDCAKSVLKQ  
LMKVDPAHRI TAKELLDNQWLTGNKLSSVRPTNVLEMMKEWKNNPESVEENTTEEK NKPS  
TEEKLKSYQPWGNVPETNYTSDEEEEEKQSTAYEKQFPATSKDNFDMCSSSFTSSKLLPAE  
IKGEMEKTPTVTPSQGTATKYPAKSGALSRTKKKL

SEQ ID NO: 166 SGK309\_H

MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTREN  
ALKVESAAQPKQVLKMEVAVLKKLQSGSLGQGDGKEEMMKPGAKRGKDHVCRFIGCGRNE  
KFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF  
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRRPVRNAGFRGTVRYASVNAHKNREMGRHD  
DLWSLFYMLVEFAVGQLPWRKIKDKEQVGMKEKYEHRMLLKHPSEFHLFLDHIASLDY  
FTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLSTSTSTPPPAEHPADGSHVWG  
GQCDASAWGPAPGEHRGCATGRAPEXPGECTPNSAREALXGAGPQSPPCPPRGSXGXSL  
GGDRCQPEQTPDQHRQSNCRQGEGRGWPFLLSPPIPSLVPLPCSSXAPCPPPISLLARPLF  
VVPSPALASLCLPSSSSSVSFTLRRPSA

SEQ ID NO: 167\_AA234451\_H

MSGGGEQLDILSVGILVKERWKVLRKIGGGGFGEIYDALDMLTRENVALKVESAAQPKQV  
LKMEVAVLKKLQGDHVCRFICGRNDRFNYVVMQLQGRNLADLRRSQSRGTFTISTTLR  
LGRQILESIESIHSVGSRHDIKPSNFAMGRFPSTCRKCYMLDFGLARQFTNSCGDVRPP  
RAVAGFRGTVRYASINAHNRNREMGRHDDLWSLFYMLVEFVVGQLPWRKIKDKEQVGSIKE  
RYDHRMLKHLPPPEFSIFLDHISSLDYFTKPDYQLLTSVFDNSIKTFGVIESDPFDWEKT  
GNDGSLTTTTTTSTTPQLHTRLTPAAIGIANATPIPGDLLRENTDEVFPDEQLSDGENGIP  
VGVSPDKLPGSLGHRPQEKDVWEEMDANKNKIKLGICKAATEEENSHGQANGLLNAPSL  
GSPIRVRSEITQPDRIPLVRKLRSIHSFELEKRLTLEPKPDTDKFLETWYKIVYFSF

SEQ ID NO: 168\_AA435956\_H

TFTIFFEMTVFDLEAKSARGGSNLLMDSVSSSFQLFMFQLLRGLAYIHHQHVLHRDLKPQN  
LLISHLGELKLADFLARAKSIPSQTYSSSEVTLWYRPPDALLGATEYSSSELDIWAGCI  
FIEMFQGQPLFPVSNILEQLEKIWEVLGVPTEDTWPVGVSKLPNYPWFPLPTPRSLHV  
VWNRLGRVPEAEDLASQMLKGFPRDRVSAQEALVHDYFSALPSQLYQLPDEESLFTVSGV  
RLKPEMCDLLASYQKGHPAQFSKCW

SEQ ID NO: 169\_AA626859\_H

NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIKICDFGFAQILIPGD  
AYTDYVATRWYRAPELLVGDYQYGSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR  
TLGKLI PRHQSI FKSNGFFHGISIPEPEDMETLEEKFSVDVHPVALNFMKGCLKMNPPDDR  
TCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQONQLLPLIPGSHISPTPDGRKQVLQLK  
FDHLPNI

SEQ ID NO: 170\_AA061797\_M

KIALREIRMLKLKHPNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVSGVSKSV  
LWQTLQALNFCHKHNCIHRDVKPENILITKQGMKICDFGFARILIPGDAYTDYVATRWY  
RAPELLVGDYKYGSSVDVWAVGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLI PRHQ  
SIFRSNQFFRGISIPEDMETLEEKFSNVQPVALSFMKGCLKMNPPDERLTCAQLLDSAYF  
ESFQEDQMKRKARSEGRSRRRQONQLLPLIPGSHISPTPDGRKQVVQLKFDHLPNI

SEQ ID NO: 171\_AA397553\_H

MPNSERHGGKKDGSAGTLQPSGGGSSNSRERHRLVSKHKRHSKHSKMDGLVTPEA  
ASLGTVIKPLVEYDDISSDSTFSDDMAFKLDRRENDERRGSDRSDDLHKHRHHQHRRSR



## FIGURE 1M

DLLKAKQTEKEKSQEVSSKSGSMKDRISGSSKRSNEETDDYGKAQVAKSSSKESRSSKLH  
 KEKTRKERELKSGHKDRSKSHRKRETPKSYKTVDSPKRRSRSPHRKWSOSSKQDDSPSGA  
 SYGQDYDLSPSRSHSTSSNYDSYKKS PGSTSRRSQSVSPPYKEPSAYQSSTRSPSPYSRRQR  
 SVSPYSRRRRSSSYERSGSGSYGRSPSPYGRRRSSSPFLSKRSLRSPLPSRKSMKSRSRSP  
 AYSRHSSSHSKKKRSSSRSRHSSISPVRPLPNSSLGAELSRKKKRAAAAAAAKMDGKES  
 KGSPVFLPRKENSSEAKDSGLESKKLPRSVKLEKSAPDTELNVNTHLNTTEVKNSSDTGK  
 VKLDENSEKHLVKDLKAQGTDRSKPIALKEEIVTPKETETSEKETPPPLPTIASPPPPPLP  
 TTTTPPQTPPLPPLPPIPALPQQPPLPPSQPAFSQVPASSTSTLPPSTHSKTSASVSSQAN  
 SQPPVQVSVKTQVSVTAAPHLKTSTLPPPLPPLPPLPGGDDMDSPKETLPSKPVKKEKEQ  
 RTRHLLTDLPLPPELPGGDLSPDSEPKAITPPQQPYKKRPKICCPRYGERRQTESDWG  
 KRCVDKFDIIGIIGEGTYGVYKARDKDTGELVALKKVRLDNEKEGFPITAIREIKILRQ  
 LIHRSVVMKEIVTDKQDALDFKKDKGAFYLVFEYMDHDLMLGLESGLVHFSEDHIKSF  
 KQLMEGLEYCHKNFLHRDIKCSNILLNNSGQIKLADFGLARLYNSEESRPYTNKVITLW  
 YRPELLELGEERYTPAIDVWSCGILGELFTKKPIFOANLELAQLELISRLCGSPCPAVW  
 PDVIKLPYFNTMKPKKQYRRRLREEFSFIPSAALDLDHMLTLDPSKRCTAEQTLQSDFL  
 KDVELSKMAPDLPHWQDCHELWSKKRRRQRQSGVVVEEPPPSKTSRKETTSGTSTEPVK  
 NSSPAPPQAPGKVESGAGDAIGLADITQQNLQSELAVLLNLLQSQTDLSPQMAQLLNI  
 HSNPEMQQLEALNQSISALTEATSQQQDSETMAPEESLKEAPSAPVILPSAEQMTLEAS  
 STPADMQNILAVLLSQLMKTQEPAGSLEENNSDKNSGQGPRTPTMPQEEAAACPPHIL  
 PPEKRPPEPPGPPPPPPPPPLVEGDLSSAPQELNPAVTAALLQLLSQPEAEPPGHLPEH  
 QALRPMEYSTRPRPNRTYGNTDGPETGFSADTDERNSGPALTESLVQTLVKNRTFSGSL  
 SHLGESSYQGTGSGVQFPGDQDLRFARVPLALHPVVGPFLKAEGSSNSVVAETKLQNY  
 GELGPGTTGASSSGAGLHWGGPTQSSAYGKLYRGPTRVPPRGGRGRGVPIY

SEQ ID NO: 172\_AA789239\_H

MEMYETLGKVGESYGTVMKCKHKNTGQIVAIKIFYERPEQSVNKIAMREIKFLKQFHHE  
 NLVNLIEVFRQKKKIHLVFEFIDHTVLDELQHYCHGLESKRLRKYLFQILRAIDYLHSSN  
 VIIHRDIKPENILVSQSGITKLCDFGFARTLAAPGDIYTDYVATRWYRAPELVLKDTSYG  
 KYVPVDI WALGCMIIEMATGNPYLPSSSDLDLLHKIVLKVXFMPKAKLLQEAQVNSLI  
 KPKESSKENELRKDERKTVYTNTLLSSSVLGKEIEKEKKPKEIKVRVIVKVGGRGDISEP  
 KKKEYEGGLQQDANENVHPMSPDTKLVTEPPNPINPSTNCNGLKENPHCGGSVTMPPI  
 NLTNSNLMAANLSSNLFHPSVRLTERAKKRTSSQSIGQVMPNSRQEDPGPIQSQMEKGI  
 FNERTGHSDQMANENKRKLNFPSRDRKEFHFPPELPVTIQSKDTKGMEVKQIKMLKRESKK  
 TESSKIPTLLNVDQNEKQEFIPLSLLSACCPIFTNICSQLTIRVEMAIARGRI

SEQ ID NO: 173\_AA124976\_M

LADIVHACLQIDPAERTSSTDLLRHDYFTRDGFIEKFIPELRAKLLQEAQVNSFIKPKEN  
 FKENEPVRDEKKS VFTNTLLYGNPSLYGKEVDRDKRAKELKVRVIKAKGGKGDVPDQKKP  
 EYEGDHRQQTADDTQPSSLDKKPSVLELTNPLNPSSENSDGVKEDPHAGGCMIMPPINLT  
 SSNLLAANLSSNLSHPNSRLTERTKKRTSSQTIGQTLNSNRQEDTGPTQVQTEKGAFNE  
 RTGQNDQISSGNKRKLNF PKDRKEFHFPPELPVTIQSKDTKGMEVKQIKVLKRESKKTDS  
 SKIPTLLSMDPNQEKQEGGDGCEGKNLKRNRFFFSR

SEQ ID NO: 174\_AA575635\_M CCRK\_M

SASGQLKIADFGLARVFS PDGGRLYTHQVATRWYRAPELLYGARQYDQGVDLWAVGCIMG  
 ELLNGSPLFPGENDIEQLCCVLRI LGTPSPRVWPEITELPDYNKISFEEQAPVPLEEVL  
 DASPQALDLLGQFLLYPPRQRIAASQALLHQYFFTA PLPAHPSELPI PQRPGGPAPKAHP  
 GPPHVHDFHVD RPIEESLLNPELIRPFIPEG

## FIGURE 1N

SEQ ID NO: 175\_AA631990\_H

MIT SISTEKS GH THYPFMITTLQYYRGRGGKTAVWRHFS AEGPF AFAEMRHSKRTHCPDW  
DSRESWGHE SYRGSHKRKRSHSSTQENRHCKPHHQFKE SDCHYLEARSLNERDYRDRRY  
VDEYRNDYCEGYVPRHYHRDIESGYRIHCSKSSVRSRRSSPKRKRNRHCSSHQSR SXEIV  
DTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAA RSEIQVLEHLNSTDPNSVFR C  
VQMLEWFDHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHHNKL  
THTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVD FGSATYDDEHHSTLVSTRH  
YRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGP I PQHMIQ  
KTRKRKYFHNNQLDWEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLF DLVRRMLEYDPTQ  
RITLDEALQHPPFDLLKKK

SEQ ID NO: 176\_AA557536\_H

MCTVVDPRIVRRYLLRRQLGQGRTFREITLLQVSGLGPPVQSPCPGTDLSRQERNWPSWA  
PEHSPSWPSSRLRLSPQEFGDHPNII SLLDVIRAENDRDIYLVFEFMDTDLNAVIRKGG L  
LQDVHVR SIFYQLLRATRFLHSGHVVRHDQKPSNVLLDANCTVKLCDFGLARSLGDLPEG  
PEDQAVTEYVATRWYRAPEVLLSSHRYTASCPRYTLGVDMWSLGCILGEMLRGRPLFPGT  
STLHQLELILETIPPPSEEXRPRQTL DALLPPDTSPEALDLLRLLVFAPDKRLSATQAL  
QHYPYVQRFHCPSDEWAREADVRPRAHEGVQLSVPEYRSRVYQMI LECGSSSGTSREKGP E  
GVSPSQAHLHKPRADPQLPSRTPVQGRPRPQSSPGHDPAEHES PRAAKNVPRQNSAPLL  
QTALLNGERPPGAKEAPPLTSLVKPSGRGAAPSLTSQAAAQVANQALIRGDWNRGGGV  
RVASVQQVPPRLPPEARPGRRMFST SALQGAQGGARALLGGYSQAYGTVCHSALGHLPLL  
EGHHV

SEQ ID NO: 177\_N28606\_H, MOK\_H

MKNYKAIGKIGEGTFSEVMKMQLRDNYYACKQMKQRFESIEQVNNLREIQALRRLNPH  
PNILMLHEVVFDKSGSLALICELMDMNIYELIRGRRYPLSEKKIMHYMYQLCKSLDHIH  
RNGIFHRDVKPENILIKQDVLKLGDFGSCRSVYSKQPYTEYISTRWYRAPECLLTDGFYT  
YKMDLWSAGCVFYEIASLQPLFPGVNELDQISKIHDVIGTPAQKILT KFKQSRAMNFD F P  
FKKGSGIPLLTNLSPOCLSLHAMVAYDPDERIAAHQALQHPYFQEQRKTEKRALGSHR  
KAGFPPEHPVAPEPLSNSCQISKEGRKQKQSLKQEEDRPKRRGPAYVMELPKLKLSGVVRL  
SSYSSPTLQSVLGS GTNGRVPVLRPLKCI PASKKTDPOKDLKPAPQQCRLPTIVRKGG R

SEQ ID NO: 178\_AB023153\_H, ICK\_H

MNRYTTIRQLGDGTYGSVLLGRSIESGELIAIKMKRKFYSWEECMNQREVKSLKKNLHA  
NVVKLKEVIRENDHLYFIFEYMKENLYQLIKERNKLPESAIRNIMYQILQGLAFIHKLG  
FFHRDLKPENLLCMGPELVKIADFGlareIRSKPPYTDYVSTRWYRAPEVLLRSTNYSSP  
IDVWAVGCIMAEVYTLRPLFPGASEIDTIFKICQVLGTPKKTDWPEGYQLSSAMNFRWPQ  
CVPNNLKTLPNASSEAVQLLRDMLQWDPKKRPTASQALRYPYFQVGHPLGSTTQNLQDS  
EKPQKGILERAGPPPYIKPVPPAQPPAKPHTRISSRQHQASQPPLHLTPYKAEVSRTDH  
PSHLQEDKPSPLLFP SLHNKHPQSKITAGLEHKNGEIKPKSRRRWGLISRSTKDSDDWAD  
LDDLDFSPSLSRIDLKNKKRQSDDTLCRFESVLDLKPSEPVG TGNSAPTQTSYQRRDTPT  
LRSAAKQHYLKH SRYLPGISIRNGILSNPGKEFIPNPWSSSGLSGKSSGTMSVISKVNS  
VGSSSTSSSGLTGNYVPSFLKKEIGSAMQRVHLAPIPDPSPGYSSLKAMRPHPGRPFLDT  
QPRSTPGLIPRPPAAQPVHGRTDWASKYPSRR

SEQ ID NO: 179\_AA839940\_M

SSNNGGMSAE EEEIGPGAEPMRGPSLATRDWRDET VGT TDLQGGIDPGAVSPEPGKDHAAG  
GPGRTEAGRVSSAAEAAIVVLDDSAAPPAPFEHRVVS IKDTLISAGYTVSQHEVLGGGRF  
GOVHRCTERSTGLALAAKIIKVKNVKDREDVKNEVNIMNQLSHVNLIQLYDAFESKNSFT  
LIMEYVDGGELFDRITDEKYHLTEL DVVLFTRQICEGVHYLHQHYILHLDLKPENILCVS

## FIGURE 10

QTGHQIKIIDFGLARRYKPREKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVITYMLL  
SGLSPFLGETDAETMNFIVNCSDWDFDADTFKGLSEEAKDFVSRLLVKEKSCRMSTQCLK  
HEWLNHLPAKASGSNVLRSQQLLQKYMAQSKWKXHFHVAAVNRLRKFPCTP

SEQ ID NO: 180\_AA460132\_H  
MAAARATTPADGEEPAPAEALAAARERSSRFLSGLLELVKQGAEARVFRGRFQGRAAVIK  
HRFPKGYRHPALEARLGRRTVQEARALLRCRRAGISAPVVFVDYASNCLYMEEIEGVS  
TVRDYIQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV  
LIDFGLSFISALPEDKGVDLYVLEKAFLLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD  
EVRLRGRKRSVMG

SEQ ID NO: 181\_SGK034\_H  
QREKVNQGNMPLQSTFLAMDTEEGVEVVWNLHFGDRKAFAAHEEKIQTVEQLVLVDH  
PNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKTKKNHKAMNARAWKRWCTQILS  
ALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNALPDDLRSPIRAEREELR  
NLHFFPPEYGEVADGTAVDIFSGMCALEMAVLEIQTNGDTRVTEEAIRARHSLSDPNM  
REFILCCLARDPARRPSAHSLLFHRVLFVHSLKLLAAHCFIQHQYLMPENNVVEEKTAM  
DLHAVLAELPRRRPPLQWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAP  
PPEEVQAKTPTPEPFDSETRKVIQMCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLL  
PTDSAQDLASELVHYGFLHEDDRMKLAAFLESTFLKYRGTQA

SEQ ID NO: 182\_AA103218\_M\_SGK034\_M  
HASAPEYGEVNDGTGFVDIFSGMCALEMAVLEIQANGDTRVTEEAIRARHSLSDPNMR  
EFILSCLARDPARRPSAHLNLLFHRVLFVHSLKLLAAHCFIQHQYLMPENNVVEEKTAM  
LHAVLAEMPQPHGPPMQWRYSEVSFLELDKFLEDVRNGIYPLMNFAAARPLGLPRVLAP  
PEEAQKAKTPTPEPFDSETRKVVQMCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLP  
TDSAQDLAAELVHYGFLHEDDRTKLAAFLETTFLKYRGTQA

SEQ ID NO: 183\_NEK7\_H, N34132\_H  
MSGGAAEKQSSTPGSLFLSPAPAPKNGSSSDSSVGEKLGAAAADAVTGRTEEYRRRRHT  
MDKDSRGAAATTTTEHRFFRRSVICDSNATALELPGLPLSLPQPSIPAAVPQSAPPEPH  
REETVTATATSQVAQPPAAAAPGEQAVAGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPP  
ARSGSGGSAKEPQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVYKGLD  
TETTVEVAVCELQDRKLTKEQRFKEEAEMLKGLQHPNIVRFYDSWESTVKGKKCIVLV  
TELMTSGTLKTYLKRFKVMKIKVLRSWCRQILKGLQFLHTRTPLIHRDLKCDNIFITGP  
TGSVKIGDLGLATLKRAFASVIGTPEFMAPEMYEEKYDESVDVYAFGMCMLMATSEY  
PYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEIEGCIRQNKDERYSIKDLLNHAFQ  
EETGVRVELAEEDDGEKIAIKLWLRIEDIKKLKGKYKDNEAIEFCFDLERDVPEDVAQEM  
VESGYVCEGDHKTMAKAIKDRVSLIKRKREQRQLVREEQENKKQEESLQQVEQSSASQ  
TGIKQLPSASTGIPTASTTSASVSTQVEPEEPEADQHQQLOYYQPSISVLSDGTVDGSGG  
SSVFTESRVSSQQTVSYGFPXHEQAHSTGTVPGHIPSTVQAQSQPHGVYPPSSVQQGIQQ  
TAPPQQTQVQYSLSQSTTSSEATTAQPVSQPQAPQVLPQVSAGKQSTQGVSQVAPAEVAV  
AQPPATQPTTLASSVDSASDVSAGMSDGNENVPSSSGRHEGRTTKRHYRKSVRSRHE  
KTSRPKLRILNVSNKGDRVVECQLETHNRKMTVFKFDLDGDNPEEIIATIMVNNDFILAE  
RESFVDQVREIEKADEMLSEDVSVEPEGDQGLSLQKDDYGFSGSQKLEGEFKQPIPA  
SSMPQQIGIPTSSLTQVVHSAGRRFIVSPVPESRLRESKVFPSEITDTVAASTAQSPGMN  
LSHSASSLSLQQAFASELRRQMTEGPNTAPPNFSHTGPTFPVPPFLSSIAGVPTTAAAT  
APVPATSSPPNDISTSVIQSEVTVPTEEGIAGVATSTGVVTSGLPPIPPVSESPVLSSV  
SSITIPAVVSISTTSPSLQVPTSTSEIVVSSTALYPSVTVSATSASAGGSTATPGPKPPA  
VVSQQAAGSTTVGATLTSVSTTTSFPSTASQLSIQLSSSTSTPTLAETVVVSAHSLDKTS

## FIGURE 1P

HSSTTGLAFSLSAPSSSSSPGAGVSSYISQPGGLHPLVIPSVIASTPILPQAAGPTSTPL  
 LPQVPSIPPLVQPVANVPAVQQTLIHSQOPALLPNQPHTHCPEVDSDTQPKAPGIDDIK  
 TLEEKLRSLFSEHSSSGAQHASVSLETSLVIESTVTPGIPTTAVAPSKLLTSTTSTCLPP  
 TNLPLGTVALPVTPVVTGQVSTPVSTTTSGVKPGTAPSKPPLTKAPVLPVGTLPAGTL  
 PSEQLPFPFGPSLTQSQQPLEDLDAQLRRTLSPEMITVTSVAVGPVSMAAPTAITEAGTQP  
 QKGVSVQKEGPVLATSSGAGVFKMGRFQVSVAADGAQKEGKNKSEDAKSVHFESSTSESS  
 VLSSSSPESTLVKPEPNGITIPGISSDVPESAHTTASEAKSDTGQPTKVGRFQVTTTAN  
 KVGRFSVSKTEDKITDTKKEGPVASPPFMDLEQAVLPAVIPKKEKPELSEPSHLNGPSSD  
 PEAAFLSRDVGSGSPHSPHQLSSKSLPSQNLSQLSLSNSFNSSYMSSDNESDIEDEDLK  
 LELRRLRDKHLKEIQDLQSRQKHEIESLYTKLGKVP PAVIIPPAAPLSGRRRRPTKSKGS  
 KSSRSSSLGNKSPQLSGNLSGQSAASVLHPQQTLPHPGNIPEGQNLQLLOPLKPSPSDN  
 LYSFTSDGAISVPSLSAPGQGNKATIIVQKQ

SEQ ID NO: 184\_BCON3\_H

MSEGESQTVLSSSGDPKVESSSAPGLTSVSPVPTSTTSAASPEEEEESEDESEILEESP  
 CGRWQKRREEVNRNVPIDISAYLAMDEEGVEVWNEVQFSEKKNYKLQEEKVRAVFDN  
 LIQLEHLNIVKFHYWADIKENKARVIFITEYMSSGSLKQFLKKTCKNHKTMNEKAWKRW  
 CTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSVAPDTINNHVKTCTREEQKNL  
 HFFAPEYGEVTNVTTAVDIYSFGMCALEMAVLEIQNGESSYVPQEAISSAIQLLEDPLQ  
 REFIQKCLQSEPARRPTARELLFHPALFEVPSLKLAAHCIVGHQHMI PENALEEITKNM  
 DTSAVLAEIPAGPGREPQVTLYSQSPALEDKFLDVRNGIYPLTAFGLPRPQQPQQEEV  
 TSPVPPSVKTPPTPEPAEVETRKVVLMQCNIESVEEGVKHHLTLLLKLEDKLNRLHSCDL  
 MPNENIPELAAELVQLGFISEADQSRLTSLLEETLNKFNFARNSTLNSAAVTVSS

SEQ ID NO: 185\_AA711829\_M

LKQFLKKTCKNHKTMNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIK  
 IGSVAPDTINNHVKTCTREEQKNLHFFAPEYGEVTNVTTAVDIYSFGMCALEMAVLEIQNG  
 GESSYVPQEAISSAIQLLEDLSLQREFIQKCLQSEPARRPTARELLFHPALFEVPSLKLAA  
 AHCIVGHQHMI PENALEEITKNMDTSAVLAEIPAGPGREPQVTLYSQSPALEDKFLDVR  
 NGIYPLTAFGLPRPQQPQQEEVTSPPVPPSVKTPPTPEPAEVETRKVVLMQCNIESVEEG  
 VKHHLTLLLKLEDKLNRLHSCDLMPNESIPDLAAELVQLGFISEADQSRLTSLLEETLNK  
 FNFTRNSTLNTATVTVSS

SEQ ID NO: 186\_AA099102\_H

MSSCVSSQPSSNRAAPQDELGGRGSSSSSESQKPCEALRGLSSLSIHLGMESFIVVTECEP  
 GCAVDLGLARDRPLEADGQEVPLDTSGSQARPHLSGRKLSLQERSQGGLAAGGSLDMNGR  
 CICPSLPYSPVSSPQSSPRLPRRPTVESHHVSI TGMQDCVQLNQYTLKDEIGKGSYG VVK  
 LAYNENDNTYYAMKVL SKKKLIRQAAPRRPPRGRTRPAPGGCIQPRGPIEQVYQEIAIL  
 KKLDHPNVVKLVEVLDDPNEDHLYMVFEVLVQGPVMEVPTLKLPLEDQARFYFQDLIKGI  
 EYLHYQKI IHRDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNYVGTPAFMAPESLS  
 ETRKIFSGKAKDVWAMGVTL YCFVFGQCPFMDERIMCLHSKI KSQALEFPDQPDIAEDLK  
 DLITRMLDKNPESRI VVPEIKLHPWVTRHGAEP LPSDENCTLVEVTEEEVENS VKHIPS  
 LATVILVKT MIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESLSELKEARQRRQP  
 PGHRPAPRGGGG SALVRGSPCVESC WAPAPGSPARMHPLRPEEAMEPE

SEQ ID NO: 187\_5R69\_17\_2\_H

MQEIPQEIQIKEIKKEQLSGSPWILLRENEVSTLYKGEYHRAPVAIKVFKKLQAGSIAIVR  
 QTFNKEIKTMKKFESPNILRIFGICIDETVTPPQFSIVMEYCELGTRELLDREKDLTLG

## FIGURE 1Q

KRMVLVLGAARGLYRLHHSEAPELHGKIRSSNFLVTQGYQVKLAGFELRKTQTSMSLGTT  
REKTRVKSTAYLSPQELEDVIFYQYDVKSEIYSFGIVLWEIATGDIPFQGECECDWLSQW  
L

SEQ ID NO: 188\_H85811\_H

MAPVYEGMASHVQVFSPTLQSSAFCSVKKLKIEPSSNWDMTGYGSHSKVYSQSKNIPLS  
QPATTTVSTSLPVPNPSPLEQTIIVPGSTGHIIVVTSASSTSVTGQVLGGPHNLMRRSTV  
SLLDTYQKCGLRKSEEIENTSSVQIIEEHPPMIQNNASGATVATATTSTATSKNSGSNS  
EGDYQLVQHEVLCSMTNTYEVLEFLGRGTFGQVVKCWKRGTNEIVAIKILKNHPSYARQG  
QIEVSILARLSTESADDYNFVRAYECFQHKNTCLVFEMLEQNLDFLKQNKFSPLPLKY  
IRPVLQQVATAMKLSLGLIHADLKPENIMLVDPSPRQPYRVKVIDFGSASHVSKAVCST  
YLQSRYYRAPEIILGLPFCEAIDMWSLGCVIAELFLGWPLYPGDSEYDQIRYISQTQGLP  
AEYLLSAGTKTTRFFNRDTSPPYPLWRLKTPDDHEAETGIKSKEARKYIFNCLDDMAQVN  
MTTDLGSDMLVEKADRREFIDLLKMLTIDADKRITPIETLNHPFVTMTHLDDFPSTH  
VKSCFQNMIEICKRRVNMVYDVTNQSCTPFITHVAPSTSTNLMTFNNQLTTVHNQPSAASM  
AAVAQRSMPLQGTGTAQICARPDFFQALIVCPPGFQGLQASPSKHAGYSVRMENAVPIVT  
QAPGAQPLQIQPGLLAQAWPSGTQQILLPPAWQQLTG VATHTSVQHATVIPETMAGTQQ  
LADWRNTHAHGSHYNPIMQQPALLTGHTVLPAAQPLNVGVAVHVMRQOPTSTTSSRSKQH  
QSSVRNVSTCEVSSSQAISSPQRSKRKENTPPRCAMVHSSPACSTSVTCGWGDVASSTT  
RERQRQTIVIPDTPSPTVSVITISSDTDEEEEQKHAPTSTVSKQRKNVISCVTVHDSPPYS  
DSSSNTSPYSVQQRAGHNNANAFDTKGSLENHCTGNPRTIIVPPLKTQASEVLVECDLSV  
PVNTSHHSSSYKSKSSSNVTSTSGHSSGSSSGAITRQQRPGPHFQQQQPLNLSQAQQHI  
TTDRGTGSHRRQAYITPTMAQAPYSFPHNSPSHGTVHPLAAAAAAHLPTQPHLYTYTA  
PAALGSTGTVAHLVASQGSARHTVQHTAYPASIVHQPVSVMGPRVLPSPTIHPSQYPAQF  
AHQTYISASPASTVYTYGYPPLSPAKVNQYPYI

SEQ ID NO: 189\_DYRK3\_H

MMIDETKCPPCSNVLCNPSEPPPPRRLNMATBQFTGDHTQHFLDGGEMKVEQLFQEFGNR  
KSNTIQSDGISDSEKCSPTVSQKSSDCLNTVKSNSSSKAPKVPLTPEQALKQYKHHLT  
AYEKLIEINYPEIYFVGPNAKKRHGVIIGPNNGGYDDADGAYIHVPRDHLAYRYEVLKII  
GKGSFGQVARVYDHLRQYVALKMVRNEKRFHRQAEEIRILEHLKKQDKTGSMNVIHML  
ESFTFRNHVCMFELLSIDLYELIKKNKFQGFVQLVRKFAQSILQSLDALHKNKIIHCD  
LKPENILLKHHGRSSTKVIDFGSSCFEYQKLYTYIQSRFYRAPEIILGSRYSTPIDIWSF  
RCILAEELLTGQPLFPGEDEGDQLACMMELLGMPPPKLLEQSKRAKYFINSKGI PRYCSVT  
TQADGRVVLVGGRSRRGKKRGPPGSKDWGTALKGCDLYLFIIEFLKRCLHWDPSARLT PAQ  
ALRHPWISKSVPRPLTTIDKVSGRVVPNPASAFQGLGSKLPPVVGIANKLKANLMSETNG  
SIPLCVLPKLIS

SEQ ID NO: 190\_AA589241\_M DYRK3\_M

TRPELLGMPPQKLLQSKRAKYFINSKGLPRYCSVSTQTDGRVVLGGRSRRGKKRGPPG  
SKDWATALKGCDLYLFIIEFLKRCLQWDPSARLT PAQALRHPWISKSTPKPLTMDKVPGKR  
VVNPTNAFQGLGSKLPPVVGIA SKLKANLMSETSGSIPLCVLPKLIS

SEQ ID NO: 191\_5R72\_16\_2\_H

MAGGRGAPGRGRDEPPESYPQRQDHELQALEAIYGADFQDLRPDACPVKPEPPEINLVLY  
PQGLTGEEVYVKVDLRVKCPPTYPDVVPPEIELKNAKGLSNESVNLLKSRLEELAKKHCGE  
VMIFELAYHVQSFLSEHNKPPPKSFHEEMLERRAQEEQORLLEAKRKEEQEQREILHEIQ  
RRKEEIKKEKKRKEMAKQERLEIASLSNQDHTSKKDPGGHRTAAI LHGGSPDFVGNKGR  
ANSSGRSRRERQYSVCNSEDSPGSCEILYFNMGSPDQLMVHKGKICIGSDEQLGKLVYNAL  
ETATGGFVLLYEWVLQWQKMGPFLLTSQEKEKIDKCKKQIQGTETEFNSLVKL SHPNVVR

## FIGURE 1R

YLAMNLKEQDDSI VVDILVEHISGVSLAAHL SHSGPI PVHQLRRYTAQLLSGLDYLHSNS  
 VVHKVLSASNVLVDAEGTVKITDYSISKRLADICKEDVFEQTRVRFSDNALPYKTGKKG  
 VWRLGLLLLLSL SQQECGEYPVTIPSDL PADFQDFLKKCVCLDDKERWSPQQLLKHSFIN  
 PQPKMPLVEQSPEDSGGQDYVETVIPS NRLPSAAFFSETQRQFSRYFIEFEELQLLGKGA  
 FGA VIKVQNKLDGCCYAVKRIPINPASRQFRRIKGEVTLLSRLHHENIVRYNNAWIERHE  
 RPAGPGTPPPDSGPLAKDDRAARGQPASDTDGLDSVEAAAPPPILSSSVIEWSTSGERSAS  
 ARFPATGPGSSDDEDDDEHGGVFSQSFLPASDSESDIIFDNEDENSKSQNQDEDCNEK  
 NGCHESEPSVTTEAVHYLYIQMEYCEKSTLRDTIDQGLYRDTVRLWRLFREILDGLAYIH  
 EKGMIHRDLKPVNI FLDSDDHVKIGDFGLATDHLAFSADSKQDDQTGDLIKSDPSGHLTG  
 MVGTALYVSPEVQGSTKSAYNQKVDLFSLGIIFFEMSYHPMTASERIFVLNQLRDPTSP  
 KFPEDFDDGEHAKQKSVISWLLNHDPKRPTATELLKSELLPPPQMEESSELHEVLHHTLT  
 NVDGKAYRTMMAQIFSQRISPAIDYTYDSILKGNFSIRTAKMQQHVCETIIRIFKRHGA  
 VQLCTPLLLPRNRQIYEHNEAALFMDHSGMLVMLPFDLRIPFARYVARNNINLNLKRYCIE  
 RVFRPRKLDRFHPKELLECAFDIVTSTTNSFLPTAEIIYTIYEIIQEFPALQERNYSIYL  
 NHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTRREVEAKFCNLSLSSNSLCRLYKF  
 IEQKGDQLDLMPTINSLIKQKTGIAQLVKYGLKDLEEVVGLLKKLGIKLQVLINLGLVYK  
 VQQHNGIIFQFVAFIKRRQRAVPEILAAGGRYDLLIPQFRGPQALGPVPTAIGVSIADK  
 ISAAVLNMEESVTISSCDLLVSVGQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQ  
 EYCRHHEITYVALVSDKEGSHVKVKSFEKERQTEKRVLETETELVDHVLQKLRTKVTDERN  
 REASDNLAVQNKGFSNASGLFEIHGATVVPISVLAPEKLSASTRRRYETQVQTRLQT  
 SLANLHQKSSEIEILAVDLPKETILQFLSLEWDADEQAFNTTVKQLLSRLPKQRYLKLVC  
 DEIYNIKVEKKVSVLFLYSYRDDYRILF

SEQ ID NO: 192\_R43524\_H, HRI\_H

MLGGNSGVRKREEEGDGAGAVAAPPAIDFPAEGPDPEYDESDVPAEIQVLKEPLQQPTFP  
 FAVANQLLLVSLLEHLSHVHEPNPLRSRQVFKLLCQTFIKMGLSSFTCSDEFSSRLHH  
 NRAITHLMRSKERVQRQPCEDISRIQKIRSREVALEAQT SRYLNEFEELVILGKGGYGR  
 VYKVRNKLDGQYYAIKKILIKGATKTVCMKVLREV KVLAGLQHPNIVGYHTAWIEHVHVI  
 QPRADRAAIELPSLEVLSDQEEDREQCGVKND ESSSSSIIFAEPTPEKEKRFGESDTENQ  
 NNKSVKYTTNLVIRESGELESTLELQENGLAGLSASSIVEQQPLRRNSHLEESFTSTEE  
 SSEENVNVLFGQTEAQYHMLMLHIQMQLCELSLWDWIVERNKRGREYVDESACPYVMANVAT  
 KIFQELVEGVFYIHNMGIVHRDLKPRNIFLHGPDQQVKIGDFGLACTDILQKNTDWTNRN  
 GKRTPTHTSRVGTCLYASPEQLEGSEYDAKSDMYSLGVVLEL FQPFQTEMERAEVLTGL  
 RTGQLPESLRKRCVPVQAKYIQHLTRRNSSQRP SAIQLLQSELFQNSGNVNLTLQMKIIEQ  
 EKEIAELKKQLNLLSQDKGVRDDGKDGGVG

SEQ ID NO: 193\_17000057519457\_H

MAAARATTPADGEEPAPAEALAAARERSSRFLSGLELVKQGAEARVFRGRFQGRAAVIK  
 HRFPKGYRHPALEARLGRRRTVQEARALLRCRRAGISAPVVFVDYASNCLYMEIEGVS  
 TVRDYIQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV  
 LIDFGLSFISALPEDKGVDLYVLEKAFLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD  
 EVRLRGRKRSMVG

SEQ ID NO: 194\_AA013524\_M

LVQQGAEARVFRGRFQGRAAVVKHRFPKSYRHPELEARLGRRRTVQEARALLRCRRAGIA  
 APVVFVDYASNCLYMEIEEDSVTVRDYIQSTMETEKDPQCLDLARRMGQVLAGMHDQD  
 LIHGDLTTSNMLLRPLAQLHIVLIDFGLSFVSGLPEDKGVDLYVLEKAFLSTHPHTETA  
 FEAFKSYGASSKKSSPVLKKLDEVRLRGRKRSMVG

## FIGURE 1S

SEQ ID NO: 195\_17000139801197\_H, IRAKM\_H  
MAGNCGARGALSAHTLLFDLPPALLGELCAVLDS CDGALGWRGLAERLSSSWLDVRHIEK  
YVDQKSGSTRELLWSWAQKNKTIGDLLQVLQEMGHRAIHLITNYGAVLSPSEKSYQEGG  
FPNILFKETANVTVDNVLIPHEHNEKGVLLKSSISFQNIIEGTRNFHKDFLIGEGEIFEVY  
RVEIQNLTYAVKLFKQEKMMQCKKHWKRFLESEVLLL FHHPNILELAAYFTETEFKCL I  
YPYMRNGTLFDRLQCVGDTAPLPWHIRIGILIGISKAIHYLHNVPQCSVICGSISSANIL  
LDDQFQPKLTDFAMAHFRSHLEHQSC TINMTSSSSKHLWYMPEEYIRQGKLSIKTDVYSF  
GIVIMEVLTGCRVVLDDPKHIQLRDLRELMEKRGDLSCLSF LDKKVP PCPRNFS AKLFC  
LAGRCAATRAKLRPSMDEV LNTLESTQASLYFAEDPPTSLKSFRCPSPLFLENVPSIPVE  
DDESQNNLLPSDEGLRIDRMTQKTPFECSQSEVMFLSLDKKPESKRNEEACNMPSSSCE  
ESWFPKYIVPSQDLRPYKVNIDPSSEAPGHSCSRPVESSCSSKFSWDEYEQYKKE

SEQ ID NO: 196\_AA840598\_M IRAKM\_M  
MWKRFLESEVLLLFRHPHILELAAYFTETEFKCLVYPYMSNGTLFDRLQCTNGTTPLSW  
HVRISVLIGIAKAIQYLHNTQPCAVICGNVSSANILLDDQLQPKLTDFAAAHFRPNLEQQ  
SSTINMTGGGRKHLWYMPEEYIRQGRLSVKTDVYSFGIVIMEVLTGCKVVLDDPKHVQLR  
DLLMELMEKRGDLSCLSF LDRKIPPCPRNFS AKLFSLAGRCVATKAKLRPTMDEV LSSLE  
STQPSLYFAEDPPTSLKSFRCPSPLFLDNVPSIPVEDDENQNNHSPVPKEVLGTDRTVQK  
TPFECSQSEVTLGLDRNRGNRGSEADCNVPSSSHEECWSPELVAPSQDLSPTVISLGSS  
WEVPGHSYSGKPMKRCSSGLFCSEHEQSKKQ

SEQ ID NO: 197\_AA088547\_H  
MASAVRGSRPWPRLGLQLQFAALLGLTSPQVHTLRPENLLL VSTLDGSLHALSKQTGDL  
KWTLRDDPVIEGPMYVTEMAFLSDPADGSLYILGTQKQGLMKLPFTIPELVHASPCRSS  
DGVFYTGKQDAWFVVDPESETQMTLTTEGPSTPRLYIGRTQYVTMHDPRAPALRWNT  
TYRRYSAPPMDGSPGKYM SHLASCGMGLLLTVDPGSGTVLWTQDLGVPVMGVYTWHDGL  
RQLPHLTLARDTLHFLALRWGHIRLPASGPRDTATLFTLDTQLLMTLYVGKDETFYVS  
KALVHTGVALVPRGLTLAPADGPTTDEVTLQVSGEREGSPSTAVRYPGSGVALPSQWLLI  
GHHELPPVLHTTMLRVHPTLGSGTAETRPENTQAPAFFLELLSLSREKLWDSELHPEEK  
TPDSYLGLGPQDLLAASLTAVLLGGWILFVMRQVVEKQOETPLAPADFAHISQDAQSLHS  
GASRRSQKRLQSPSKQAQPLDDPEAEQLTVVGKISFNPKDVLGRGAGGTFVFRGQFEGRA  
VAVKRLRECFGLVRREVQLQESDRHPNVLR YFCTERGPQFHYIALELCRASLQEYVEN  
PDLDRGGLEPEVVLQQLMSGLAHLHSLHIVHRDLKPGNILITGPD SQGLGRVVLSDFGLC  
KKLPAGRCFSFLHSGIPGTEGWMAPELLQLLPDPSPTSAVDIFSAGCVFYVLSGGSHPF  
GDSL YRQANILTGAPCLAHLEEEVHDKVVARDLVGAMLSPLPQPRPSAPQVLAPFFWSR  
AKQLQFFQDVS DWLEKESEQEPLVRALEAGGCAVVRDNWHEHIS MPLQTDLRKFRSYKGT  
SVRDLLRAVRNKKHHYRELPEVVRQALGQVPDGFVQYFTNRFPRLLLHTHRMRSCASES  
LFLPYYPDSEARRPCPGATGR

SEQ ID NO: 198\_HGP\_6644466  
MEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFMQKLGFGTGVNVYLMKRSRGLSHSP  
WAVKKINPICNDHYRSVYQKRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGE  
KSLNDLIEERYKASQDPFPAAILKVALNMARGLKYLHQEKLLHGD IKSSNVVIKGD FE  
TIKICDVGVSPLDENMTVTDPEACYIGTEPWKPKEAVEENGVI TDKADIFAFGLTLWEM  
MTLSIPHINLSNDDDDDKTFDESDFDEAYYAALGTRPPINMEELDESYQKVIELFSVC  
TNEDPKDRPSAAHIVEALETDV

SEQ ID NO: 199\_AA449542\_M  
SPRGLSHSPWAVKKISLLCDDHYRTVYQKRLTDEAKILKLNHPNIGYRAFTEASDGSL  
CLAMEYGEKSLNDLIEERNKDSGSPFPAAVILRVALHMARGLKYLHQEKLLHGD IKSS

## FIGURE 1T

NVVIKGFETIKICDVGVSLPLDENMTVTDPEACYIGTEPWKPKEALEENGIITDKADV  
AFGLTLWEMMTLCIPHVNLPDDDDVEDATFDESDFDDEAYYAALGTRPSINMELDDSYQK  
AIELFCVCTNEDPKDRPSAAHIVEALELDGQCCGLSESKH

SEQ ID NO: 200\_5R57\_10\_2\_M TESK2\_M  
LLDSDLYLPWTVRVKLAYGIAVGLSYLHFKGIFHRDLTSKV

SEQ ID NO: 201\_AA232253\_H  
MSSLGASFVQIKFDDLQFFENC GGGSFGSVYRAKWISQDKEVAVKLLKIEKEAEILSVL  
SHRNIQFYGVILEPPNYGIVTEYASLGSLYDIINSNRSEEMDMHIMTWATDVAKGMHY  
LHMEAPVKVIHRDLKSRNVVIAADGVVKICDFGASRFHNHTTHMSLVGTFFPWMAPEVIQS  
LPVSETCDTYSYGVVLWEMLTREVPFKGLEGLQVAWLVEKNERLTIPSSCPRSFAELLH  
QCWEADAKKRPSFKQIISILESMSNDTSLPDKCNSFLHNKAERCEIEATLERLKKLERD  
LSFKEQELKERERRLKMWEQKLTQSNTPLLPSEIGAWTEDDVYCWWQQLVRKGDSSAE  
MSVYASLKFENITGKRLLLLLEEDLKDGMIVSKGHIHFKSAIEKLTHDYINLFHFPPL  
IKDSGGEPEENEKEIVNLELVFGFHLKPGTGPQDCKWKMYMEMDGDEIAITYIKDVTFTNT  
NLPDAEILKMTKPPFVMEKWIIVGIAKSQTVECTVTYESDVRTPKSTKHVHLIQWSRTKPQ  
DEVKAVQLAIQTLFTNSDGNPGRSDSSADCQWLDTLRMRQIASNTSLQRSQSNPILGSP  
FFSHFDGQDSYAAAVRRPQVPIKYQQITPVNQSRSSPTQYGLTKNFSSLHLNSRDSGFS  
SGNTDTSSERGRYSDRSRKYGRGSI LNSSPRGRYSGKSQHSTPSRGRYPGKFYRVSQS  
ALNPHQSPDFKRSRDLHQPNITPGMPLHPETDSRASEEDSKVSEGGWTKVEYRKKPHRP  
SPAKTNKERARGDHRGWRNF

SEQ ID NO: 202\_AI375137\_H  
MGNYKSRTQTCTDEWKKKVSESYVITIERLEDDLQIKEKELTELNRNIFGSDEAFSKVNL  
NYRTENGLSLLHLCCICGKKSHIRTLMLKGLRPSRLTRNGFTALHLAVYKDNAELITSL  
LHSGADIQQVGYGGLTALHIATIAHLEAADVLLQHGANVNIQDAVFFTPLHIAAYYGHE  
QVTRLLLLKFGADVNVSGEVGDRPLHLASAKGFLNIAKLLMEEGSKADVNAQDNEDHVP  
FCSRFGHHDIVKYLQSDLEVQPHVNIYGDTPHLACYNKGFEVAKETIQISGTESLTK  
ENIFSETAFHSACTYKSIDLVKFLLDQNVININHQRDGTGLHSACYHGHIRLVQFLL  
DNGADMNLVACDPSRSSGEKDEQTCMLWAYEKGHDAIVTLLKHYKRPQDELPCNEYSQPG  
GDGSYVSVSPPLGKIKSMTKEKADILLRAGLP SHFHLQLSEIEFHEIIGSGSFGKVYKG  
RCRNKIVAIKRYRANTYCSKSDVDMFCREVSILCQLNHPCVIQFVGACLN DPSQFAIVTQ  
YISGGSLSLLEHQKRILDQSKLIIAVDVAKGMEYLHNLTPQIHRDLNSHNILLYEDG  
HAVVADFGESRFLQSLDEDNMTKQPGNLRWMAPEVFTQCTRYTIKADVFSYALCLWEILT  
GEIPFAHLKPAAAAADMAHYHIRPPIGYSIPKPISSLLIRGWNACPEGRPEFSEVVMKLE  
ECLCNIELMSPASSNSSGSLSPSSSSDCLVNRGGPGRSHVAALRSRFELEYALNARSYAA  
LSQSAGQYSSQGLSLEEMKRSLQYTPIDKYGYVSDPMSSMHFHSRNSSSSFEDSS

SEQ ID NO: 203\_H97685\_H  
MESERSPLYRQLIDLGYLSSSHWNCGAPGQDTKAQSMLVEQSEKLRHLSTFSHOVLQTRL  
VDAAKALNLVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMNIANRKQEE  
MKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEVGTREIKCCIRQIQELIISRLNQA  
VANKLISSVDYLRESFVGTLERCLQSLEKSQDVSVHITSNYLKQILNAAHYHEVTFHSGS  
SVTRMLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAKSICSQFRTRLNS  
SHEAFAASLRQLEAGHSGRLEKTEDLWLRVRKDHAPRLARLSLESRLQDVLHHRKPKLG  
QELGRGQYGVVYLCNWDGHHFPCALKSVVPPDEKHWNDLALFHYMRSLPKHERLVDLHG  
SVIDYNYGGGSSIAVLLIMERLHRDLTYTGLKAGLTLETRLQIALDVVEGIRFLHSQGLVH  
RDIKLNVLDDKQNRAKITDLGFCKPEAMMSGSI VGTPIHMAPELFTGKYDNSVDVYAFG

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## FIGURE 1U

ILFWYICSGSVKLPEAFERCASKDHLWNNVRRGARPERLPVFDDEECWQLMEACWDGDPLK  
RPLLGIQVQMLQGIMNRLCKSNSEQPNRGLDDST

SEQ ID NO: 204\_W20810\_M

DVNLKASKASDVYSFGILVWAVLAGREAELVDKTSLIRETVCDRQSRPPLTELPPGSPET  
PGLEKLKELMIHCWGSQSENRPSPQDCEPKTNEVYNLVKDKVDAAVSEVKHYLSQHRSSG  
RNLSAREPSQRGTEMDCPRETVMVKMLDRHLLEEPSGPVPGKCPERQAQDTSVGPATPAR  
TSSDPVAGTPQIPHTLPFRGTTGPGVFTETPGPHPQRNQDGRHGTPWYPWTPPNPMTGP  
PALVFNNCSEVQIGNYNLSLVAPPRTTASSSAKYDQAQFGRGRGWQPFHK

SEQ ID NO: 205\_AA744236\_H

MSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYKRENEDKVNKAAKHLKTL  
RHPCLLRFLSCTVEADGIHLVTERVQPLEVALETLSAEVCAGIYDILLALIFLHDRGHL  
THNNVCLSSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPPEEMSPEFTT  
LPECHGHARDAFSFGTLVESLLTILNEQVSADVLSSFQQLHSTLLNPIPKCRPALCTLL  
SHDFFRNDLFLEVNVFLKSLTLKSEEEKTEFFKFLDRVSCLEELIASRLVPLLLNQLVF  
AEPVAVKSFLPYLLGPKKDHQGETPCLLSPALFQSRVIPVLLQLFEVHEEHVRMVLSSH  
IEAYVEHFTQEQLKKVILPQVLLGLRDTSDSIVAITLHSLAVLVSLLGPEVVVGGERTKI  
FKRTAPSFTKNTDLSLEGDPFSQPIKFPINGLSDVKNSTEDSENFPSSSKKSEEWPDWSE  
PEEPENQTVNIQIWPPEPCDDVKSQCTTLDVEESSWDDCEPSSLDTKVNPGGGITATKPV  
TSGEQKPIPALLSLTEESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSELG  
LGEEFTIQVKKKPVKDPMDWFMADIPEIKPSAAFLILPELRTEMVPKKDDVSPVMQFSS  
KFAAAEITEGEAEGWEEEGELNWNEDNNW

SEQ ID NO: 206\_AI052250\_H

MESMLNKLKSTVTKVTADVTSAVMGIPVTREFDVGRHIASGCNGLAWKIFNGTKKSTKQE  
VAVVFVDKKLIDKYQKFEKQIIDSCLKRGVQQLTRLRHPRLLTVQHPLEESRDCLAFCTE  
PVFASLANVLGNWENLPSPISPDIKDYKYDVETKYGLLQVSEGLSFLHSSVKMVHGNI  
PENIILNKSGAWKIMGFDFCVSSTNPSEQEPKFPCKEWDPNLPSLCLPNPEYLAPEYILS  
VSCETASDMYSLGTVMYAVFNKGKPIFEVKNQDIYKSFSRQLDQLSRLGSSSLTNIPEEV  
REHVKLLLNVTPTVRPDADQMTKIPFFDDVGAVTLQYFDTLFQRDNLQKSQFFKGLPKVL  
PKLPKRIVIVQRILPCLTSEFVNPDMPVFLPNVLLIAEECTKEEYVKLILPELGPVFKQQ  
EPIQILLIFLQKMDLLLTKTPPDEIKNSVLPVYRALEAPSIQIQELCLNIIPTFANLID  
YPSMKNALIPRIKNACYKHLPLRFV

SEQ ID NO: 207\_AA278842\_H

MWFFARDPVRDFPFELIPEPPEGGLPGPWALHRGRKKATGSPVSI FVYDVKPGAEETQV  
AKAAFKRFTLRHPNIIAYIDGLETEKCLHVVTAVTPLGIYLKARVEAGGLKELEISWG  
LHQIVKALSFLVNDCSLIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQGNNGGPPRKGIPE  
LEQYDPPELADSSGRVVREKWSADMWRLGCLIWEVFNGLPRAAALRNPGKIPKTLVPHY  
CELVGANPKVRPNPARFLQNCRAPGGFMSNRFVETNLFLEEIQIKEPAEKQKFFQELSKS  
LDAFPEDFCRHKVLPLQLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVKMFSS  
TDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVHGFLLDTNPAIREQTVKSMLLLAPKLN  
EANLNVELMKHFARLQAKDEQGPIRCNTTVCLGKIGSYLSASTRHRVLTSAFSTRATRDPF  
APSRVAGVLGFAATHNLYSMNDCAQKILPVLCLGLTVDPKSVRDQAFKAIRSFLSKLESV  
SEDPTQLEEVKDVHAASSPGMGGAASWAGWAVTGVSLSKLIRSHPTTAPTETNIPQ  
RPTPEGVPAPAPTVPATPTTSGHWETQEEDKDTAEDSSSTADRWDDWGSLEQEAESVL  
AQQDDWSTGGQVSRASQVNSDHKSSKSPESDWSSWEAEGSWEQGWQEPSSQEPDPGTR  
LASEYNWGGPESDKGDPFATLSARPSTQPRPDSWGEDNWEGLTDSRQVKAEALARKKRE  
ERRREMEAKRAERKVAKGPMKLGARKLD

## FIGURE 1V

SEQ ID NO: 208\_AA599286\_H

MAFMEKPPAGKVLLDDTVPLTAAIEASQSLQSHTEYIIRVQGGISVENSWQIVRRYSDFD  
LLNNSLQIAGLSLPLPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFLD  
PNNYSANYTEIALQQVSMFFRSEPKEVVEPLKDIGWRIRKKYFLMKIKNQPKERLVLWS  
ADLGPDKYLSKDFQCLIKLLPSCLHPYIYRVTFATANESSALLIRMFNEKGTLDLIYK  
AKPKDPFLKKYCNPKKIQGLELQIKTYGRQILEVLKFLHDKGFPYGHLLHASNVMLDGD  
CRLLDLENSLLGLPSFYRSYFSQFRKINTLESVDVHCFGHLLYEMTYGRPPDSVPVDSFP  
PAPSMVAVLESTLSCEACKNGMPTISRLLQOMPLFSDVLLTTSEKPQFKIPTKLKEALR  
IAKECIEKRLIEEQKQIHQHRRLTRAQSHHGSEERKKRILARKKSKRSALENSEEHSA  
KYSNSNNSAGSGASSPLTSPSSPTPPSTSGISALPPPPPPPPPPAAPLPPASTEAPAQLS  
SQAVNGMSRGALLSSIQNFQKGTLRKAKPVITVLRSAEASCLHLEGKVLFYSSPLPPN  
YPLPGKVIAEPVQPQTVLFCRCSCQQLFERNNSLSRIKLGWHAKKKKKK

SEQ ID NO: 209\_AA425725\_H

MSASTGGGGDGGSGGSSSSSQASCGPESSGSELALATPVPQMLQGLLGSDDDEEQEDPKD  
YCKGGYHPVKIGDVFNGRYHVVRKLGWGHFSTVWLCWDIQRKRFVALKVVKSAHYTETA  
VDEIKLLKCVRSDSPDPKRETIVQLIDDFRISGVNGVHVMVLEVLGHQLLKWI IKSNY  
QGLPVPCKVKSIVRQVLHGLDYLHTKCKI IHTDIKPENILLCVGDAYIRRLAAEATEWQQA  
GAPPPSRISIVSTAPQEVLTGKLSKNKRKKMRRKRKQOKRLLEERLRDLQRLAEMAATQA  
EDSGRLRDGGSGSTSSSGFSGSLFSPASCSILSGSSNQRETGGLSPSTPFGASNLLVNP  
LEPQNADKIKIKIADLGNACWVHKHFTEDIQTRQYRAVEVLIGAEYGPADIWSTACMAF  
ELATGDYLFEPHSGEDYSRDEDHIAHIVELLGDI PPAPALSGRYSREFFNRRGELRHIHN  
LKHWGLEYEVLMEKYEWPLEQATQFSAFLPMMEYIPEKRASAADCLOHPWLNP

SEQ ID NO: 210\_SGK022\_H

MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKVIDKMGGPSEFIQRFLPRELQ  
IVRTL DHKNI IQVYEMLESADGKICLVMELAEGGDVDFCVLNGGPLPESRAKALFROMVE  
AIRYCHGCGVAHRDLKCENALLQG FNKL TDFGFAKVL PKSHRELSQTFCGSTAYAAPEV  
LQGI PHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSPFTHLSISADCQD  
LLKRLLEPDMILRPSIEEVSHPWLAST

SEQ ID NO: 211\_AA060026\_M SGK022\_M

MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKIIDKMGGPEEFIQRFLPRELQ  
IVRTL DHKNI IQVYEMLESADGKIYLVMELEAGGDVDFCVLNGGPLPESRAKALFROMVE  
AIRYCHGCGVAHRDLKCENALLQG FNKL TDFGFAKVL PKSRRELSQTFCGSTAYAAPEV  
LQGI PHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSPFTHLGISTECQD  
LLKRLLEPDMILRPSIEEVSHPWLAST

SEQ ID NO: 212\_AA399669\_H

MGKGDVLEAAPT TTTAYHSLMDEYGYEVGKAIGHGSYGSVYEA FYTKQKVMVAVKIISKKK  
ASDDYLNKFLPREIQQVMKVL RHKYLINFYRAIESTSRVYIILELAQGGDVLEWIQRYGA  
CSEPLAGKWFSQLTLGIAYLHKSIVHRDLKLENLLLDKWENVKISDFGFAKMVPSNQPV  
GCSPXYRQVNCFSHLSQTYCGSFAYACPEILRGLPYNPFLSDTWSMGVILYTLVVAHLPF  
DDTNLKKLLRETQKEVTFPANHTISQECKVQLLIACVAQWRKTQARPLSPLL

SEQ ID NO: 213\_AA758539\_H

MDDATVLRKKGYIVGINLGKGSYAKVKSAYSERLKFNVAVKIIDRRKTPTDFVERFLPRE  
MDILATVNHGSI IKT YEIFETSDGRIYIIMELGVQGDLLFIKQCQALHEDVARKMFROL  
SSAVKYCHDLDIVHRDLKCENLLLDKDFNIKLSDFGFSKRCLRDSNGRIILSKTFCGSAA

## FIGURE 1W

YAAPEVLQSI PYQPKVYDIWSLGVILYIMVCGSMPYDDSDIRKMLRIQKEHRVDFPRSKN  
LTCECKDLIYRMLQPDVSQLHIDEILSHSWLQPPKPKATSSASFKEGEGKYRAECKLD  
TKTGLRPDHRPDHKLGAKTQHRLLVVPENENRMEDRLAETSRAKDHHISGAEVGKAST

SEQ ID NO: 214\_AA883975\_H

MSGDKLLSELGYKLGRTIGEGSYSKVKVATSKKYKGTVAIKVVDRRRAPPDFVNKFLPRE  
LSILRGVRPHPHIVHVFIEVCNGKLYIVMEAAATDLLQAVQRNGRIPGVQARDLFAQIA  
GAVRYLHDHHLVHRDLKCENVLLSPDERRVKLTDFGFGROAHGYPDLSTTYCGSAAYASP  
EVLGIPYDPKKYDVWSMGVVLYVMVTGCMFDDSDIAGLPRRQKRGVLYPEGLELSERC  
KALIAELLQFSPSARPSAGQVARNCWLRAGDSG

SEQ ID NO: 215\_AA905446\_H

VGRQETGVRRWAFLICQPI SPPLTSSEFIQRFLPRELQIVRTL DHKNI IQVYEMLESADG  
KICLVMELAEAGDVFDCVLNGGPLPESRAKALFROMVEAIRYCHGCGVAHRDLKCENALL  
QGFNLKLTDFGFAKVLPKSHRELSQTFCGSTAYAAPEVLQGI PXKMLWQQQKGVSFPTH  
SISADCQDLLKRLLPEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 216\_H29974\_H

YSLLAIEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVELALAEFWALTSLKRRHQNV  
VQFEECVLQRNGLAQRM SHGNKSSQLYLRLVETSLKGERILGYAEPCYLWFVMEFCEGG  
DLNQYVLSRRPDPATNKSFMLQLTSAIAFLHKNHIVHRDLKPDNILITERSGTPILKVAD  
FGLSKVCAGLAPRGKEGNQDNKNVNVNKYWLSSACGSDFYMAPEVWEGHYTAKADIFALG  
IIIWAMIERITFIDSETKKELLGTYIKQGT EIVPVGEALLENPKMELHIPQKRRTSMSEG  
IKQLLKDMLAANPQDRPDAFELETRMDQVTCAA

SEQ ID NO: 217\_AA498104\_M H29974\_M

PLLLPPPPAAMETGKENGARRGKSPERKRRSPVQORVLCEKLRPAAQAMPAGAEVPGEA  
FLARRRPDGGGDV PARPRYSLLAEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVE  
LALAEFWALTSLKRRHQNVVQFEECVLQRNGLAQRM SHGNKNSQLYLRLVETSLKGERIL  
GYAEPCYLWFVMEYCEGGDLNQYVLSRRPDPATNKSFMLQLTSAIAFLHKNHIVHRDLK  
PDNILITERSGTPILKVADFGLSKVCAGLAPRGKEGNQDNKNVNVNKYWLSSACGSDFYM  
APEVWEGHYTAKADIFALGIIIWAMIERITFIDSETKKELLGTYIKQGT EIVPVGEALLE  
NPKMELHIPQKRRTSMSEGVKQLLKDMLAANPQDRPDAFELETRMDQVTCAA

SEQ ID NO: 218\_AA215311\_H

MVSSQPKYDLIREVGRGSYGVVYEAVIRKTSARVAVKKIRCHAPENVELALREFWALSSI  
KSQHPNVIHLEECILQKDMVQKMSHGSNSSLYLQLVETSLKGEIAFDPR SAYYLWFVMD  
FCDGGDMNEYLLSRKPNRKTNTSFMLQLSSALAFHKNQI IHRDLKPDNILISQTRLDT  
DLEPTLKVADFGLSKVCSASGQNPEEPVSVNKCFLSTACGTD FYMAPEVWEGHYTAKADI  
FALGIIIWAMLERITFIDTETKKELLGSYVKQGT EIVPVGEALLENPKMELLI PVKKKSM  
NGRMKQLIKEMLAANPQDRPDAFELELRVLVQIAFKDSSWET

SEQ ID NO: 219\_AA018361\_H

MRAAFPAGGAGGSVEPPSARPAPQAGTAARSEEAPARAQAAGMAGPGWGPRLDGFILT  
ERLGS GTYATVYKAYAKD TREVVAIKCVAKKSLNKASVENLLTEIEILKGIRHPHIVQL  
KDFQWSDNIYLIMEFCAGGDL SRFIHTRRILPEKVARVFMQQLASALQFLHERNISHLD  
LKPQNILLSSLEKPHLKLADFGFAQHMSPWDEKHVLRGSPLYMAPEMVCQRQYDARVDLW  
SMGVILYEALFGQPPFASRSFSELEEKIRSNRVIELPLRPLLSRDCRDLLQRLLERDPSR  
RISFQDFFAHPWVDLEHMPSGESLGRATALVVQAVKKDQEGDSAAALSLYCKALDFFVPA

## FIGURE 1X

LHYEVDQRKEAIKAKVGQYVSRAEELKAIVSSSNQALLRQGTSARDLLREMARKPRLL  
AALEVASAAMAKEEAAGGEQDALDLYQHSLGELLLLLRSRPRAGGSCFTLRFRRTSWPELN  
T

SEQ ID NO: 220\_AA311714\_H  
MENFILYEEIGRSKTVVYKGRRKGTINFVAILCTDKCRRPEITNWVRLTREIKHKNIIVT  
FHEWYETSNHLWLXENLPEDVVREFGIDLISGLHHLHKLGLFCDISPRKILLEGPGTL  
KFSNFCLAKVEGENLEEFFALVAAEEGGDNGENVLKKSMKSRVKGSPVYTAPEVVRGAD  
FSISSDLWSLGCCLLYEMFSGKPPFFSESSELTEKILCEDPLPPIPKDSSRPKASSDFIN  
LLDGLLQDRDPQKRLTWTRLLQHSFWKKAFAAGADQESSVEDLSLSRNTMECSGPDQSKELL  
QNSQSRQAKGHKSGQPLGHSFRLENPTFRPKSTLEGQLNESMFLSSRPTPTSTAVEV  
SPGEDMTHCSPQKTSPLTKITSGHLSQODLESQMRELIYTDSDLVVTPIIDNPKIMKQPP  
VKFDAKILHLPTYSVDKLLFLKDQDWNDFLQQVCSQIDSTEKSMGASRAKLNLLCYLCVV  
AGHQEVATRLLHSPLFQLLIQHLRIAPNWDIRAKVAHVIGLLASHTTELQENTPVVETTS  
SIGIGILNCLVQHSTPVPRQCLVYV

SEQ ID NO: 221\_SGK384\_H  
SLAHVLRARQILTEPEVRDYLRLGLVSGRLRYLHQRCILHR

SEQ ID NO: 222\_AA210451\_M SGK384\_M  
MGQQHGTRNGLTHRELPRGVGLLLAMALMNVALYLCLDQLFISPRSTADSRRCPPGYFR  
MGRMRNCSRWLSCEELRTEVRQLKRVGEGAVKRVFLSEWKEHKVALSRLTRLEMKEDFLH  
GLQMLKSLQSEHVVTLVGYCEEDGTILTEYHPLGSLSNLEETLNLSKYQDVNTWQHRQL  
AMEYVSIINYLHHSPLGTRVMCDSDNLPKTLQYLLTSNFSIVANDLDALPLVDHDSGLV  
IKCGHRELHGDFVAPEQLWPYGEDTPFQDDLMPSYNEKVDIWKIPDVSSFLLGHVEGSDM  
VRPHLFDIHKACKSQIPAERPTAQNVLDAYQRVFHSRLRDTVMSQTKEML

SEQ ID NO: 223\_SGK071\_2\_H  
EVVAVQMMVECMDDHYASQALEELMPLLLKLRHAHISVYQELFITWNGEISSLYLCLVMEF  
NELSFQEVIEDKRKAKKIIDSEWMQNVLGQVLDALAYLHHLDIHRNLKPSNIILISSDH  
CKLQDLSSNVLMTDKAKWNIRAEEDPFRKSWMAPEALNFSFSQKSDIWSLGCIIIDMTSC  
SFMDGTEAMHLRKSLRQSPGSLKAVLKTMEEKQIPDVETFRNLLPLMLQIDPSDRITIKD  
VVHITFLRGSFKSSCVSLTLHRQMVPASITDMLLEGNVASILGDAGDTKGERALKLLSMA  
LASYCLVPEGSLFMPLALLHMDQWLSCDQDRVPGKRDFAVLGKLGLLGPPIPKGLPWPP  
ELVEVVVTTMELHDRVLDVQLCACSLLLHLLGQALVHHPEAKAPCNQAITSTLLSALQSH  
PEEEPLLVMVYSLLAITTTQESESLSSEELQNAGLLEHILEHLNSSLERDVCASGLGLLW  
ALLLDDPILALQRPKRKRAPNHGKPGKPNPASTQSIIVNKAPLEKVPDLISQVLATYPA  
DGEMAEASCQVFWLLSLLGCIKEQQFEQVVALLLQSIRLCQDRALLVNNAYRGLASLVKV  
SELAAFKVVVQEEGGSGLSLIKETYQLHRDDPEVVENVGMLLVHLASYEEILPELVSSSM  
KALLQEIKERFTSSSLVSDSSAFSKPGLPPGGSPQLGCTTSGGLE

SEQ ID NO: 224\_AA118352\_M SGK071\_M  
EEDPCQKSWMAPEALKFSFSTKSDIWSLGCIIIDMATCSFLNDTEAMQLRKAIRHHPGSL  
KPILKTMEEKQIPGTDVYYLLLPFMLHINPSDRLAIKDVMQVTFMSNSFKSSSVLNMQR  
QKVPFITDVLLEGNMANILGSWLCASFVNDNRHCDSGIGSQRLGFDQSVSWTEHPLKD  
VMQNFSSRPEVQLRAINKLLTMPEDQLGLPWPTELLEEVISIIKQHGRILDILLSTCSLL  
LRVLGQALAKDPEAEIPRSSLIISFLMDTLRSHPNSERLVNVVYNVLAIISSQGQISEEL  
EEGLFQLAQENLEHFQEDRDICLSILSLLWSLLVDVVTVDKEPLEQLSGMVTWVLATHP  
EDVEIAEAGCAVLWLLSLLGCIKESQFEQVVLLLSRIQLCPGRVLLVNNAFRGLASLAK

## FIGURE 1Y

VSELVAFRIVVLEEGSSGLHLIQDIYKLYKDDPEVVENLCMLLAHLTSYKEILPEMESGG  
IKDLVQVIRGRFTSSLELISYADEILQVLEANAQPGLOEDQLEPPAGQEAPLQGEPLFRP

SEQ ID NO: 225\_018653.9\_H

GRGRGAGHARGLGRGPAGRRAPPRSLSRPGPGPSRAGPAGRGEGSDAAPAGGSGRGFL  
RLLPAGLRPQRALRSGSEPPRPGQSPEPSPAPGAGRRGGRGELARQIRARYEEVQRYSRG  
GPGPGAGRPERRRLMDLAPGGPGLPRPRPPWARPLSDGAPGWPPAPGPGSPGPGPRLGCA  
ALRNVSGAQYMGSGYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGVRRGCYRLAA  
HKLLKEMVLLERLRHPNVLQLYGYCYQDSEDIPTLTITITELGAPVEMIQLLQTSWEDRF  
RICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVDGELKVTDLDDARVEETPCAGSTDCI  
LEFPARNFTLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDISVNATGE  
LAWGVDETLAQLEKVLHLYRSGQYLQNSTASSSTEYQCI PDSTI PQEDYRCWPSYHHGSC  
LLSVFNLAEAVDVCESHAQCRAFVVTNQTTWTGRQLVFFKTGWSQVVPDPNKTTYVKASG

SEQ ID NO: 226\_AA396601\_M

TRPGCAALRNVSGAQYVGSYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGARRG  
CYRLAAHKLLKEMVLLERLRHPNVLQLYGYCYQDSEGIPTLTITITELGAPVEMIQLLQTSWEDRF  
RICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVNGELKVTDLDDARVEETPCT  
SSADCTLEFPARNFSLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDISI  
VNATGELAWGVDETLAQLETAHLFRSGQYLQNSTSSRAEYQRI PDSAITQEDYRCWPSY  
HHGGCLLSVFNLAEAIDVCESHAQCRAFVVTNQTTWTGRKL VFFKTGWNQVVPDAGKTTY  
VKAPG

SEQ ID NO: 227\_VRK3\_H

MISFCPDCGKSIQAAFKFCPYCGNSLPVEEHVGSQTFVNPHVSSFQGSKRGLNSSFETSP  
KKVKWSSTVTSRRLSLFSDGDSSESEDTLSSSERSKSGSGSRPPTPKSSPQKTRKSPQVTR  
GSPQKTSCSPQKTRQSPQTLKRSRVTTSLALPTGTVLTDKSGRQWKLKSFQTRDNQIL  
YEAAPTSTLTCDSGPQKQKFSKLDAKDGRLFNEQNFFQRAAKPLQVNWKKLYSTPLLA  
IPTCMGFGVHQDKYRFLVLP SLGRSLQSALDVSPKHVLSERSVLQVACRLDDALEFLHEN  
EYVHGNVTAENIFVDPEDQSQVTLAGYGFAFRYCPSGKHVAYVEGSRSPHEGDLEFISMD  
LHKGCGPSRRSDLQSLGYCMLKWLYGFLPWTNCLPNTEDIMKQKQKFVDKPGPFVGP CGH  
WIRPSETLQKYLKVMALTYEEKPPYAMLRRNNLEALLQDLRVSPYDPIGLPMVP

SEQ ID NO: 228\_S71575\_M VRK3\_M

IPTCIGFGIHQDKYRFLVFP SLGRSLQSALDDNPKHVVSERCVLQVACRLDDALEYLHEN  
EYVHGNLTAENVFVNPEDLSQVTLVGYGFTYRYCPGGKHVAYKEGSRSPHDGDLEFISMD  
LHKGCGPSRRSDLQTLGYCMLKWLYGSLPWTNCLPNTTEKITRQKQKYLDSPERLVGLCGR  
WNKASETLREYLKVMALNYEEKPPYATLRNSLEALLQDMRVSPYDPLDLQMPV

SEQ ID NO: 229\_AA45427\_H

MGHALCVCSRGTVIIDNKRYLFIQKLGEFFSYVDLVEGLHDGHFYALKRILCHEQQDRE  
EAQREADMHRFLFNHPNIRLVAYCLRERGAKHEAWLLLPFFKRGTLWNEIERLKDKNFL  
TEDQILWLLLGICRGLEAIHAKGYAHRDLKPTNILLGDEGQPVLM DLGSMNQACIHVEGS  
RQALTLDWAAQRCTISYRAPELFSVQSHCVIDERTDVWSLGCVLAMMFEGEPYDMVFQ  
KGDSVALAVQNQLSIPQSPRHSSALRQLLNSMMTVDPHQRP HILLLSQLEALQPPAPGQ  
HTTQI

SEQ ID NO: 230\_H05721\_H

MAVRQALGRGLQLGRALLLRFTGKPGRAYGLGRPGPAAGCVRGERPGWAAGPGAEP RRVG  
LGLPNRLRFFRQSVAGLAARLQRQFVVRWAGCAGPCGRAVFLAFGLGLGLIEEKQAESRR

## FIGURE 12

AVSACQEIQAIFTQKSKPGPDPLDTRRLQGFRLEEYLIGQSIGKGCSAAVYEATMPTLPQ  
 NLEVTKSTGLLPGRGPGTSAPGEGQERAPGAPAFPLAIKMMWNI SAGSSSEAILNTMSQE  
 LVPASRVALAGEYGAVTYRKS KRGPQLAPHPNI IRVLRAFTSSVPLLPGALVDYPDVLP  
 SRLHPEGLGHGRTLFLVMKNYPCTLRQYLCVNTSPRLAAMMLLQLEGGVDHLVQQGIAH  
 RDLKSDNILVELDPDGPWLVIADFGCCLADESIGLQLPFSSWYVDRGGNGCLMAPEVST  
 ARPGPRAVIDYSKADAWAVGAIAYEIFGLVNPFGYQGKAHLESRSYQEAQLPALPESVPP  
 DVRQLVRALLQREASKRPSARVAANVLHLSLWGEHILALKNLKLDKMVGWLLQOSAATLL  
 ANRLTEKCCVETKMKMLFLANLECETLCQAALLLCSWRAAL

SEQ ID NO: 231\_AI086865\_H

MEKYERIRVVGRAFGI VHLCLRKADQKLVIIKQIPVEQMTKEERQAAQNECQVLKLLNH  
 PNVIEYYENFLEDKALMIAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALHHVH  
 THLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSTPCYISPCLCEGKPYNQKSDIW  
 ALGCVLYELASLKRAFEAANLPALVLKIMSGTFAPISDRYSPELRQLVLSLLSLEPAQRP  
 PLSHIMAQPLCIRALLNLHTDGREVRGPQQHREQDHQCPLQGI IMTFGSGSNGCLGHGS  
 LTDISQPTIVEALLGYEMVQQVEEALSFTLLGSAPLDQEPLLSIDLGTASAAVTGEEDL  
 GSGDVNRLPSWERGHLLAGVASSTDVSTFSEGDCKEPKCCWRHKQCTGHI IYPFASDCV  
 RHSLHLHSVNHNCNSRLKDSSSEDSSSRGAGPTCSHVIESPCFELTPEEEHVERFRYGW  
 CKSYRPSVAVIHHPLYHECGADDLNKXKRKRKRKRKSKPPIPTQVGPATASPDLTSMAT  
 GTPDSTAPITIWRSSEPTGKGQGSKVIKKVKKKKEKEKDKEEMDEKAKLKKKAKKGQLTK  
 KKSPVKLEPSPDPVSRSL SARQLARMSSESPESREELESEDSYNGRGQGELSSSEDI VESS  
 SPRKRENTVQAKKTGAKPSQARKVNKRKSPPGSNPNLS

SEQ ID NO: 232\_AA836348\_H

MSVLGEYERHCDSINSDFGSESGCGDSSPGPSASQGPRAGGAAEQEELHYIPIRVLGR  
 GAFGEATLYRRTEDDSL VVWKEVDLTRLSEKERRDALNEIVILALLQHDNI IAYYNHFM  
 NTTLLIELEYCNGGNLYDKILRQKDKLFEEEMVVWYLFQIVSAVSCIHKAGILHRDIKTL  
 NIFLTKANLIKLG DYGLAKKLNSEYSMAETLVGTPYYMSPELCQGVKYNFKSDIWAVGCV  
 IFELLTLKRTFDATNPLNLCVKIVQGIRAMEVDSSQYSLELIQMVHSCLDQDPEQRPTAD  
 ELLDRPLLKRKRSSSTVTEAPIAVVTSRTSEVYVWGGGKSTPQKLDVIKSGCSARQVCAG  
 NTHFAVVTVKELYTWNMQGGTKLHGQLGHGDKASYRQPKHVEKLQGKAIRQVSCGDDF  
 TVCVTDEGQLYAFGSDYYGCMGVDKVAGPEVLEPMQLNFFLSNPVEQVSCGDNHVVVLT  
 NKEVYSWGCGEYGRGLDSEEDYYTPQKVDVPKALI I VAVQCGCDGTFLLTQSGKVLACG  
 LNEFNKLGLNQCMSGI INHEAYHEVPYTTSFTLAKQLSFYKIRTIAPGKTHTA AIDERGR  
 LLTFGCNKCGQLGVGNKKRLGINLLGGPLGKQVIRVSCGDEFTIAATDEKVLNSKTIR  
 SNSSGLSIGTVFQSSSPGGGGGGGGEEEDSQQESETPDPSGGFRGTMEADRGMEGLISP  
 TEAMGNSNGASSCPGWLRKELENAEFI PMPDPSPLSAAFSESEKDTLPYEELQGLKVA  
 SEAPLEHKPQVEASVTELFAPESQLVTSAESCSNLCWEGNTTDS SCVCVQLSAGGG

SEQ ID NO: 233\_R86668\_H, MKK6\_H

MNLLLSYRDVQDYSAI IELVETLQALPTCDVAEQHNVC FHYTFALNRRNRPGDRAKALSV  
 LLPLVQLEGSVAPDLYCMCGRIYKDMFFSSGFQDAGHREQAYHWYRKAFDVEPSLHSGIN  
 AAVLLIAAGQHFEDSKELRLIGMKLGCLLARKGCVEKMQYYWDVGFYLGAI LANDPTQV  
 VLAAEQLYKLNAPIWYLVSMETFLLYQHFRPTPEPPGGPPRAHFWLHFLQSCQPFKT  
 ACAQGDQCLVLVLEMNKVL LPAKLEVRGTDVPSTVTL SLEPETQDIPSSWTFPVASICG  
 VSASKRDERCCFLYALPPAQDVQLCFPSVGHQCQWFCGLIQAVVTNPDSTAPAEAEAGAGE  
 MLEFDYEYTETGERLVLGKGTYG VYAGRDRHTRVRIAIKEI PERDSRFSQPLHEEIALH  
 RRLRHKNIVRYLGSASQGGYLKIFMEEVPGGSLSSLLRSVWGPKDNESTISFYTRQILQ  
 GLGYLHDNHI VHRDIKGDNLINTFSGLLKI SDFGT SKRLAGITPCTETFTGTLOQYMAPE  
 IIDQGRGYGKAADIWSLGCTVIEMATGRPPFHELGSPPQAAMFQVGMKVHPPMPSSLSA

## FIGURE 1AA

EAQAFLLRTFEPDPRLRASAQTLLGDPFLQPGKRSRSPSSPRHAPRPSDAPSASPTPSAN  
STTQSQTFPCPQAPSQHPSPPKRCLSYGGTSQLRVPEEPAAEEPASPEESSGLSLLHQE  
SKRRAMLAHVLEQELPALAENLHQEQKQEQGARLGRNHVEELLRCLGAHIHTPNRRQLAQ  
ELRALQGRLRAOGLGPALLHRPLFAFPDAVKQILRKRQIRPHWMFVLDSSLRAVRAALG  
VLGPEVEKEAVSPRSEELSNEGDSQQSPGQQSPLPVEPEQGPAPLMVQLSLLRAETDRLR  
EILAGKEREYQALVQORALQRLNEEARTYVLAPEPPTALSTDQGLVQWLQELNVDSGTIQM  
LLNHSFTLHTLLTYATRDDLITYTRIRGGMVCRIWRAILAQRAGSTPVTSGP

SEQ ID NO: 234\_PAK6\_H

MFGKKKKKIEISGPSNFEHRVHTGFDPOEQKFTGLPQQWHSLLADTANRPKPMVDPSCIT  
PIQLAPMKTIVRGNKPKETSINGLLEDFDNISVTRSNLSRKESPPTPDQGASSHGPCHA  
EENGFITFSQYSSSEDTTADYTTKEYREKSLYGGDLDPYYRGSHAQKQNGHVMKMKHGEA  
YYSEVKPLKSDFAFSAFYHSHLDSLKPSSEYSDLKWEYQRASSSSPLDYSFQFTPSRTA  
GTSGCSKESLAYSESEWGPSLDDYDRPKSSYLNTSPQPTMRQSRSGSGLQEPMPFPG  
ASAFKTHPQGHSYNSYTPRLSEPTMCIPKVDYDRAQMVLSPPLSGSDTYPRGPAKLQPS  
QSKSGYSSSSHQYPSGYHKATLYHHPSLQSSSQYISTASYLSSLSLSSSTYPPPSWGSSS  
DQQPSRVSEHQFRAALQLVVSPGDPREYLANFIKIGEGSTGIVCIATEKHTGKQVAVKKM  
DLRKQQRRELLFNEVVMRDYHHDNVVDMYSSYLVGDELWVVMFLEGGALTDIVTHTRM  
NEEQIATVCLSVLRALSYLHNQGVHRDIKSDSILLTSDGRIKLSDFGFCQVSKVPRK  
KSLVGTPTYWMAPEVISRLPYGTEVDIWSLGIMVIEMIDGEPPYFNEPPLQAMRIRDSLP  
PRVKDLHKVSSVLRGFLDLMLVREPSQRATAQELLGHPFLKLAGPPSCIVPLMRQYRHH

SEQ ID NO: 235\_SURTK106\_H

MNDRNEIQMEAKLQSLTIIAQEILCRFFITLRRHARFLLTKLGRQGMARSGITHSCAVCI  
LCGPSREGDSPVAMGMTRMLLECSLSDKLCVIEKQYEVIIVPTLLVTIFLILLGVILWL  
FIREQRTQQQRSGPQGIAPVPPPRDLSWEAGHGGNVALPLKETSVENFLGATTPALAKLQ  
VPREQLSEVLEQICSGSCGPIFRANMNTGDPSKPKSVILKALKEPAGLHEVQDFLGRIQF  
HQYLKGKHNVLVQLEGCTEKLPLYMVLEDVAQGDLLGFLWTCRRDVMTMDGLLYDLTEKQ  
VYHIGKQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSTQT  
IPLKWLAPERLLLRPASIRADVWSFGILLYEMVTLGAPPYPEVPPTSILEHLQRRKIMKR  
PSSCTHTMYSIMKSCWRWREADRPSRELRLRLEAAIKTADDEAVLQVPELVVPELYAAV  
AGIRVESLFYNYSML

SEQ ID NO: 236\_AA098024\_M

LQEKHLFHGDVAARNILIQSDLTPKLCHLGLAYEVHAHGAISSARSSTIPLKWLAPERLL  
LRPASIRGDIWSFGILLYEMVTLGAPPYPEVPPTSILQYLQKKIMKRPSSCSHAMYNIM  
KCCWRWSEDSRPLLQVLLQRLLEAASRSADDKAVLQVPELVVPELYADVAGIRAESISYSF  
SVL

SEQ ID NO: 237\_SGK2ALPHA\_H

MNSSPAGTPSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNYGKVLLAKRKSDGAF  
YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE  
LFFHLQRRERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVVLTDVGL  
CKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSDVS  
QMYENILHQPLQIPGGRTVAACDLLQSLLLHKDQQRQLGSKADFLEIKNHVFFSPINWDDL  
YHKRLTPFPNPNTGPADLKHFDPFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPE  
DDDILDC

## FIGURE 1BB

SEQ ID NO: 238\_CCRK\_H

MDQYCILGRIGEGAHGIVFKAKHVETGEI IALKKVALRRLEDGFPNQALREIKALQEMED  
NQYVVQLKAVFPHGGGFVLAFAEFMLSDLAEVVRHAQRPLAQAQVKSQMLLKGVAFCHA  
NNIVHRDLKPANLLISASGQLKIADFGLARVFS PDGSRLYTHQVATRSVGCIMGELLNGS  
PLFPGKNDIEQLCYVLRILGTPNPQVWPELTELPDYNKISFKEQVPMPL EEVL PDVSPQA  
LDLLGQFLLYPPHQRIAASKALLHQYFF TAPLPAHPSELPI PQLGGPAPKAHPGPPHIH  
DFHVDRLLEGVAVEPRADSALHPGGVRSWPWSRLPAPQDHSVHLFLCHLPGF TLQGLPMA  
TVGPHHTLPLSPCEGWSRGRGHVPSQEYENIQSSRGDSWPVLGEPYLLCATDVPIRTVSS  
AASQGLHMQNDDACLGAASPECCLLVKEKCRE

SEQ ID NO: 239\_TESK2\_H

MDRSKRNSIAGFPFPRVERLEEFEGGGGGEGNV SQVGRVWPSSYRALISAFSRLTRLDDFT  
CEKIGSGFFSEVFKVRHRASGQVMALKMNTLSSNRANMLKEVQLMNRLSHPNILRYINSG  
NLEQLLDSNLHLPWTVRVKLAYDIAVGLSYLHFKGI FHRDLTSKNCLIKRDENGYS AVVA  
DFGLAEKIPDVSMGSEKLAVVGSPFWMAPEVLRDEPYNEKADVFSYGIILCEIIARIQAD  
PDYLPRTENFGLDYDAFQHMVGDCPPDFLQLT FNCCNMDPKLRPSFVEIGKTLEEILSRL  
QEEEQERDRKLQPTARGLLEKAPGVKRLSSLDDKIPHKSPCPRRTIWL SRSQSDIFSRKP  
PRTVSVLDPYRPRDGAARTPKVNPFSARQDL MGKIKFFDLPSKSVISLVFDLDAPGPG  
TMPLADWQEPLAPPIRRWRS LPGSPEFLHQEACPFVGREESLSDGPPRLSSLKYRVKEI  
PPFRASALPAAQAHEAMDCSILQEENGFGSRPQGTSPCPAGASEEMEVEER PAGSTPATF  
STSGIGLQTQKQDG



## FIGURE 2A

SEQ ID NO: 1\_X69117\_H BARK2\_H

ATGGCGGACCTGGAGGCCGTGCTGGCCGATGTCAGTTACCTGATGGCCATGGAGAAGAGC  
AAGGCGACCCCGGCCCGCCGCGCCAGCAAGAGGATCGTCCTGCCGGAGCCAGTATCCGG  
AGTGTGATGCAGAAGTACCTTGCGAGAGAGAAATGAAATAACCTTTGACAAGATTTTCAAT  
CAGAAAATTGGTTTCTTGCTATTTAAAGATTTTTGTTTGAATGAAATTAATGAAGCTGTA  
CCTCAGGTGAAGTTTTATGAAGAGATAAAGGAATATGAAAACTTGATAATGAGGAAGAC  
CGCTTTTGCGAGAAGTCGACAAATTTATGATGCCTACATCATGAAGGAACCTTCTTCCCTGT  
TCACATCCTTTCTCAAAGCAAGCTGTAGAACACGTACAAAGTCATTTATCCAAGAAACAA  
GTGACATCAACTCTTTTTCAGCCATACATAGAAGAAATTTGTGAAAGCCTTCGAGGTGAC  
ATTTTTCAAAAATTTATGGAAGTGACAAGTTCCTAGATTTTGTGAGTGGAAAAACGTT  
GAATTAATATCCATTTGACCATGAATGAGTTCAGTGTGCATAGGATTATTGGACGAGGA  
GGATTCGGGGAAGTTTATGGTTGCAGGAAAGCAGACACTGGAAAAATGTATGCAATGAAA  
TGCTTAGATAAGAAGAGGATCAAAATGAAACAAGGAGAAACATTAGCTTTAAATGAAAGA  
ATCATGTTGTCTCTTGTGTCAGCACAGGAGACTGTCCTTTTCAATTGTATGTATGACCTATGCC  
TTCCATACCCCGAGATAAACTCTGCTTCATCCTGGATCTGATGAACGGGGGCGATTTGCAC  
TACCACCTTTCACAACACGGTGTGTTCTCTGAGAAGGAGATGCGGTTTTATGCCACTGAA  
ATCATTTCTGGGTCTGGAACACGTGCACAATCGGTTTGTGTCTACAGAGATTGAAGCCA  
GCAAATATTCTCTTGGATGAACATGGACACGCAAGAATATCAGATCTTGGTCTTGCCTGC  
GATTTTTCCAAAAGAAGCCTCATGCGAGTGTGGCACCCATGGGTACATGGCTCCCGAG  
GTGCTGCAGAAGGGGACGGCCTATGACAGCAGTGGCGACTGGTTCTCCCTGGGCTGCATG  
CTTTTCAAACCTTCTGAGAGGTACAGCCCTTTCAGACAACATAAAACCAAAGACAAGCAT  
GAAATTGACCGAATGACACTCACCGTGAATGTGGAACCTTCAGACACCTTCTCTCCTGAA  
CTGAAGTCCCTTTTGGAGGGCTTGCTTCAGCGAGACGTTAGCAAGCGGCTGGGCTGTAC  
GGAGGCGGCTCACAGGAAGTAAAGAGCACAGCTTTTTCAAAGGTGTTGACTGGCAGCAT  
GTCTACTTACAAAAGTACCCACCACCCTTGATTCCTCCCCGGGGAGAAGTCAATGCTGCT  
GATGCCCTTGATATTGGCTCATTTGATGAAGAGGATACCAAAGGGATTAAGCTACTTGAT  
TGCGACCAAGAAGTCTACAAGAAGTTCCTTTGGTTCATCTCTGAACGCTGGCAGCAAGAA  
GTAACGGAAACAGTTTATGAAGCAGTAAATGCAGACACAGATAAAATCGAGGCCAGGAAG  
AGAGCTAAAAATAAGCAACTTGGCCACGAAGAAGATTACGCTCTGGGGAAGGACTGTATT  
ATGCACGGGTACATGCTGAACTGGGAAACCCATTTCTGACTCAGTGGCAGCGTCGCTAT  
TTTTACCTCTTTCAAATAGACTTGAATGGAGAGGAGAGGGAGAGTCCCGGCAAAATTTA  
CTGACAATGGAACAGATTCTCTCTGTGGAAGAACTCAAATTAAGACAAAAATGCATT  
TTGTTTCAATAAAAGGAGGGAAACAATTTGTCTTGCAATGTGAGAGTGATCCAGAGTTT  
GTGCAAGTGAAGAAAGAGTTGAACGAAACCTTCAAGGAGGCCAGCGGCTATTGCGTCGT  
GCCCCGAAGTTCCTCAACAAACCTCGGTGAGTACTGTGGAGCTCCCAAAGCCATCCCTC  
TGTCACAGGAACAGCAACGGCCTCTGA

SEQ ID NO: 2\_AA144574\_M BARK2\_M

CTGCTTCGTAGTCTACAGAGACCTGAAGCCTGCGAACATCCTCCTAGATGAATATGGGCA  
CGTGAGGATATCGGATCTCGGCCTTGCTGTGATTTCTCCAAAAGAAGCCTCATGCCAG  
CGTGGGCACCCATGGGTACATGGCTCCCGAGGTGTTGCAGAAGGGAACGTGCTATGACAG  
CAGCGCCGACTGGTTCTCCCTGGGCTGTATGCTCTTCAAACCTTCTGCGGGGCCACAGCCC  
CTTCAGGCAGCATAAAACCAAAGACAAGCATGAGATAGACCGAATGACCCTGACCGTGAA  
CGTGCAGCTTCCAGATGCCCTTCTCCCCTGAGCTGAGGTCCCTCTTAGAGGGTTTGCTCCA  
GCGGGACGTGAGCCAGCGGCTGGGCTGCGGAGGAGGAGGGGCACGAGAGTTGAAGGAGCA  
CATCTTCTTCAAGGGCATTGACTGGCAGCATGTGTACTTACGGAAGTACCCGCCACCCCT  
AATCCCTCCTCGGGGAGAGGTCAACGCTGCAGATGCCTTCGATATCGGCTCCTTCGATGA  
GGAAGACACCAAAGGCATTAAGCTGTTGGACTGTGACCAGGACCTCTATAAGAACTTCCC  
ACTGGTGATCTCCGAGCGCTGGCAGCAAGAAGTGGTGGAGACCATCTATGACCGCGTCAA  
TGCTGATACTGATAAAATCGAGGCCAGGAAGAAGGCTAAAAATAAGCAACTTGGTCAAGA

## FIGURE 2B

GGAAGATTACGCTATGGGGAAGGACTGCATCATGCACGGGTACATGCTGAAGCTGGGGAA  
CCCCTTTCTCACACAGTGGCAAAGACGCTATTTTTACCTGTTCCCCAACAGACTGGAGTG  
GAGAGGAGAGGGCGAGTCTCGGCAAAGTCTACTGACCATGGAACAGATCATGTCTGTGGA  
GGAGACCCAGATTAAAGACAGAAAAGTGCATCTTACTCAGGATAAAGGGAGGGGAAGCAATT  
TGTCTTGCAATGTGAGAGTGACCCCGAGTTTGCACAGTGGCTGAAGGAGCTGACCTGCAC  
CTTCAATGAGGCCAGAGACTGCTGCGCCGTGCCCCAAATTCCTCAACAAACCACGGGC  
CGCCATCCTGGAGTTCTCCAAGCCACCCTGTGTACAGAAATAGCAGCGGCCTCTGAAC  
CACAGAGCAGCGGGGCCTGAAGGAGGGGCCCCAGCTCTTCAGCCCAGGAGTGGAACGAAG  
CCACGGGGAAACCGTGTGGGGCTAAGACACAGTGTCTTCTGAGCACTGACGGGGCTGCTCCA  
AGCCGAGGAGGCTCAGGACACCAGGGCGGCCTTCTGGGAGCTGGGACATCCTCGGGGCTG  
TCCTATCCACACTCGAAATTACTGAAGAAGCAGAGGCATTCTGCTGTG

SEQ ID NO: 3\_AA826850\_H

GAAGAGGATGGGCTCGTCCATGTTCGGCGGCCACCGCGCGGAGGCCGGTGTGTTGACGACAA  
GGAGGACGTGAACCTTCGACCACTTCAGATCCTTCGGGCCATTGGGAAGGGCAGCTTTGG  
CAAGGTGTGCATTGTGCAGAAGCGGGACACGGAGAAGATGTACGCCATGAAGTACATGAA  
CAAGCAGCAGTGCATCGAGCGCGACGAGGTCCGCAACGTCTTCGGGAGCTGGAGATCCT  
GCAGGAGATCGAGCACGTCTTCCTGGTGAACCTCTGGTACTCCTTCAGGACGAGGAGGA  
CATGTTTCATGGTTCGTGGACCTGCTACTGGGCGGGGACCTGCGCTACCACCTGCAGCAGAA  
CGTGCAGTTCTCCGAGGACACGGTGAGGCTGTACATCTGCGAGATGGCACTGGCTCTGGA  
CTACCTGCGCGGCCAGCACATCATCCACAGAGATGTCAAGCCTGACAACATTCTCCTGGA  
TGAGAGAGGACATGCACACCTGACCGACTTCAACATTGCCACCATCATCAAGGACGGGGA  
GCGGGCGACGGCATTAGCAGGCACCAAGCCGTACATGGCTCCGGAGATCTTCCAXTCTTT  
TGTC AACGGCGGGACCGGCTACTCCTTCGAGGTGGACTGGTGGTGGTGGGGGTGATGGC  
CTATGAGCTGCTGCGAGGATGGAGGCCCTATGACATCCACTCCAGCAACGCCGTGGAGTC  
CCTGGTGCAGCTGTTTCAGCACCGTGAGCGTCCAGTATGTCCCCACGTGGTCCAAGGAGAT  
GGTGGCCTTGCTGCGGAAGCTCCTCACTGTGAACCCCGAGCACCGGCTCTCCAGCCTCCA  
GGACGTGCAGGCAGCCCCGGCGCTGGCCGGCGTGCTGTGGGACCACCTGAGCGAGAAGAG  
GGTGGAGCCGGGCTTCGTGCCAAACAAAGGCCGTCTGCACTGCGACCCACCTTTGAGCT  
GGAGGAGATGATCCTGGAGTCCAGGCCCTGCACAAGAAGAAGAAGCGCCTGGCCAAGAA  
CAAGTCCCGGGACAACAGCAGGGACAGCTCCAGTCCGAGAATGACTATCTTCAAGACTG  
CCTCGATGCCATCCAGCAAGACTTCGTGATTTTTTAACAGAGAAAAGCTGAAGAGGAGCCA  
GGACCTCCCGAGGGAGCCTCTCCCCGCCCTGAGTCCAGGGATGCTGCGGAGCCTGTGGA  
GGACGAGGCGGAACGCTCCGCCCTGCCCATGTGCGGCCCCATTGCCCCCTCGGCCGGGAG  
CGGCTAGGCCGGGATGCCCCGTGGTCTCACCCCTTGAGCTGCTTTGGAGACTCGGCTGCC  
AGAGGGAGGGCCATGGGCCGAGGCCTGGCATTCACGTTCCCACCCAGCCTGGCTGGCGGT  
GCCCACAGTGCCCCGGACACATTTACACCTCAGGCTCGTGGTGGTGCAGGGGACAAGAG  
GCTGTGGGTGCAGGGGACACCTGTGGAGGGCATTTCCTGTTGGGCCCCCGAGACCCGCCTA  
GATGGAGGAAGCGCTGCTGGGCGCCCTCTTACCGCTCACGGGGAGCTGGGGCCATGGATG  
GGACAGGAGTCTTTGTCCCTGCTCAGCCCGGAGGCTGTGCACGGCCCTCGTCACAAGGTG  
ACCCCTGCAGCACAGGCCGCGGGTGCCCCAGGCTCGGCTCAGTTCTTGGAGGTCAAGGGC  
ATGGGTGGGGTAGTGGGTGGGGAGGTGAATGTTTTCTAGAGATTCAAAGTCTCCAGCA  
ATTTCTGTATAGTTTTTCACCTCTGAGAATTACAATGTGAGAACCGCTC

SEQ ID NO: 4\_AA960957\_H

GTCCCACATCCCGCATCCGGCATCCAGCGGCCGGGCATGTAGCAGCGGCAGCAACGGCG  
GAATATGGGCGGGAACCACTCCACAAGCCCCCGTGTGTTGACGAGAATGAGGAAGTCAA  
CTTTGACCATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCAT  
CGTGCAGAAGCGAGACACTAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTG  
CATCGAGAGGGATGAGGTTCCGAATGTTTTCCGGGAGCTGCAGATCATGCAAGGGCTGGA

FIGURE 2C

GCACCCCTTCCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGACATGTTTCATGGT  
GGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTTAC  
AGAGGGGACTGTGAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAG  
GTACCACATCATCCACAGAGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACA  
TGTTTCACATTACAGACTTCAACATAGCGACGGTAGTGAAAGGAGCAGAAAGGGCTTCCTC  
CATGGCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCAGGTGTACATGGACAGAGG  
CCCCGATACTCGTACCCTGTGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCT  
GCGGGGCTGGAGGCCGTACGAAATCCACTCGGTACGCCCATCGATGAAATCCTCAACAT  
GTTCAAGGTGGAGCGTGTCCACTACTCCTCCACGTGGTGCAAGGGGATGGTGGCCCTGCT  
GAGGAAGCTCCTGACCAAGGATCCTGAGAGCCGCGTGTCCAGCCTTCATGACATACAGAG  
CGTGCCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGCACTGATGCCCGG  
CTTTGTGCCCAATAAAGGGAGGTTGAACTGCGATCCACATTTGAGCTTGAAGAGATGAT  
TCTAGAATCCAAGCCACTTCACAAAAAGAAGAAGCGATTGGCAAAGAACAGATCCAGGGA  
TGGCACAAGGACAGCTGCCCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCG  
GGAGGAATTCATCATATTCAACAGAGAGAAGCTCAGGAGGCAGCAGGGACAGGGCAGCCA  
GCTCTTGGACACCGACAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCTCCAGGACGGGTG  
CAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGCCCACACTTG  
TTGCTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCACCCAGAGCCCCCTCTTTGTGC  
CCTGATGGTCCCTGTCTCACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGA  
GCTGGGAAGCCTGGGTTCTGGTCCCATCTCCATGACTGATTACGTGTGACCTCAGACAA  
GTCACGCCCTCTCTGTGCCTCCGTTTTCTGCATCTGCCAAAGGGGTTAAACACTTCTGCC  
CCACTTCAAATTACAAGATTATGGGGAGAACCCAATTAGGTAGGAAACATGAAAAACCTT  
TGATATTTATAAAATCATTTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCC  
ATTCCCCAAAGCAATCAAACCGTCATGACTTTGCAATTTGGCACATCCTAGCTTGTTAGA  
GGGCACCTCCGAAAAACACAGCCCTGACAGCAAAATAAAGGTCTGATATGTTGGCCCCCTT  
CTATGGAAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTTCATGTGCATTCT  
CTGGCAGGCCACAGTCTGAGCTTGTAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC  
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCCCTCATTTAAGAAGACTATCCTTACCTTTT  
AGTTTCAGCAGTCCTCACCACCACCATATCCCCAGTGCTGGGATGGCACACAGGTGTCCA  
TTCAGATGAGAGTTGGGTGCTGAGCATTGGTTACTCCTGCAGAGTGTAATCAGCACCCC  
ATCCAAGTGGCCCCGAAAGCCAGACCTGCAGCAGAACTCTCCAAGTCTCTATCAGCTTTC  
AGGGTTTTCTCTCCTGGGAAGGGTGTAAAATCAGCTTGTGAGATTCTTCTTACAGAGAGT  
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAG  
AAAGTTTTATTTTCAAGGAGGAAATGGGTTACACAAAAAGCAAACCTACATTCTGATCTGCT  
CAGGGAGAAGCTTGCCTTTGAAGTGAAGATGTTGGGATGAGCAGGGAAAGCTTAGACTT  
TGGAGTCAGGTTTGTGTTTCAAGATCCAGCCCTGCTGGCTACTAAGTAACTGGGAGACCTT  
AGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCTCATTTTTTAAACAGGGATAATAAA  
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTG  
GATGACTCATAGAATGGCCTTTTTTGTGAGCATAATCGTCATCATTATTTAGATACTTTC  
TTCCTTCACTCACCCAGCAGGTGAGTTTCTGTGCAAAACAAACCTGTTTAGGATTCTTCC  
AAATGTTCTTCTGGGGTCTTTGATATTTGTTTGTACATCCTGCTGAAGTTCGACTGTG  
TTTTTATTTTTTTCATCCAAGTTCATTTTCACTTTTTTACATGATTACTCAATCCTTGGG  
GCTGTCCATGTCTCTTAGATTTCTTAAAGACATTTTAAATGTATGGTTAGGTTTTAT  
ATTTTTATTTTTTAAAAAGAAATAGTCAGTGTTTTCTCCTTTCAACCGAGACTATTTTC  
TGGATTGTGTGCTCCTCGTCAGTTGACTTGTGTTTGCACACTTTTCTTACTTCATGTCCC  
CATCAACAACCGTCTCTGCTCCCCACCTCCCCCAGGAAATAAGGGGCCTGCTCCTCTCCCT  
ACTGTGACCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTTATTGGGCTGAGTTCACGA  
ATTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCCTGGTTCTGTTCAAGT  
TGGCATTTCTTGTGTTGGAATAAACTATTTCTTGGACATTCTTTC

## FIGURE 2D

SEQ ID NO: 5\_TBK1\_H

TCCTGAGTCTCGAGGAGGCCGCGGGAGCCCCGCGCGGTGGCGCGCGGAGACCCGGCTG  
GTATAACAAGAGGATTGCCTGATCCAGCCAAGATGCAGAGCACTTCTAATCATCTGTGGC  
TTTTATCTGATATTTTAGGCCAAGGAGCTACTGCAAATGTCTTTCGTGGAAGACATAAGA  
AAACTGGTGATTTATTTGCTATCAAAGTATTTAATAACATAAGCTTCCTTCGTCCAGTGG  
ATGTTCAAATGAGAGAATTTGAAGTGTTGAAAAAACTCAATCACAAAAATATTGTCAAAT  
TATTTGCTATTGAAGAGGAGACAACAACAAGACATAAAGTACTTATTATGGAATTTGTCTC  
CATGTGGGAGTTTATACACTGTTTTAGAAGAACCCTTCTAATGCCTATGGACTACCAGAAT  
CTGAATTCCTAATTGTTTTGCGAGATGTGGTGGGTGGAATGAATCATCTACGAGAGAATG  
GTATAGTGCACCGTGATATCAAGCCAGGAAATATCATGCGTGTTATAGGGGAAGATGGAC  
AGTCTGTGTACAACTCACAGATTTTGGTGCAGCTAGAGAATTAGAAGATGATGAGCAGT  
TTGTTTTCTCTGTATGGCACAGAAGAATATTTGCACCCTGATATGTATGAGAGAGCAGTGC  
TAAGAAAAGATCATCAGAAGAAATATGGAGCAACAGTTGATCTTTGGAGCATTGGGGTAA  
CATTTTACCATGCAGCTACTGGATCACTGCCATTTAGACCCTTTGAAGGGCCTCGTAGGA  
ATAAAGAAGTGATGTATAAAATAATTACAGGAAAGCCTTCTGGTGCAATATCTGGAGTAC  
AGAAAGCAGAAAATGGACCAATTGACTGGAGTGGAGACATGCCTGTTTTCTTGCACTCTTT  
CTCGGGGTCTTCAGGTTCTACTTACCCCTGTTCTTGCAAACATCCTTGAAGCAGATCAGG  
AAAAGTGTTGGGGTTTTGACCAGTTTTTTGCGAGAACTAGTGATATACTTCACCGAATGG  
TAATTCATGTTTTTTTCGCTACAACAAATGACAGCTCATAAGATTTATATTCATAGCTATA  
ATACTGCTACTATATTTTATGAAGTGGTATATAAAACAAACCAAATTTATTTCTTCAAATC  
AAGAAGTTATCTACGAAGGGCGACGCTTAGTCTTAGAACCTGGAAGGCTGGCACAACATT  
TCCCTAAAACCTACTGAGGAAAAACCTATATTTGTAGTAAGCCGGGAACCTCTGAATACCA  
TAGGATTAATATATGAAAAAATTTCCCTCCCTAAAGTACATCCACGTTATGATTTAGACG  
GGGATGCTAGCATGGCTAAGGCAATAACAGGGGTTGTGTGTTATGCCTGCAGAATTGCCA  
GTACCTTACTGCTTTATCAGGAATTAATGCGAAAGGGGATACGATGGCTGATTGAATTAA  
TTAAAGATGATTACAATGAAACTGTTTCAAAAAAGACAGAAGTTGTGATCACATTGGATT  
TCTGTATCAGAAACATTGAAAAAACTGTGAAAGTATATGAAAAGTTGATGAAGATCAACC  
TGGAAGCGGCAGAGTTAGGTGAAATTTTACAGACATACACACCAAATTTGTTGAGACTTTCCA  
GTTCTCAGGGAACAATAGAAACAGTCTTACAGGATATCGACAGCAGATTATCTCCAGGTG  
GATCACTGGCAGACGCATGGGCACATCAAGAAGGCACTCATCCGAAAGACAGAAATGTAG  
AAAAACTACAAGTCTGTAAATTCATGACAGAGATTTACTATCAGTTCAAAAAAGACA  
AAGCAGAACGTAGATTAGCTTATAATGAAGAACAAATCCACAAATTTGATAAGCAAAAAAC  
TGTATTACCATGCCACAAAAGCTATGACGCACTTTACAGATGAATGTGTTAAAAAGTATG  
AGGCATTTTGAATAAGTCAGAAGAATGGATAAGAAAGATGCTTCATCTTAGGAAACAGT  
TATTATCGCTGACTAATCAGTGTTTTGATATTGAAGAAGAAGTATCAAAATATCAAGAAT  
ATACTAATGAGTTACAAGAACTCTGCCTCAGAAAAATGTTTACAGCTTCCAGTGGAATCA  
AACATAACCATGACCCCAATTTATCCAAGTTCTAACACATTAGTAGAAATGACTCTTGGA  
TGAAGAAATTAAGGAAGAGATGGAAGGGGTGGTTAAAGAACTTGCTGAAAATAACCACA  
TTTTAGAAAGGTTTGGCTCTTTAACCATGGATGGTGGCCTTCGCAACGTTGACTGTCTTT  
AGCTTTCTAATAGAAGTTTAAGAAAAGTTTCCGTTTGCACAAGAAAATAACGCTTGGGCA  
TTAAATGAATGCCTTTATAGATAGTCACTTGTCTTCTACAATCCAGTATTTGATGTGGTCG  
TGTAATATGTACAATATTGTAAATACATAAAAAATATACAAATTTTGGCTGCTGTGAA  
GATGTAATTTTATCTTTTAAACATTTATAATTATATGAGGAAATTTGACCTCAGTGATCAC  
GAGAAGAAAGCCATGACCGACCAATATGTTGACATACTGATCCTCTACTCTGAGTGGGGC  
TAAATAAGTTATTTTCTCTGACCGCCTACTGGAAATATTTTTAAGTGAACCAAATAGG  
CATCCTTACAAATCAGGAAGACTGACTTGACACGTTTGTAATGGTAGAACGGTGGCTAC  
TGTGAGTGGGGAGCAGAACCGCACCACTGTTTACTGGGATAACAATTTTTTTGAGAAGG  
ATAAAGTGGCATTATTTTATTTTACAAGGTGCCAGATCCCAGTTATCCTTGTATCCATG  
TAATTTTCAGATGAATTATTAAGCAAACATTTTAAAGTGAATTCATTATTAAGAACTATTC  
ATTTTTTTCTTTGGCCATAAATGTGTAATTGTCAATTAATTTCTAAGGTCATTTCAACT

## FIGURE 2E

GTTTTAAGCTGTATATTTCTTTAATTCTGCTTACTATTTTCATGGAAAAAATAAATTTCT  
CAATTTTAAAAAA

SEQ ID NO: 6\_AA305176\_H

TGGCTGCTCGCGGAGGGGCGAGTGTACGCGGGGCCGCTGTAGGCTGTCCAGCGATGGATCC  
CACC CGGGAAGCAAGAAGGAGCCTGGAGGAGGCGCGGCGACTGAGGAGGGCGTGAATAG  
GATCGCAGTGCCAAAACCGCCCTCCATTGAGGAATTGAGCATAGTGAAGCCCATAGCCG  
GGGCGCCTTCGGGAAAGTGTATCTGGGGCAGAAAGGCGGCAAATTGTATGCAGTAAAGGT  
TGTTAAAAAAGCAGACATGATCAACAAAAATATGACTCATCAGGTCCAAGCTGAGAGAGA  
TGCACTGGCACTAAGCAAAAGCCCATTCATTGTCCATTTGTATTATTCACTGCAGTCTGC  
AAACAATGTCTACTTGGTAATGGAATATCTTATTGGGGGAGATGTCAAGTCTCTCCTACA  
TATATATGGTTATTTTGATGAAGAGATGGCTGTGAAATATATTTCTGAAGTAGCACTGGC  
TCTAGACTACCTTCACAGACATGGAATCATCCACAGGGACTTGAAACCGGACAATATGCT  
TATTTCTAATGAGGGTCATATTAACTGACGGATTTTGGCCTTTCAAAGTTACTTTGAA  
TAGAGATATTAATATGATGGATATCCTTACAACACCATCAATGGCAAAACCTAGACAAGA  
TTATTTCAAGAACCCAGGACAAGTGTTATCGCTTATCAGCTCGTTGGGATTTAACACACC  
AATTGCAGAAAAAATCAAGACCCTGCAACATCCTTTGAGCCTGTCTGTCTGAAACATC  
ACAGCTTTCTCAAGGACTCGTATGCCCTATGTCTGTAGATCAAAAGGACACTACGCCTTA  
TTCTAGCAAATTACTAAAAATCATGTCTTGAAACAGTTGCCTCCAACCCAGGAATGCCTGT  
GAAGTGTCTAACTTCTAATTTACTCCAGTCTAGGAAAAGGCTGGCCACATCCAGTGCCAG  
TAGTCAATCCCACACCTTCATATCCAGTGTGGAATCAGAATGCCACAGCAGTCCCAAATG  
GGAAAAAGATTGCCAGGTTTGAGGGACATTTATCTTAATGAAAATCAATTATGTATGTCA  
AATGAATGTGAGAAATATTATACCTTTTCATATAAATTCCATAAAGAAATGAAATTGTTA  
CATGAATGGCAGTCATAGTATTAATCAGAAATTCATTTTCTGCACATTCTGTCAAATTC  
TTTTGAAATATTTCAATTTCTCATTCAATTGTGACATTGTTCTTACTTGATTATATAATGA  
GATTCTTGCAAGTAAATTGATAATAAATGCTTGGCTTCTGTGTATCTAGGTGGACCTCACT  
TGTTTTTAGAAGTCCTTCCCATGATACAGACATTGGCTTGTTGGTTTTGTTTTATTTTGT  
TTTTAACATATGTCATTTAAAAACTCATATTACCTCCTTTT

SEQ ID NO: 7\_AA116841\_M

CCACGCGTCCGATCCCATGGCCAGAAGGCGAAGAAAAGCTATCTGATAATGCTCAAAGTG  
CAATGGACATGCTTTTAAACCATTTGATGATTCAAAGAGAGCTGGAATGAGAGAACTAAAAC  
AGCATCCTCTCTTCAGTGAAGTGGACTGGGAAAATCTGCAGCATCAGACTATGCCTTTTCG  
TACCCCAACCAGACGACGAAACAGATACATCCTATTTTGAAGCCAGAAATAATGCTCAAC  
ATCTGACCGTATCTGGGTTTAGTCTGTAGCACATGCGTGTCAATTTTATCTAACTTGTGA  
TATAGAATTAAGTTTTACAGTAATATGCTACTTAATACTAGATTGGTCTAAATGGGATAA  
AAGTCATTATTTTACCCAGACTGAACAGCTTTTAAATTACTAAGTACAACAGTTTTTACAG  
AATTAATAATACTATAAGCAATATAATCAGTAATTAATCTTTACCTTAGAAGTGTATATAA  
GCCATAATAGCTTTTTTTCATCTTATTTATTCACTGCACCTTTATGAAGAGCAAAGTATCAA  
TAACTAAAACACTACCACTCTAAATAGAGGGAGTGAGCCGT

SEQ ID NO: 8\_AA256100\_H

AGGGAGCTGACGGGCGCCCGGCTGCGGTCCGTGCGGAGGCTGAGCCGGCCGCGGGC  
GCGACCGGAGGCAGTTTCCGTTACTATGGCAATGACGGCAGGGACTACAACAACCTTTCC  
TATGAGCAACCATACCCGGGAAAGAGTGAAGTGTAGCCAAGCTCACATTGGAGAATTTTA  
TAGCAACCTAATTTTACAGCATGAAGAGAGAGAAAACAGGCAGAAGAAATTAGAAGTGGC  
CATGGAAGAAGAAGGATTAGCAGATGAAGAGAAAAAGTTACGTCGATCACAACACGCTCG  
CAAAGAAACAGAGTTCTTACGGCTCAAAGGACCAGACTTGGCTTGGATGACTTTGAGTC  
TCTGAAAGTTATAGGAAGAGGAGCTTTTGGAGAGGTGCGGTTGGTCCAGAAGAAAGATAC  
AGGCCATATCTATGCAATGAAGATATTGAGAAAGTCTGATATGCTTGAAAAAGAGCAGGT

FIGURE 2F

GGCCCATATCCGAGCAGAAAGAGATATTTTGGTAGAAGCAGATGGTGCCTGGGTGGTGAA  
GATGTTTTACAGTTTTTCAGGATAAGAGGAATCTTTATCTAATCATGGAATTTCTCCCTGG  
AGGTGACATGATGACATTGCTAATGAAGAAAGACACCTTGACAGAAGAGGAAACACAGTT  
CTACATTTTCAGAGACTGTTCTGGCAATAGATGCGATCCACCAGTTGGGTTTCATCCATCG  
GGATATTAAGCCAGACAACCTTTTATTGGATGCCAAGGGTCATGTAAAATTATCTGATTT  
TGGTTTTATGTACGGGATTAAAGAAAGCTCACAGGACTGAATTTTATAGAAATCTCACACA  
CAACCCACCAAGTGACTTCTCATTTTCAGAACATGAACTCAAAGAGGAAAGCAGAACTTG  
GAAGAAGAACAGGAGACAACCTGGCATATTCCACAGTTGGGACACCAGATTACATTGCTCC  
AGAAGTATTCATGCAGACTGGTTACAACAAATTTGTGTGACTGGTGGTCTTTGGGAGTGAT  
TATGTATGAAATGCTAATAGGATATCCACCTTTCTGCTCTGAAACACCTCAAGAAACATA  
CAGAAAAGTGATGAACTGGAAAGAACTCTGGTATTTCTCCAGAGGTACCTATATCTGA  
GAAAGCCAAGGACTTAATTTCTCAGATTTTGTATTGATTCTGAAAACAGAATTGGAAATAG  
TGGAGTAGAAGAAATAAAAGGTCATCCCTTTTTTGAAGGTGTCGACTGGGAGCACATAAG  
GGAAAGGCCAGCAGCAATCCCTATAGAAATCAAAGCATTGATGATACTTCAAATTTTGA  
TGACTTCCCTGAATCTGATATTTTACAACCAAGTGCCAAATACCACAGAACCGGACTACAA  
ATCCAAAGACTGGGTTTTTCTCAATTATACCTATAAAAGGTTTGAAGGGTTGACTCAACG  
TGGCTCTATCCCCACCTACATGAAAGCTGGGAAGTTATGAATGAAGATAACATTCACCCA  
TAACCAAGAGAACTCAGGTAGCTGCATCACCAGGCTTGCTTGGCGTAGATAACAATACAC  
TGAAATACTCCTGAAGATGGTGGTGCTTATTGACTACAAGAGGAAATTCTACAGGATTAG  
GATTTCTAAGACTACTATAGGAATTGGTTGGCAGTGCCAGCTGGCTCTTTTTTTTAATAT  
TTTATTATTTTTTGTAACTTTATTATATGAAGGTACTGGAATAAAAGGAACAGACATCCC  
TTTCTAACTGCACTGCCATACATGCGTATTAAGGTCCATTCTGCCTGTGTGTGCTGTGGCT  
TTGAACTGTAACACCTCTAATCAATTCAGGAGAAACACATATCATTTAAAGCAACATAGG  
CTAACCTGTAGGTAACACTGCAGTATTGATGTTTTACTGCAAATCTTATGGGTCTAGATA  
ATCAGTAAAAGCCATCTTCCATAGTTGGTGTTAGAACATTGCCCTATTGGTTTGGACATC  
TGTAAGATATATATGAAGACAATTTCTGTAATGGTTTTAAGAGATTTAAAAAGAAATTCA  
CTGGTTCTTTACAAAATAGAATTTATCATCAAGTTATTACACAAACTTCACAGTAAGGAG  
TGACAAGTTTATAATAAGGAAGACAAAGTTTAAACACCTTCACTCAAGCACTCCACTAATA  
TATTTACGTTGCATTTCAGAAATACTGATGACCTTCATATACGTAGTCTGTATACTCATAG  
GGAGATGTACTGTATTATATAACATGTAAAGTTGATTTTTCTTGTGACAAGAGAACTTCTT  
TTTTTAAACAAGAGGACATGGCATTATTTTAAATTTGATTATGGTGAGTTGAATTTAAGACA  
TGACCATGAAGGCTGCTTGTAGAATTAGTGATTTTTTATTAAACTATTTTTTTAAATGTC  
AAACTTCTATCATGTAAATGGACTTATAGAGAACAAAAAGCTATTTACTTTGGTTTTCTA  
GAAAGTTGTTACATATCATGGCTGGTTAACTTTTATTTCTTTTGATGAAAATTTTTCTTT  
TGATAGTACTTGTATTATTGTGCCATTATTTTCTTATGCTCCAAATGTACCAAAGATCTT  
GAACAGAGTGGATGTTTCACACTGAGTAGAATTTTCTTTTCTGTGGGCATGCTGTATTTC  
AGACCTGACAGATCTTTGATAGAGGTCAGCTTATTAAAGGGCAATATTGTTCTTGTTTAG  
CTACATCACTGTGGTGAATATAGATGGAATTAAGGAAGTAAATGCAGGCCAGGGGTTGT  
GATGAGAGGATAGGGGAGATAATATCAGCATCAAATTCCTTTGGGTATCTCTCTAAGAATT  
AAATAATCTTTTCTAGCTTAATATTTTAAATTCATTTCAAACAACCTCTGAGGTTTTTGGTT  
TCATTAGTAATAGTTGAGGAATAATATACTAGCAAAGAATGGCCTAATGTTTGTCTAATC  
TGTTAATGGATGAAATTTTTTAAAGATACAACCATGATAACCATTAATGATCTATGA  
TCAAATCTAAAGTGATGAATTATTTGTAGGAATGTCTTCCTAATGGGGAAGAATTGCAT  
AGGAGCATTATGCAAATCTACACAAGCTTTTATAAATGTTGCTGCTGGGTAGCTCCACAG  
TGTTTCATAAGGCCATCCTGTTTCCCCCACTCCCCCATTTTTTGGTTTGTTCCTTTTAA  
ATATTTGTTGAGTACTTACGTGTTTATCTAACAGTTCCTTCCATTTTTCTAGTCTGGAT  
TTTTTGAGTATTTAGGAAAGAGAGCTATTAAAACTCTGGGGATTTCTCAATGTGACTAA  
CTCTAATTTTTCTAATTATAACTGCCTTTAATTAACATAATATTAATTTTGCTGAGGTT  
TATGAGATTTTCTACCCACATCGCTCCCTTTTTTTTAAAGGACTGTTTTGCTAGTG  
TGATAATGAATAGGTAAGATATGAGATAATTGCAACATTGTCTAGTTCTAGTATGGTAA

FIGURE 2G

CTATTCTTGAAATGGTATTGAAAAATACCGTTAATTCAAATTGACAGAGATTGATAAAAA  
GAAACTGATTTACCTAAGTTTACTTTTAAATTGCATAATAGAGCATTTTTTTGTTTTGAGT  
TCCCTCATTCTTATTACCAGAAAGAGCTTGCAAATAGTTTTACTTTCTTGGCACTGGAAG  
GGTAGTTCTGGAAAGCTACTTTGTTGAGAGTCTCATTCTTCCCTGGAGTTAATAGAGTGA  
TTCACAATCTTTGGGGTTTTCTCCTCATCAAAGCATTCTTAAGTGCCTATCTAAAAGC  
AATTAAAGACTGTGTCTGCCCTTTAGAAGCTAAGAATTTGATTCATGATGCAAATTAAC  
AGATAATTTGCAAAGTACCCTTGAGATTGAATTTTCTCTATTATATATTTCCCATATTTT  
AGGTGAATAATTTAATTTAAATGACAAAACCTATCTAGTCAACTGGGCATAATGACATT  
TTCTTTAAATTAGACTCTATTTTGAATTAAGAGTTTTATTATAAACCGTGTGTTTTTG  
GTTTTTCTAAGTATATAGAAAGCTTGATAATTCAGATTTATCAATTTCTGATTTAATG  
TAGACTTTGACTTTTTTATTAAAAACCTTTGTATTAAAGCAAGTTATGTTATTTTTCTTT  
TATGCATTTATTACTAACATAGCTTTAAATCTTTAAATGTATTGAAGCATTGTGCTGTCT  
GAAAATAAGGAATTGCTTATAAACCCAGCCACTTCTGAATACAATATGTAGCTGATTTAAT  
AAGCTAGTTAGTGAATGGAAATAAGTGTGGAGTATTAAAAATGTTCTTTGGTTGGTAAG  
GCCTAAGATAGGGTTTCATTTATTTCTATACTTTTTCTGTTTTTTAAACACCTGCATATT  
TTTATGTAAATCTCTAAATTTAAATATTTTAAAGTACATTTATTTTTGGTGTGTTTATTGT  
ATAAACCTTAGACAATCAATCAGTCAGTCTTTACTGACAGGAGCAGCAGCTATCTGTCT  
TTTGCTGATCTACAAATAAATGAATTGAGAATTTAGTCCATAGAGGTCCCTGGCTACCAA  
ACACATTTCTCCTTTGAATTGTTAAATTCAGAACATTCAAAATAACTGTTTTGCTACAAC  
CCATGATTATTTTCTGTGTGTTTATTTAAATTTACTTTCTCTTTAGAAGTGCATTTAT  
TTCTGAAAAATCTTAATGAAACAAACGCTTAGAACAAATATAAATATGAGACACTTGGGA  
CTACTAGAGATATTTTAGATTTTTATGAAAAAAATGTGAGGGGATATTGCTGCTTTAAAA  
AGGAATAAAGTAATAAAAAATATATCTCAGCTATTTTTTTAAAGCAATATAATTGAGCAAT  
TGTCTAGAAAAGTAATCATGAGGCTACTGAGTTTGGTGTTTCTGTTACTGAGTTTCAAAAA  
TGTTTTGGTGGCATGAGGACAAAATTTTATTGAAGGTAAGATAAGAATAAAAACTATGTT  
TAC

SEQ ID NO: 9\_AA210825\_H

CACGAGGGCTACTGGCGCCTGGCGACCCTCCCTGCCCCCACCCAACCCCGCTCCGGCAA  
CGCCCCCTTCCTCACGGCTCCCGACCGAACTTTCTCCAACTTCTGCGACTCGTGAGATT  
CCCTTCTACCCACTCCGGCCCTCGGGACCCCTCTGCCCATCCCTGGCCGGTCCGGTCCC  
TGCGAACCCCTTTATCTCTGGAATCCACTCGGTCCCCGACTCAGAGACTCCTGCCCTCCA  
CCCCAAGGACCCCGCCATCCTCAGGTCCCTCCGCTGCCAGATCTTTTCTCGGATCCC  
CGCTCTCCACACCTGCTCACGAGATCCCGCGGATCTAGAACCAGGGTCCCCCGGGC  
CCCCCGGCGGTCCCGGGTGGGCTCCAGGCGGGCGGTCCCGGCCCTCCCCCATGGCCAC  
CGCCCCCTCATTATCCCGCCGGGCTCCCTGGCTCTCCCGGGCCGGGTCTCCTCCGCCCC  
CCGGCGGCTAGAGCTGCAGTCGCCGCCACCGCTACTGCCCCAGATCCCGGCCCGGGTT  
CCGGGGTCTCCTTTCACATCCAGATCGGGCTGACCCGCGAGTTCGTGCTGTTGCCCGCCG  
CCTCCGAGCTGGCTCATGTGAAGCAGCTGGCCTGTTCCATCGTGGACCAGAAGTTCCCTG  
AGTGTGGCTTCTACGGCCTTTACGACAAGATCCTGCTTTTCAAACATGACCCACGTCCG  
CCAACCTCCTGCAGCTGGTGCCTCGTCCGGAGACATCCAGGAGGGCGACCTGGTGGAGG  
TGGTGTCTCGGCCTCGGCCACCTTCGAGGACTTCCAGATCCGCCCGCACGCCCTCACGG  
TGCACTCCTATCGGGCGCCTGCCTTCTGTGATCACTGCGGGGAGATGCTCTTCGGCCTAG  
TGCGCCAGGGCCTCAAGTGCAGTGGCTGCGGGCTGAAC'TACCACAAGCGCTGTGCCTTCA  
GCATCCCCAACAACTGTAGTGGGGCCCCGAAACGGCGCCTGTATCCACGTCTCTGGCCA  
GTGGCCACTCGGTGCGCCTCGGCACCTCCGAGTCCCTGCCCTGCACGGCTGAAGAGCTGA  
GCCGTAGCACCAACCGAACTCCTGCCTCGCCGTCCCCCGTCATCCTCTTCTCCTCTCTG  
CCTCATCGTATACGGGCCGCCCCATTGAGCTGGACAAGATGCTGCTCTCCAAGGTCAAGG  
TGCCGCACACCTTCTCATCCACAGCTATACACGGCCCACCGTTTGCCAGGCTTGCAAGA  
AACTCCTCAAGGGCCTCTTCCGGCAGGGCCTGCAATGCAAAGACTGCAAGTTTAACTGTC

## FIGURE 2H

ACAAACGCTGCGCCACCCGCGTCCCTAATGACTGCCTGGGGGAGGCCCTTATCAATGGAG  
ATGTGCCGATGGAGGAGGCCACCGATTTTCAGCGAGGCTGACAAGAGCGCCCTCATGGATG  
AGTCAGAGGACTCCGGTGTTCATCCCTGGCTCCCACTCAGAGAATGCGCTCCACGCCAGTG  
AGGAGGAGGAAGGCGAGGGAGGCAAGGCCAGAGCTCCCTGGGGTACATCCCCCTAATGA  
GGGTGGTGCAATCGGTGCGACACACGACGCGGAAATCCAGCACCACGCTGCGGGAGGGTT  
GGGTGGTTTATTACAGCAACAAGGACACGCTGAGAAAGCGGCACTATTGGCGCCTGGACT  
GCAAGTGTATCAGCTCTTCCAGAACAACACGACCAACAGATACTATAAGGAAATTCGCG  
TGTCAGAAATCCTCAGGTGGAGTCCGCCAGAACTTCAGCCTTGTGCCGCCGGGCACCA  
ACCCACACTGCTTTGAGATCGTCACTGCCAATGCCACCTACTTCGTGGGCGAGATGCCTG  
GCGGGACTCCGGGTGGGCCAAGTGGGCAGGGGGCTGAGGCCGCCCGGGGGCTGGNNGAGA  
CAGCCATCCGCCAGGCCCTGATGCCCGTCATCCTTCAGGACGCACCCAGCGCCCCAGGCC  
ACGCGCCCCACAGACAAGCTTCTCTGAGCATCTCTGTGTCCAACAGTCAGATCCAAGAGA  
ATGTGGACATTGCCACTGTCTACCAGATCTTCCCTGACGAAGTGCTGGGCTCAGGGCAGT  
TTGGAGTGGTCTATGGAGGAAAACACCGGAAGACAGGCCGGGACGTGGCAGTTAAGGTCA  
TTGACAAACTGCGCTTCCCTACCAAGCAGGAGAGCCAGCTCCGGAATGAAGTGGCCATTC  
TGCAGAGCCTGCGGCATCCCGGGATCGTGAACCTGGAGTGCATGTTGAGACGCCTGAGA  
AAGTGTGTTGTGGTGATGGAGAAGCTGCATGGGGACATGTTGGAGATGATCCTGTCCAGTG  
AGAAGGGCCGGCTGCCTGAGCGCCTCACCAAGTTCCTCATCACCAGATCCTGGTGGCTT  
TGAGACACCTTCACTTCAAGAACATTGTCCACTGTGACTTGAAACCAGAAAACGTGTTGC  
TGGCATCAGCAGACCCATTTCCTCAGGTGAAGCTGTGTGACTTTGGCTTTGCTCGCATCA  
TCGGCGAGAAGTCGTTCCGCCGCTCAGTGGTGGGCACGCCGGCCTACCTGGCACCCGAGG  
TGCTGCTCAACCAGGGCTACAACCGCTCGCTGGACATGTGGTCAGTGGGCGTGATCATGT  
ACGTCAGCCTCAGCGGCACCTTCCCTTTCAACGAGGATGAGGACATCAATGACCAGATCC  
AGAACGCCGCCCTTCATGTACCCGGCCAGCCCCCTGGAGCCACATCTCAGCTGGAGCCATTG  
ACCTCATCAACAACCTGCTGCAGGTGAAGATGCGCAAACGCTACAGCGTGGACAAATCTC  
TCAGCCACCCCTGGTTACAGGAGTACCAGACGTGGCTGGACCTCCGAGAGCTGGAGGGGA  
AGATGGGAGAGCGATACATCAGCATGAGAGTGACGACGCGCGCTGGGAGCAGTTTGCAG  
CAGAGCATCCGCTGCCTGGGTCTGGGCTGCCCACGACAGGGATCTCGGTGGGGCCTGTC  
CACCACAGGACCACGACATGCAGGGGCTGGCGGAGCGCATCAGTGTCTCTGAGGTCTTG  
TGCCCTCGTCCAGCTGCTGCCCTCCACAGCGGTTCTTTCACAGGATCCCAGCAATGAACTG  
TTCTAGGGAAAGTGGCTTCTTGGCCAAACTGGATGGGACACGTGGGAGTGGGGTGGGGG  
GAGCTATTTCAGGCCCTCCCTGTTTCCCAGCAATTAAACGGACTCATCTCTGGCC  
CCATGGCCTTGATCTCAGCAAAA

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ATTCAATTCATAATTGTTGGTGCAAAAGATTTGCTTGCTATGGATTCAAATGGTCTTTCT  
GATCCTTACATCAAAATCACAAATCTTTCTCAAAAAACGAAAGTGATTAAGAAAACCTTG  
ACTCCAACCTTGGAAATGAACTTTTTTTGTGCATTTTCCAGAAAAACAACCCTTGAATTA  
GAATGTTGGGACCACGATACTTTTTCAGATGATTTTATTGGCAAGGCTCCATTTCTTTG  
GCAGAGATTCCAGCTTTGGCAGAAGTTGATATGTGGATAGATATGAAAACGAAAAAAGGA  
GAATTTGCAGGAAAA

SEQ ID NO: 11\_AA316804\_H

ATGTCTGCAAATAATTCCCCTCCATCAGCCCAGAAGTCTGTATTACCCACAGCTATTCCCT  
GCTGTGCTTCCAGCTGCTTCTCCGTGTTCAAGTCTTAAGACGGGACTCTCTGCCCGACTC  
TCTAATGGAAGCTTCAGTGACCATCACTACCAACTCCAGAGGCTCAGTGCATACAGTT  
TCATTTCTACTGCAAATTGGCCTCACACGGGAGAGTGTTACCATTGAAGCCCAGGAACTG  
TCTTTATCTGCTGTCAAGGATCTTGTGTGCTCCATAGTTTATCAAAAGTTTCCAGAGTGT  
GGATTCTTTGGCATGTATGACAAAATCTTCTCTTTTCGCCATGACATGAACTCAGAAAAAC  
ATTTTGCAGCTGATTACCTCAGCAGATGAAATACATGAAGGAGACCTAGTGGAAGTGGTT



FIGURE 21

CTTTCAGCTTTAGCCACAGTAGAAGACTTCCAGATTTCGTCCACATACTCTCTATGTACAT  
TCTTACAAAGCTCCTACTTTCTGTGATTACTGTGGTGAGATGCTGTGGGGATTGGTACGT  
CAAGGACTGAAATGTGAAGGCTGTGGATTAAATTACCATAAACGATGTGCCTTCAAGATT  
CCAAATAACTGTAGTGAGTAAGAAAGAGACGTCTGTCAAATGTATCTTTACCAGGACCC  
GGCCTCTCAGTTCCAAGACCCCTACAGCCTGAATATGTAGCCCTTCCCAGTGAAGAGTCA  
CATGTCCACCAGGAACCAAGTAAGAGAATTCTTCTTGGAGTGGTCGCCCCAATCTGGATG  
GAAAAGATGGTAATGTGCAGAGTGAAAGTTCCACACACATTTGCTGTTCACTCTTACACC  
CGTCCCACGATATGTCACTACTGCAAGCGGTTACTGAAAGGCCTCTTTCGCCAAGGAATG  
CAGTGTAAGATTGCAAATTCAACTGCCATAAACGCTGTGCATCAAAAGTACCAAGAGAC  
TGCCTTGGAGAGGTTACTTTCAATGGAGAACCTTCCAGTCTGGGAACAGATACAGATATA  
CCAATGGATATTGACAATAATGACATAAATAGTGATAGTAGTCGGGGTTTGGATGACACA  
GAAGAGCCATCACCCCCAGAAGATAAGATGTTCTTCTTGGATCCATCTGATCTCGATGTG  
GAAAGAGATGAAGAAGCCGTTAAAACAATCAGTCCATCAACAAGCAATAATATTCCGCTA  
ATGAGGGTTGTACAATCCATCAAGCACACAAAGAGGAAGAGCAGCACAAATGGTGAAGGAA  
GGGTGGATGGTCCATTACACCAGCAGGGATAACCTGAGAAAGAGGCATTATTGGAGACTT  
GACAGCAAATGTCTAACATTATTTTCAAGATGAATCTGGATCAAAGTATTATAAGGAAATT  
CCACTTTTCAGAAATTCTCCGCATATCTTACCACGAGATTTTCAAAACATTTTACAAGGC  
AGCAATCCACACTGTTTTTGAATCATTACTGATACTATGGTATACTTCGTTGGTGAGAAC  
AATGGGGACAGCTCTCATAATCCTGTTCTTGCTGCCACTGGAGTTGGACTTGATGTAGCA  
CAGAGCTGGGAAAAAGCAATTTCGCCAAGCCCTCATGCCTGTTACTCCTCAAGCAAGTGTT  
TGCACCTTCTCCAGGGCAAGGGAAAGATCACAAAGATTTGTCTACAAGTATCTCTGTATCT  
AATTGTCAAGTTTCAAGGAGAATGTGGATATCAGTACTGTTTACCAGATCTTTGCAGATGAG  
GTGCTTGGTTTCAAGGCCAGTTTGGCATCGTTTTATGGAGGAAAACATAGAAAAGACTGGGAGG  
GATGTGGCTATTAAAGTAATTGATAAGATGAGATTCCCCACAAAACAAGAAAGTCAACTC  
CGTAATGAAGTGGCTATTTTACAGAATTTGCACCATCCTGGGATTGTAAACCTGGAATGT  
ATGTTTGAACCCCAAGACGAGTCTTTGTAGTAATGGAAAAGCTGCATGGAGATATGTTG  
GAAATGATTCTATCCAGTGAGAAAAGTCGGCTTCCAGAACGAATTACTAAATTCATGGTC  
ACACAGATACTTGTGTGCTTTGAGGAATCTGCATTTTAAAGAAATATTGTGCACTGTGATTTA  
AAGCCAGAAAATGTGCTGCTTGCATCAGCAGAGCCATTTCCCTCAGGTGAAGCTGTGTGAC  
TTTGGATTTGCACGCATCATTGGTGAAAAGTCATTCAAGGAGATCTGTGGTAGGAACCTCCA  
GCATACTTAGCCCTGAAGTTCTCCGGAGCAAAGGTTACAACCGTTCCCTAGATATGTGG  
TCAGTGGGAGTTATCATCTATGTGAGCCTCAGTGGCACATTTCCCTTTAATGAGGATGAA  
GATATAAATGACCAAATCCAAAATGCTGCATTTATGTACCCACCAAATCCATGGAGAGAA  
ATTTCTGGTGAAGCAATTGATCTGATAAAACAATCTGCTTCAAGTGAAGATGAGAAAACGT  
TACAGTGTGACAAATCTCTTAGTCATCCCTGGCTACAGGACTATCAGACTTGGCTTGAC  
CTTAGAGAATTTGAAACTCGCATTGGAGAACGTTACATTACACATGAAAGTGATGTGCT  
CGCTGGGAAATACATGCATACACACATAACCTTGTATACCCAAAGCACTTCATTATGGCT  
CCTAATCCAGATGATATGGAAGAAGATCCTTAA

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ATGGAGGAGGGGGCGCCGCGCAGCCTGGGCGGAGCCAGTGGCCCCCAGAGGATGAGAAG  
GAGGTGATCCGCCGGGCCATCCAGAAAGAGCTGAAGATCAAGGAGGGGGTGGAGAACCTG  
CGGCGCGTGGCCACAGACCGCCCACTTGGGCCATGTGCAGCAGCTGCTGCGGTCTCTCC  
AACCGCCGCCTGGAGCAGCTGCATGGCGAGCTGCGGGAGCTGCACGCCCCGAATCCTGCTG  
CCCCGGCCCTGGGCCTGGCCCAGCTGAGCCTGTGGCCTCAGGACCCCGGCCGTGGGCAGAG  
CAGCTCAGGGCTCGGCACCTAGAGGCTCTCCGGAGGCAGCTGCATGTGGAGCTGAAGGTG  
AAACAGGGGGCTGAGAACATGACCCACACGTGCGCCAGTGGCACCCCCAAGGAGAGGAAG  
CTCCTTGCAGCTGCCCAGCAGATGCTGCGGGACAGCCAGCTGAAGGTGGCCCTGCTGCGG  
ATGAAGATCAGCAGCCTGGAGGCCAGTGGGTCCCCGGAGCCAGGGCCTGAGCTACTGGCG  
GAGGAGCTACAGCATCGACTGCACGTTGAGGCAGCGGTGGCTGAGGGCGCCAAGAACGTG

## FIGURE 2J

GTGAAACTGCTTAGTAGCCGGAGAACACAGGACCGCAAGGCACTGGCTGAGGCCAGGCC  
CAGCTACAGGAGTCCTCTCAGAACTGGACCTCCTGCGCCTGGCCTTGGAGCAGCTGCTG  
GAGCAACTGCCTCCTGCCACCCCTTTGCGCAGCAGAGTGACCCGAGAGTTGCGGGCTGCG  
GTGCCTGGATACCCCCAGCCTTCAGGGACACCTGTGAAGCCCACCGCCCTAACAGGGACA  
CTGCAGGTCCGCCTCCTGGGCTGTGAACAGTTGCTGACAGCCGTGCCTGGGCGCTCCCCA  
GCGGCCGCACTGGCCAGCAGCCCCCTCCGAGGGCTGGCTTCGGACCAAGGCCAAGCACCAG  
CGTGGCCGAGGCGAGCTTGCCAGTGAGGTGCTGGCTGTGCTAAAGGTGGACAACCGTGTT  
GTGGGGCAGACGGGCTGGGGCAGGTGGCCGAACAGTCCTGGGACCAGACCTTTGTCATC  
CCACTGGAGCGAGCCCGTGAGCTGGAGATTGGGGTACACTGGCGGGACTGGCGGCAGCTA  
TGTGGCGTGGCCTTCCTGAGACTTGAAGACTTCCTGGACAATGCCTGTCACCAACTGTCC  
CTCAGCCTGGTACCGCAGGGACTGCTTTTTGCCCAGGTGACCTTCTGCGATCCTGTCAAT  
GAGAGGCGGCCCCGGCTGCAGAGGCAGGAACGCATCTTCTCTAAACGCAGAGGCCAGGAC  
TTCCTGAGGCGTTCGCAGATGAACCTCGGCATGGCGGCCTGGGGGCGCCTCGTCATGAAC  
CTGCTGCCCCCTGCAGCTCCCCGAGCACAATCAGCCCCCTAAAGGATGCCCTCGGACC  
CCAACAACACTGCGAGAGGCCTCTGACCCTGCCACTCCAGTAATTTCTGCCCAAGAAG  
ACCCCTTGGGTGAAGAGATGACACCCCCACCAAGCCCCCAGCCTCTACCTCCCCAG  
GAGCCAACATCCGAGGAGACTCCGCGCACCAACAGTCCCATATGGAGCCTAGGACTCGA  
CGTGGGCCATCTCCACCAGCCTCCCCACCAGGAAACCCCTCGGCTTCAGGACTTCCGC  
TGCTTAGCTGTGCTGGGCCGGGACACTTTGGGAAGGTCTCTGGTCCAGTTCAAGGGG  
ACAGGGAAATACTACGCCATCAAAGCACTGAAGAAGCAGGAGGTGCTCAGCCGGGACGAG  
ATAGAGAGCCTGTACTGCGAGAAGCGGATCCTGGAGGCTGTGGGCTGCACAGGGCACCTT  
TTCCTGCTCTCCCTCCTTGTCTGCTTCCAGACCTCCAGCCATGCCCGCTTTGTGACTGAG  
TTTGTGCCTGGTGGTGACCTCATGATGCAGATCCACGAGGATGTCTTCCCCGAGCCCCAG  
GCCCCGCTTCTACGTGGCTTGTGTTGTCTGGGGCTGCAGTTCTTACACGAGAAGAAGATC  
ATTTACAGGGACCTGAAGTTGGATAACCTTCTGCTGGATGCCCAGGGATTCTGAAGATC  
GCAGACTTTGGACTCTGCAAGGAAGGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGT  
GGCACCCCGAGTTCTTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACACAGGCCGTC  
GACTGGTGGGCGCTGGGTGTGCTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCCA  
GGGGACACAGAGGAAGAGGTGTTTGAATGCATCGTCAACATGGACGCCCCCTACCCCGGC  
TTTCTGTGCGGTGCAAGGGCTTGAGTTCATTGAGAAGCTCCTCCAGAAGTGCCCGGAGAAG  
CGCCTCGGGGCAGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACC  
ACCAACTGGCAAGCCCTGCTCGCCCGCACCATCCAGCCCCCTTCGTGCCTACCCTGTGT  
GGCCCTGCGGACCTGCGCTACTTTGAGGGCGAGTTCACAGGGCTGCCGCTGCCCTGACC  
CCACCTGCACCCACAGCCTCTCACTGCCCGCCAACAGGCCGCCTTCCGGGACTTCGAC  
TTTGTGTGAGAGCGATTCTTGAACCTGA

SEQ ID NO: 13\_AI021023\_M\_PKNBETA\_M

GCTGAAGTGGGATAACCTTCTGCTGGATGCCCAGGGATTCTGAAGATCGCAGACTTTGG  
ACTCTGCAAGGAAGGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGTGGCACCCCGGA  
GTTCTTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACAGGGCTGTGGACTGGTGGGG  
GCTGGGTGTGCTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCAGGGGACACAGA  
GGAAGAGGTGTTTGAATGCATCGTCAACATGGACGCCCCCTACCCCGGCTTTCTGTGCGT  
GCAAGGGCTTGAGTTCATTGAGAAGCTCCTCCAGAAGTGCCCGGAGAAGCGCCTCGGGGC  
GGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACCACCAACTGGCA  
AGCCCTGCTCGCCCGCACCATCCAGCCCCCTTGTGCTTACCCTGTGTGGCCCTGCGGA  
CCTGCGCTACTTTGAGGGCGAGTTCACAGGGCTGCCGCTGCCCTGACCCACCTGCACC  
CCACAGCCTCCTCACTGCCCGCCAACAGGCCGCCTTCCGGGACTTCGACTTTGTGTGAGA  
GCGATTCTTGAACCTGAGGGCATCTCCTGGCACCTCTGTCCCTTCCCCACAGACTG  
TTAGAGCCTCTGCTCGTTACCCGTGCGCCCTGCCTGGAGGTCCAGGCCTTGCTGGGTAC  
TTCTGAGCCCTTGGGATTCAAAGTGGCAGCCATGGGGCCACTGTTGTGGGCTTTGCTCAG

## FIGURE 2K

TGTCACTGGGCAAAGTGTGTCCCTTCCCCCTCCAGCTCGCCCTCTTCTACCTCCCAGCGA  
GACCTGGCCAGAAAGGTGCCGAGCAAGGAGTGATATGGTTTGTCTTTTAAGACTGG  
ACTTGCTTTATATTAAATTTGTAAAAGTG

SEQ ID NO: 14\_H19102\_H

GGTGGCAACATCCGGGGTCCCTGGGCCCCGAGGCTGGAAGAGCCTCTGGACAGGTTTGGGA  
ACCATCAGGTCAGATCTGGAAGAACTCTGGGAACTACGGGGGCACCACTATCTGCACCAG  
GAATCCCTAAAGCCAGCCCCAGTACTGGTAGAGAAGCCTCTGCCAGAGTGGCCAGTGCCT  
CAGTTCATCAACCTCTTTCTACCAGAGTTTCCCATTAGGCCCATTAGGGGGCAGCAGCAG  
CTGAAGATTTTAGGCCCTCGTGGCTAAAGGCTCCTTTGGAACTGTCCTCAAGGTGCTAGAT  
TGCACCCAGAAAGCTGTATTTGCAGTGAAAGGTGGTGCCCAAGGTAAAGGTCTACAGAGG  
GATACCGTGAGGCAGTGCAAAGAGGAGGTTAGCATCCAGCGACAGATCAACCATCCCTTT  
GTACACAGCTTGGGGGACAGCTGGCAGGGGAAAACGGCACCTTTTCATTATGTGTAGCTAC  
TGCAGCACAGATCTGTACTCCCTTTGGTCCGCTGTTGGCTGCTTTCTGAGGCTTCCATC  
CGTCTCTTTGCTGCCGAGTTGGTGCTGGTACTGTGTTATCTCCATGACTTGGGCATCATG  
CATCGAGATGTGAAGATGGAGAATATTCTTCTAGATGAACGAGGCCATCTGAAACTGACA  
GACTTTGGTCTGTCCCGCCACGTGCCCCAGGGAGCTCAAGCCTACACTATCTGTGGCACT  
CTTCAGTACATGGCCCCAGAGGTCCTAAGTGGAGGACCTTACAACCATGCTGCTGATTGG  
TGGTCCCTGGGTGTCTTGCTTTTCTCTCTGGCGACTGGAAAAGTTTCCAGTGGCTGCAGAG  
AGAGATCATGTGGCCATGTTGGCAAGTGTGACCCACAGTGACTCTGAGATCCCAGCTTCT  
CTTAACCAGGGCCTCTCACTCCTGCTCCATGAGCTCTTATGCCAGAACCCCCCTCCATCGT  
CTACGTTATCTGCATCACTTCCAGGTCCACCCTTTCTTTTCGGGGTGTGGCCTTCGACCCA  
GAGCTCCTACAGAAAGCAGCCAGTGAACCTTTGTACGGAGACACAAGCTACCCAGCCCAGT  
TCAGCGGAGACCATGCCCTTTGACGACTTTGACTGTGATCTGGAGTCCTTCTTGCTCTAC  
CCTATCCCTGCTTGA

SEQ ID NO: 15\_AA476563\_H

ATGGAATTCTTTAGGATAGACAGTAAGGATAGCGCAAGTGAACCTCTGGGACTTGACTTT  
GGAGAAAAATTGTATAGTCTAAATCAGAACCTTTGAAACCATTCCTTTACTCTTCCAGAT  
GGAGACAGTGCTTCTAGGAGTTTAAATACTAGTGAAAGCAAGGTAGAGTTTAAAGCTCAG  
GACACCATTAGCAGGGGCTCAGATGACTCAGTGCCAGTTATTTCTGTTTAAAGATGCTGCT  
TTTGATGATGTGAGTGCTGATGAAGGAAGACCTGATCTTCTTGTAATTTACCTGGT  
GAATTGGAGTCAACAAGAGAAGCTGCAGCAATGGGACCTACTAAGTTTACACAAACTAAT  
ATAGGGATAATAGAAAATAAATCTTGGAGCCCTGATGTTTATGCCTCAGGCTTAGT  
ACTGAACAATGCCAAGCACATGAGGAGAAAAGGCATAGAGGAACTGAGTGATCCCTCTGGG  
CCCAAATCCTATAGTATAACAGAGAAACACTATGCACAGGAGGATCCCAGGATGTTATTT  
GTAGCAGCTGTTGATCATAGTAGTTCAGGAGATATGTCTTTGTTACCCAGCTCAGATCCT  
AAGTTTCAAGGACTTGGAGTGGTTGAGTCAGCAGTAACTGCAAACAACACAGAAGAAAGC  
TTATTCGTATTTGTAGTCCACTCTCAGGTGCTAATGAATATATTGCAAGCACAGACACT  
TTAAAAACAGAAGAAGTATTGCTGTTTACAGATCAGACTGATGATTGGCTAAAGAGGAA  
CCAACCTCTTTATTCCAGAGAGACTCTGAGACTAAGGGTGAAAGTGGTTTAGTGCTAGAA  
GGAGACAAGGAAATACATCAGATTTTTGAGGACCTTGATAAAAAATTAGCACTAGCCTCC  
AGGTTTTACATCCCAGAGGGCTGCATTCAAAGATGGGCAGCTGAAATGGTGGTAGCCCTT  
GATGCTTTACATAGAGAGGGGAATTGTGTGCCGCGATTTGAACCCAAACAACATCTTATTG  
AATGATAGAGGACACATTCAGCTAACGTATTTAGCAGGTGGAGTGAGGTTGAAGATTCC  
TGTGACAGCGATGCCATAGAGAGAATGTACTGTGCCCCAGAGGTTGGAGCAATCACTGAA  
GAACTGAAGCCTGTGATTGGTGGAGTTTGGGTGCTGTCTCTTTGAACTTCTCACTGGC  
AAGACTCTGGTTGAATGCCATCCAGCAGGAATAAATACTCACACTACTTTGAACATGCCA  
GAATGTGTCTCTGAAGAGGCTCGCTCACTCATTCAACAGCTCTTGCAGTTCAATCCTCTG

## FIGURE 2L

GAACGACTTGGTGCTGGAGTTGCTGGTGTTGAAGATATCAAATCTCATCCATTTTTTACC  
CCTGTGGATTGGGCAGAACTGATGAGATGA

SEQ ID NO: 16\_AA626690\_H

ATGCTACCATTCGCTCCTCAGGACGAGCCCTGGGACCGAGAAATGGAAGTGTTTCAGCGGC  
GGCGGCGCGAGCAGCGCGAGGTAAATGGTCTTAAATGGTTGATGAGCCAATGGAAGAG  
GGAGAAGCAGATTCTTGTCATGATGAAGGAGTTGTTAAAGAAATCCCTATTACTCATCAT  
GTTAAGGAAGGCTATGAGAAAGCAGATCCTGCACAGTTTGAGTTGCTCAAGGTTCTTGGT  
CAGGGGTCATTTGGAAAGGTTTTTCTTGTTAGAAAGAAGACCGGTCCTGATGCTGGGCAG  
CTCTATGCAATGAAGGTGTTAAAAAAGCCTCTTTAAAGTTTCGAGACAGAGTTCCGACA  
AAGATGGAGAGGGATATACTGGTGGAAGTAAATCATCCATTTATTGTCAAATTGCACTAT  
GCCTTTCAGACTGAAGGGAACTGTACTTAATACTGGATTTTCTCAGGGGAGGAGATGTT  
TTCACAAGATTATCCAAAGAGGTTCTGTTTACAGAGGAAGATGTGAAATCTACCTCGCA  
GAACCTGGCCCTTGCTTTGGATCATCTGCACCAATTAGGAATTGTTTATAGAGACCTGAAG  
CCAGAAAACATTTTGCTTGATGAAATAGGACATATCAAATTAACAGATTTTGGACTCAGC  
AAGGAGTCAGTAGATCAAGAAAAGAAGGCTTACTCATTTTGTGGTACAGTAGAGTATATG  
GCTCCTGAAGTAGTAAATAGGAGAGGCCATTCCCAGAGTGCTGATTGGTGGTCATATGGT  
GTTCTTATGTTTGAAATGCTTACTGGTACTCTGCCATTTCAAGGTAAAGACAGAAATGAG  
ACCATGAATATGATATTAAAGCAAACTTGGAATGCCTCAATTTCTTAGTGCTGAAGCA  
CAAAGTCTTCTAAGGATGTTATTCAAAAGGAATCCAGCAAATAGATTGGGATCAGAAGGA  
GTTGAAGAAATCAAAAGACATCTGTTTTTGC AAATATTGACTGGGATAAAATTATATAAA  
AGAGAAGTTCAACCTCCTTTCAAACCTGCTTCTGGA AAAACCAGATGATACTTTTTGTTTT  
GATCCTGAATTTACTGCAAAAACACCTAAAGATTCTCCCGGTTTGCCAGCCAGTGCAAAT  
GCTCATCAGCTCTTCAAAGGATTGAGCTTTGTTGCAACTTCTATTGCAGAAGAAATATAAA  
ATCACTCCTATCACAAGTGCAAATGTATTACCAATTGTTGAGATAAATGGAATGCTGCA  
CAATTTGGTGAAGTATATGAATTGAAGGAGGATATTGGTGTGGCTCCTACTCTGTTTGC  
AAGCGATGCATACATGCAACTACCAACATGGAATTTGCAGTGAAGATCATTGACAAAAGT  
AAGCGAGACCCTTCAGAAGAGATTGAAATATTGATGCGCTATGGACAACATCCCAACATT  
ATTACTTTGAAGGATGTCTTTGATGATGGTAGATATGTTTACCTTGTTACGGATTTAATG  
AAAGGAGGAGAGTTACTTGACCGTATTCTCAAACAAAATGTTTCTCGGAACGGGAGGCT  
AGTGATATACTATATGTAATAAGTAAGACAGTTGACTATCTTCATTGTCAAGGAGTTGTT  
CATCGTGATCTTAAACCTAGTAATATTTTATACATGGATGAATCAGCCAGTGAGATTCA  
ATCAGGATATGTGATTTTGGGTTTGCAAAACAACTTCGAGGAGAAAATGGACTTCTCTTA  
ACTCCATGCTACACTGCAAACTTTGTTGCACCTGAGGTTCTTATGCAACAGGGATATGAT  
GCTGCTTGTGATATCTGGAGTTTAGGAGTCCTTTTTTACACAATGTTGGCTGGCTACACT  
CCATTTGCTAATGGCCCCAATGATACTCCTGAAGAGATACTGCTGCGTATAGGCAATGGA  
AAATTCTCTTTGAGTGGTGGA AACTGGGACAATATTTTCAGACGGAGCAAAGGATTTGCTT  
TCCCATATGCTTCATATGGACCCACATCAGCGGTATACTGCTGAACAAATATTAAAGCAC  
TCATGGATAACTCACAGAGACCAGTTGCCAAATGATCAGCCAAAGAGAAATGATGTGTCA  
CATGTTGTTAAGGGAGCAATGGTTGCAACATACTCTGCCCTGACTCACAAGACCTTTCAA  
CCAGTCCTAGAGCCTGTAGCTGCTTCAAGCTTAGCCAGCGACGGAGCATGAAAAAGCGA  
ACATCAACTGGCCTGTAA

SEQ ID NO: 17\_AA215680\_H

ATGAGCCTGGTGGCCTGTGAGTGCTGCCCAGCCCCGGCCTGGAGCCTGAGCCTTGCTCA  
CGAGCACGGTCCCAAGCTCACGTGTACCTGGAGCAGATTGCAACAGGGTGGCTCTGGGA  
GTGCCTGACATGACAAAACGTGACTATCTGGTGGATGCGGCCACGCAGATCCGGCTGGCC  
CTGGAGCGGATGTTAGTGAGGACTATGAGGCGGCCTTCAACCACTATCAGAATGGCGTG  
GACGTGCTGCTCCGTGGCATAACGTTGACCCCAACAAGGAGCGACGTGAGGCTGTGAAG  
CTGAAAATTACCAAATACCTGCGGCGGGCAGAGGAGATCTTCAACTGCCACCTGCAGCGG

## FIGURE 2M

CCGCTGAGCAGTGGAGCCAGCCCCAGCGGGGTTTCAGCAGCCTGAGGCTCCGGCCCATT  
CGCACGCTGAGCTCTGCCGTGGAGCAGCTGAGGGGCTGCAGGGTGGTCGGGGTCATCGAG  
AAGGTGCAGCTGGTCCAGGACCCGGCAACCGGAGGGACCTTTGTGGTGAAGAGCCTACCC  
AGGTGCCACATGGTGAGCAGGGAGCGGCTGACCATCATCCCACACGGAGTCCCCACATG  
ACGAAGCTGCTCAGGTACTTTGTGAGCGAGGACTCCATCTTCCTGCACCTGGAGCATGTG  
CAAGGAGGCACTCTCTGGTCCCACCTGCTCTCCCAGGCGCACTCCCGACATTCTGGGCTC  
AGCTCTGGCTCTACCCAGGAGAGGATGAAGGCTCAGCTCAACCCCCACCTCAACCTCCTG  
ACCCAGCGAGGCTTCCCTCAGGCCATGCCCCTGCCAGGACAGAATCGCCCTGGAGCCT  
CCTAGGACTTCTCCGAACCTTCTCCTAGCTGGGGAGGCCCCATCCACCAGACCCAGAGG  
GAGGCTGAAGGTGAACCCACAGCCAGGACCAGCACCTCTGGCTCCTCGGACCTTCCAAAG  
GCCCCAGGTGGCCACCTGCACCTTCAAGCTAGGAGGGCTGGCCAGAACTCAGACGCTGGG  
CCCCCTCGGGGGCTCACTTGGGTTCTTGAGGGGGCCGGCCCGGTGCTAGGGGGCTGTGGC  
CGAGGCATGGATCAGAGCTGCCTGTCAGCAGATGGGGCCGGCCGGGGCTGTGGCAGGGCC  
ACCTGGAGTGTGAGAGAGGAGCAGGTGAAGCAGTGGGCGGCAGAGATGCTGGTAGCGCTG  
GAGGCGCTGCACGAGCAGGGGGTGTGTGCCGGGACCTCCACCCCGGGAACCTGCTCCTG  
GACCAGGCAGGTCACATCCGGCTCACATATTTTGGCCAGTGGTCAGAGGTGGAGCCCCAG  
TGCTGCCGGGAGGCCGTGGACAATCTCTACAGCGCCCCAGAGGTGGGTGGGATTTCCGAG  
CTGACGGAAGCCTGTGACTGGTGGAGCTTTGGGTCTCTACTGTATGAACTGCTGACGGGA  
ATGGCACTGTCCCAGAGCCACCCTTCAGGAATCCAGGCCCACACCCAGCTCCAGCTGCCC  
GAGTGGCTCAGTCGCCCAGCGCCTCTCTGCTGACTGAGCTGCTGCAGTTCGAGCCTACC  
CGGCGCCTGGGCATGGGAGAAGGTGGTGTGAGCAAACTCAAGTCCCATCCCTTTTTTCAGT  
ACCATCCAATGGAGCAAGCTGGTGGGGTAA

SEQ ID NO: 18\_SGK\_H

ATGACGGTGAAAACCTGAGGCTGCTAAGGGCACCCCTCACTTACTCCAGGATGAGGGGCATG  
GTGGCAATTCTCATCGCTTTTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTTATTTCAG  
AAGATTGCCAATAACTCCTATGCATGCAAACACCCTGAAGTTCAGTCCATCTTGAAGATC  
TCCCAACCTCAGGAGCCTGAGCTTATGAATGCCAACCCCTTCTCCTCCACCAAGTCCTTCT  
CAGCAAATCAACCTTGGCCCGTCTGTCCTCAATCCTCATGCTAAACCATCTGACTTTTCACTTC  
TTGAAAGTGATCGGAAAGGGCAGTTTTTGGAAAGGTTCTTCTAGCAAGACACAAGGCAGAA  
GAAGTGTCTATGCAGTCAAAGTTTTACAGAAGAAAGCAATCCTGAAAAAGAAAGAGGAG  
AAGCATATTATGTCGGAGCGGAATGTTCTGTTGAAGAATGTGAAGCACCCCTTTCTGGTG  
GGCCTTCACTTCTTTCCAGACTGCTGACAAATTGTAATTTGTCTTAGACTACATTAAT  
GGTGGAGAGTTGTTCTACCATCTCCAGAGGGAACGCTGCTTCTTGGAACCAACGGGCTCGT  
TTCTATGCTGCTGAAATAGCCAGTGCCCTTGGGCTACCTGCATTCACTGAACATCGTTTAT  
AGAGACTTAAAACCAGAGAATATTTTGCTAGATTACAGGGACACATTGTCCTTACTGAT  
TTCGGACTCTGCAAGGAGAACATTGAACACAACAGCACAAACATCCACCTTCTGTGGCACG  
CCGGAGTATCTCGCACCTGAGGTGCTTCATAAGCAGCCTTATGACAGGACTGTGGACTGG  
TGGTGCTGGGAGCTGTCTTGTATGAGATGCTGTATGGCCTGCCGCCTTTTTATAGCCGA  
AACACAGCTGAAATGTACGACAACATTCTGAACAAGCCTCTCCAGCTGAAACCAAATATT  
ACAAATTCCGCAAGACACCTCCTGGAGGGCCTCCTGCAGAAGGACAGGACAAAGCGGCTC  
GGGGCCAAGGATGACTTCATGGAGATTAAGAGTCATGTCTTCTCTCTTAATTAACCTGG  
GATGATCTCATTAATAAGAAGATTACTCCCCCTTTTAACCCAAATGTGAGTGGGCCCCAAC  
GAGCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTCCCCAACTCCATTGGCAAG  
TCCCCTGACAGCGTCTCGTCAAGCCAGCGTCAAGGAAGCTGCCGAGGCTTCTCTAGGC  
TTTTCTATGCGCCTCCCACGGACTCTTCTCTCTGA

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CGGGTCGACCCACGCTCCGCCGGTTTCACTGCTCCCCTCAGTCTCTTTTGGGCTCTTTC  
CGGGCATCGGGACGATGACCGTCAAAGCCGAGGCTGCTCGAAGCACCCCTTACCTACTCCA

## FIGURE 2N

GAATGAGGGGAATGGTAGCGATTCTCATCGCTTTTATGAAACAGAGAAGGATGGGCCTGA  
ACGATTTTATTTCAGAAGATTGCCAGCAACACCTATGCATGCAAACACGCTGAAGTTCAGT  
CCATTTTGAAAATGTCCCATCCTCAGGAGCCGGAGCTTATGAACGCTAACCCCTCTCCTC  
CGCCAAGTCCCTCTCAACAAATCAACCTGGGTCCGTCCTCCAACCCCTCACGCCAAACCT  
CCGACTTTCACCTTCTTGAAAGTGATCGGAAAGGGCAGTTTTTGAAAGGTTCTTCTGGCTA  
GGCACAAGGCAGAAGAAGTATTCTATGCAGTCAAAGTTTTACAGAAGAAAGCCATCTGA  
AGAAGAAAGAGGAGAAGCATATTATGTGAGAGCGGAATGTTCTGTTGAAGAATGTGAAGC  
ACCCTTTCTGGTGGGCCTTCACTTCTCATTCCAGACCGCTGACAAGCTCTACTTTGTCC  
TGGACTACATTAATGGTGGAGAGCTGTTCTACCATCTCCAGAGGGAGCGCTGCTTCTGG  
AACCACGGGCTCGATTCTACGCAGCTGAAATAGCCAGTGCCCTGGGCTATCTGCACTCCC  
TAAACATCGTTTATAGAGACTTAAAACCTGAGAATATTCTCCTAGACTCCCAGGGGCACA  
TCGTCTCACTGACNTATTTAGCTGCGTAGAATCGAGCATAACGGGACAACATCTACCT  
TCTGTGGCACGCTGAGTATCTGGCTCCTGAGGTCTCCATAAGCAGCCGTATGACCGGA  
CGGTGGACTGGTGGTGTCTTGGGGCTGTCTGTATGAGATGCTCTACGGCCTGCCCCCGT  
TTTATAGCCGGAACACGGCTGAGATGTACGACAATATTCTGAACAAGCCTCTCCAGTTGA  
AACCAAATATTACAAACTCGGCAAGGCACCTCTGGAAGGCCTCTGCAGAAGGACCGGA  
CCAAGAGGCTGGGTGCCAAGGATGACTTTTATGGAGATTAAGAGTCATATTTTCTTCTCTT  
TAATTAAGTGGGATGATCTCATCAATAAGAAGATTACACCCCATTTAACCCAAATGTGA  
GTGGGCCCAGTGACCTTCGGCACTTCGATCCCGAGTTTACCGAGGAGCCGGTCCCCAGCT  
CCATCGGCAGGTCCCCTGACAGCATCCTTGTACGGCCAGTGTGAAGGAAGCAGCAGAAG  
CCTTCCTCGGCTTCTCCTATGCACCTCCTGTGGATTCTTCCTCTGAGTGCTCCCGGGAT  
GGTTCTGAAGGACTTCCTCAGCGTTTCTTAAAGTGTTTTCGTTAGCCTTTGGTGGAGTTG  
CCAGCTGACAGAACATTTTAAAAGAATTTGCACACCTGGAAGCTTGGCAGTCTCGCCTGC  
CCGGCGTGGCGCGACGCAGCGCGCTGCTTGATGGGAGCTTTCCGAAGAGCACACCCTC  
CTCTCAATGAGCTTGTGAGGTCTTCTTTCTTCTCTTCTTCCACGTGGTGCTAGCTCC  
AGGCGAGCGAGCGTGAGAGTGCCGCTGAGACAGACACCTTGGTCTCAGTTAGAAGGAAG  
ATGCAGGTCTAAGAGGAATCCCCGAGGTCTGTCTGAGCTGTGATCAAGAATATTCTGCA  
ATGTGCCTTTTCTGAGATCGTGTTAGCTCCAAAGCTTTTTCCTATCGCAGAGTGTTTCAGT  
TTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTTCCTTGGCGGATTTCCCGTGTGTGCA  
GTGGCGTGAGTGCTATGCCTGATCACAGACGGTTTTGTGTTGAGCATCAATGTGACAC  
TTGCAGGACACTACAATGTGGGACATTGTTGTTTCTTCCACATTTGGAAGATAAATTTA  
TGTGTAGACTGTTTTGTAAGATATAGTTAATAACTAAAACCTATTGAAACGGTCTTGCAA  
TGACGAGCATTGAGATGCTTAAGGAAAGCATTGCTGCTACAAATATTTCTATTTTTAGAA  
AGGGTTTTTATGGACCAATGCCCCAGTTGTCAGTCAAAGCCGTGGTGTGTTTTCATTGTTT  
AAAATGTACCTATAAAAACGGGCATTATTTATGTTTTTTTTTCCCTTTGTTTCATATTCTTT  
TGCATTCTGATTATTGTATGTATCGTGTAAGGAAGTCTGTACATTGGGTTATAACACT  
AGATATTTAAACTTACAGGCTTATTTGTAAACCATCATTTTAATGTACTGTAATTAACAT  
GGGTTATAATATGTACAATTCCTCCTCCTTACCACACAACCTTTTTTTGTGTGCGATAAAC  
CAATTTTGGTTTGCAATAAAATCTTGAAAACCT

SEQ ID NO: 20\_AA109508\_M

CCACCTGCAGCGGGAGCGCGGTTCTGGAGCCCCGGGCCAGGTTCTACGCTGCTGAGGT  
GGCCAGCGCCATTGGCTACCTGCACTCCCTCAACATCATTTACAGGGATCTGAAACCAGA  
GAACATTTCTTTGGAAGTCCAGGGACACGTGGTGCTGACGGATTTTGGCCTCTGCAAGGA  
AGGTGTAGAGCCTGAAGACACCACATCCACATTTCTGTGGTACCCCTGAGTACTTGGCACC  
TGAAGTGCTTCGGAAAGAGCCTTATGATCGAGCAGTGGACTGGTGGTGGTGGGCGCAGT  
CCTCTACGAGATGCTCCATGGCCTGCCGCCCTTCTACAGCCAAGATGTATCCCAGATGTA  
TGAGAACATTTCTGCACCAGCCGCTACAGATCCCCGAGGCCGGACAGTGGCCCGCTGTGA  
CCTCCTGCAAAGCCTTCTCCACAAGGACCAGAGGCAGCGCTGGGCTCCAAAGCAGACTT  
TCTTGAGATTAAGAACCATGTATTCTTACGCCCCATAAACTGGGATGACCTGTACCACAA

FIGURE 20

GAGGCTAACTCCACCCTTCAACCCAAATGTGACAGGACCTGCTGACTTGAAGCATTTTGA  
CCCAGAGTTCACCCAGGAAGCTGTGTCCAAGTCCATTGGCTGTACCCCTGACACTGTGGC  
CAGCAGCTCTGGGGCCTCAAGTGCATTCTCTGGGATTTTCTTATGCGCCAGAGGATGATGA  
CATCTTGGATTGCTAGAAGAGAAGGACCTGTGAACTACTGAGGCCAGCTGGTATTAGTA  
AGGAATTACCTTCAGCTGCTAGGAAGAGCGACTCAAACCTAACAATGGCTTCAACGAGAAG  
CAGGTTTATTTTTTCCAGCACATAAAAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAG  
GACAGGTCATCAGATACTCAGAGGCTGTATCTCTGCCCTGCCAACCTTGACAAATGGCTT  
CCAATGTTAGGTTTGTCTACAAGATGGTTACTGGAGCTCTAGCTGCCTATTTTGTGTTTAG  
GGAAGGGAAAATGGAGGAAAGGGGAGAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAA  
AAGCTCCACCCAATGACTTCTGCTTCCATCTCACTAACCACCCACCCCTACCTGGAATGG  
AGGCTGGGAGATGTGGCTTATTTGCTGGGTACGTGACTATCCCTAATAACAAAGGGGTTT  
TGACACTAAGACATTAGGGGAGAATGTTGGGTAGGCAGCCAGCACTCTTTTACCAGAGGG  
CCTCCTGGTGTGTTGGATTTTGATCTCAATGTGTAAATGACAGAGATGTAACAAGCTCAT  
AGGGTATCAATATCTCTTATTGTTCT

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CGGATGCATTTNTTGGTGTGCTCTTGAGGGATTAAATGCAAAGAGATCACACCATGGACT  
ACAAGGAAAGCTGCCCAAGTGTAAGNATTCACAGCTCCGATGAACACAGAGAGAAAAAGA  
AGAGGTTTACTGTTTATAAAGTTCTGGTTTTCAGTGGGAAGAAGTGAATGGTTTGTCTTCA  
GGAGATATGCAGAGTTTGATAAACTTTATAACACTTTAAAAAACAGTTTCCTGCTANGG  
CCCTGAAGATTCTGCCAAGAGAATATTTGGTGATAATTTTGATCCAGATTTTATTAAAC  
AAAGACGAGCAGGACTAAACGAATTCATTTCAGAACCTAGTTAGGTATCCAGAACTTTATA  
ACCATCCAGATGTCAGAGCATTCTTCAAATGGACAGTCCAAAACACCAGTCAGATCCAT  
CTGAAGATGAGGATGAAAGAAGTTCTCAGAAGCTACACTCTACCTCACAGAACATCAACC  
TGGGACCGTCTGGAAATCCTCATGCCAAACCAACTGACTTTGATTTCTTAAAAGTTATTG  
GAAAAGGCAGCTTTGGCAAGGTTCTTCTTGCAAAACGGAAACTGGATGGAAAATTTTATG  
CTGTCAAAGTGTTACAGAAAAAATAGTTCTCAACAGAAAAGAGCAAAAACATATTATGG  
CTGAACGTAATGTGCTCTTGAAAAATGTGAAACATCCGTTTTTGGTTGGATTGCATTATT  
CCTTCCAAACAACTGAAAAGCTTTATTTTGTCTGGATTTTGTAAATGGAGGGGAGGGAC  
ATGTTGTCTTAACAGATTTTGGGCTTTGTAAAGAAGGAATTGCTATTTCTGACACCACTA  
CCACATTTTGTGGGACACCAGAGTATCTTGCACCTGAAGTAATTAGAAAACAGCCCTATG  
ACAATACTGTAGATTGGTGGTGCCCTTGGGGCTGTTCTGTATGAAATGCTGTATGGATTGC  
CTCCTTTTTTATTGCCGAGATGTTGCTGAAATGTATGACAATATCCTTCACAAACCCCTAA  
GTTTGAGGCCAGGAGTGAGTCTTACAGCCTGGTCCATTCTGGAAGAACTCCTAGAAAAAG  
ACAGGCAAAATCGACTTGGTGCCAAGGAAGACTTTCTTGAAATTCAGAATCATCCTTTTT  
TTGAATCACTCAGCTGGGCTGACCTTGTACAAAAGAAGATTCCACCACCATTTAATCCTA  
ATGTGGCTGGACCAGATGATATCAGAACTTTGACACAGCATTTACAGAAGAAACAGTTC  
CATATTCTGTGTGTATCTTCTGACTATTCTATAGTGAATGCCAGTGTATTGGAGGCAG  
ATGATGCATTTCGTTGGTTTCTCTTATGCACCTCCTTCAGAAGACTTATTTTGTGAGCAG  
TTTGCCATTTCAGAAACCATTCAGCAAAATAAGTCTATAGATGGGACTGAAACTTCTATTT  
GTGTGAATATATTCAAATATGTATAACTAGTGCCTCATTTTATATGTAATGATGAAAAC  
TATGAAAAAATGTATTTCTTCTATGTGCAAGAAAAATAGGGCATTTCAAAGAGCTGTTT  
TGATTAAAATTTATATTCTTGTTTAATAAGCTTATTTTAAACAATTTAAAGCTATTAT  
TCTTAGCATTAACTATTTTAAAGAAACCTTTTTTGCTATTGACTGTTTTTCCCTCTA  
AGTTTACACTAACATCTACCCAAGATAGACTGTTTTTTAACAGTCAATTTCAGTTTCAGCT  
AACATATATTAAATACCTTTGTAACCTTTTGCTATGGCTTTTGTATCACACCAAACTAT  
GCAATTGGTACATGGTGTGTTAAGAAGAAACCGTATTTTCCATGATAAATCACTGTTTG  
AAATATTTGGTTCATGGTATGATCGAAATGTAAAAGCATAATTAACACATTGGCTGCTAG  
TTAACAATTGGAATAACTTTATTCTGCAGATCATTTAAGAAGTAACAGGCCGGGCGCGGT  
GGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGCAGATCACCTGAGGTCA

## FIGURE 2P

GGAGTTGGAGACCAGCCTGACCAACATGGACAAACCCCGTCTCTACTAAAAATACAAAAT  
TGGCAGGGTGTGGTGGCACATGCCTATAATCCCAGCTACTTGGGAGGCTAAGGCAGGAGA  
ATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCACCATTGCACTCCTG  
CCTGGGCAACAAGAGTGAAACTCCATCTCC

SEQ ID NO: 22\_R47805\_H

ATGGCGCACCAAACGGGCATCCACGCCACGGAAGAGCTGAAGGAATTCTTTGCCAAGGCA  
CGGGCTGGCTCTGTGCGGCTCATCAAGGTTGTGATTGAGGACGAGCAGCTCGTGCTGGGT  
GCCTCGCAGGAGCCAGTAGGCCGCTGGGATCAGGACTATGACAGGGCCGTGCTGCCACTG  
CTGGACGCCCAGCAGCCCTGCTACCTGCTCTACCGCTCGACTCACAGAATGCTCAGGGC  
TTCGAATGGCTCTTCCTCGCCTGGTCGCCTGATAACTCCCCCGTGGGCTGAAGATGCTG  
TACGCGGCCACGCGGGCCACAGTGAAAAAGGAGTTTGGAGGTGGCCACATCAAGGATGAG  
CTCTTCGGGACTGTGAAGGATGACCTCTCTTTTGCTGGGTACCAGAAACACCTGTCTGCTCC  
TGTGCGGCACCTGCCCGCTGACCTCGGCTGAGAGAGAGCTCCAGCAGATCCGCATTAAC  
GAGGTGAAGACAGAGATCAGTGTGAAAGCAAGCACCAGACCCTGCAGGGCCTCGCCTTC  
CCCCTGCAGCCTGAGGCCAGCGGGCACTCCAGCAGCTCAAGCAGAAAATGGTCAACTAC  
ATCCAGATGAAGCTGGACCTAGAGCGGAAACCATTGAGCTGGTGCACACAGAGCCCACG  
GATGTGGCCAGCTGCCCTCCCGGGTGCCCCGAGATGCTGCCCGCTACCACTTCTTCCTC  
TACAAGCACACCCATGAGGGCGACCCCTTGAGTCTGTAGTGTTTCATCTACTCCATGCCG  
GGGTACAAGTGCAGCATCAAGGAGCGAATGCTCTACTCCAGCTGCAAGAGCCGCCTCCTC  
GACTCCGTGGAGCAGGACTTCCATCTGGAGATCGCCAAGAAAATTGAGATTGGCGATGGG  
GCAGAGCTGACGGCAGAGTTCCTCTACGACGAGGTGCACCCCAAGCAACACGCCTTCAAG  
CAGGCCTTCGCCAAGCCCAAGGGCCAGGGGGCAAGCGGGGCCATAAGCGCCTCATCCGC  
GGCCCGGGTGAAAATGGGGATGACAGCTAG

SEQ ID NO: 23\_H60215\_H

CCACGCGTCCGGCGCCGCAGCCATGGAGGGAGGCGGCGGGCGGCGGGCGGGCTCGGG  
TGGCTGCGCTGGGAGGCGGCGGTGAGAGGCTCGCACGCCTCCAGCCCGGCCCCGGCCCCC  
CGGGAGGGAGAGCCGAGCAGCCCCGGCTCTGGGCTACGGACTATGGGCGAATAGCTCTGA  
CCACCCGGCGAAGTGCACACACCCAGAAGCTATGTCCTTCGGCAGTAAAAGTTTTACAGC  
ACAATATATGTGCTCTGCTCTCCTCCCGCAATCCTGCTCCAAGAGATCTTAAGCTGGAGG  
CACCAGGTCTGAATTCAGACTCCTCCCCACCACCCACACTTCACCTCCAAGTGGAGCAT  
GACCACAGACCCATTGAGGAGGCTGGCGGACTCTTCATCCTGGACAGTCCCTTACTGTA  
TGTCAAAGCTGAGAATGAAGCGGAGAGCATCAGACAGAGGAGCTGGGGAAACGTCGGCCA  
GGGCCAAGGCTCTAGGAAGTGGGATTTCTGGAAATAATGCAAAGAGAGCTGGACCATTC  
TCCTTGGTCCCCGTCTGGGCAACTCACCGGTGCCAAGCATAGTGCAAGTGTGCGGAGGA  
AAGATGGCACGGATGACTTCTATCAGCTGAAGATCCTGACCCTGGAGGAGAGGGGGGACC  
AAGGCATAGAGAGCCAGGAAGAGCGGCAGGGCAAGATGCTGCTGCACACCGAGTACTCAC  
TGCTGTCTCTCCTGCACACGCAGGATGGCGTGGTGCACCACCACGGCCTCTTCCAGGACC  
GCACCTGTGAAATCGTTGAGGACACAGAATCCAGCCGGATGGTTAAGAAGATGAAGAAGC  
GCATCTGCCTCGTCTGGACTGCCTCTGTGCTCATGACTTCAGCGATAAGACCGCTGACC  
TCATCAACCTGCAGCACTACGTTCATCAAGGAGAAGAGGCTCAGCGAGAGGGAGACTGTGG  
TAATCTTCTACGACGTGGTCCGCGTGGTGGAGGCCCTGCACCAGAAAAATATCGTGACA  
GAGACCTGAAGCTGGGGAACATGGTGCTCAACAAGAGGACACATCGGATAACCATCACCA  
ACTTCTGCCTCGGGAAGCATCTGGTGAGCGAGGGGGACCTGCTGAAGGACCAGAGAGGGA  
GCCCTGCCTACATCAGTCCCGACGTGCTCAGCGGCCCGGCCGTACCGTGGCAAGCCCAGTG  
ACATGTGGGCCCTGGGCGTGGTGCTCTTCACCATGCTGTATGGCCAGTTCCCTTCTACG  
ACAGCATCCCCGAGGAGCTCTTCCGCAAGATCAAGGCTGCCGAGTATACCATTCCTGAGG  
ATGGACGGGTTTCTGAGAACACCGTGTGTCTCATCCGGAAGCTGCTGGTCTTGACCCCC  
AGCAGCGCCTGGCCGCCGCCGACGTCTGGAGGCCCTCAGTGCCATCATTGCATCATGGC



## FIGURE 2Q

AGTCCCTGTCATCTCTGAGTGGGCCTTTGCAAGTGGTTCCTGACATTGATGACCAAATGA  
GCAATGCGGATAGCTCCCAGGAGGCGAAGGTGACGGAGGAGTGCTCCCAGTACGAGTTTG  
AGAACTACATGCGTCAGCAGCTGCTGCTGGCCGAGGAGAAGAGCTCCATCCATGACACCC  
GGAGCTGGGTACCCAAGCGGCAGTTTCGGCAGCGCACACCACCGGTGCGACGGCTGGGCCACG  
ACGCACAGCCCATGACCTCCTTGACACGGCCATCCTGGCGCAGCGCTACCTGCGGAAAT  
AACAGCCTCAGCCGGGGCCACCAGCACTGCTGCCACTTCTTCCAGCCCCAGCCAAAGGCG  
TGGCTGTGAGGGCTGGGCCCTGTAGTGCTGGACTCTCCCGGGCCACAATAGGGACAGGGC  
AGGGACAGGGACAGCCAGGTCACACGTGGGGTCAGCAGAGGTACCACGAAGCTACCTTT  
TGGGATGATTGCTCGATTGTTTGGTTTTTAAATCTGAGAAGCCTAGATAACTAATCTGCT  
TTTAATCACGATGTTTTAATCTACCTCTGTCTCTTTAACCATGCTGTCTCTGGACTGAGC  
AAGAGGGAGGAGGGAGCCTGCTCACCCCACTCCAGGGCCTTCCCCAGCGGCCACCAACTG  
ACCTGGGGCGCTGCTCCCCACAGTCAAATAAGCTGAAAGTGACGCTCGCTGCAGGCCCC  
AGAGCGAGCTTCCCCCTCTCCCTGCTCTCCAGGCCCCCTGCCACAGCCTCTTCCGTCCC  
TCTCTTTCTGATCCAGGCCCTCAGTCCAAGCTTTGGAAAACCTTCACCTCATCTTAAAC  
CAAAC TCAAATATATTTATTTTTTTTACCAT

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GCCGCGATGGCCAGCACCAGGAGTATCGAGCTGGAGCACTTTGAGGAACGGGACAAAAGG  
CCGCGGCCGGGGTCGCGGAGAGGGGCCCCCAGCTCCTCCGGGGGCAGCAGCAGCTCGGGC  
CCCAAGGGGAACGGGCTCATCCCCAGTCCGGCGCACAGTGCCCACTGCAGCTTCTACCGC  
ACGCGGACCCTGCAGGCCCTCAGCTCGGAGAAGAAGGCCAAGAAGGCGCGCTTCTACCGG  
AACGGGGACCGCTACTTCAAGGGCCTGGTGTTTGCCATCTCCAGCGACCGCTTCCGGTCC  
TTCGATGCGCTCCTCATAGAGCTCACCCGCTCCCTGTGCGACAACGTGAACCTGCCCCAG  
GGTGTCGCGCACTATCTACACCATCGACGGCAGCCGGAAGGTCACCAGCCTGGACGAGCTG  
CTGGAAGGTGAGAGTTACGTGTGTGCATCCAATGAACCATTTTCGTAAAGTCGATTACACC  
AAAAATATTAATCCAAACTGGTCTGTGAACATCAAGGGTGGGACATCCCGAGCGCTGGCT  
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AAGACTGCTCATTCTTTGAACAAGTCTTAACAGATATCACCGAAGCCATTAAACNAGCC  
TCAGGAGTCGTCAAGAGGCTCTGCACCTGGATGGAAAGCAGGTGAGAGTTACGTGTGTG  
CATCTGCCAGACTTTTTTGGTGATGACGATGTTTTTATTGCATGTGGACCAGAAAAATTT  
CGTTATGCCCAAGATGACTTTGTCTGGATCATAGTGAATGTCGTGTCTGAAGTCATCT  
TATTCTCGATCCTCAGCTGTTAAGTATTCTGGATCCAAAAGCCCTGGGCCCTCTCGACGC  
AGCCAGATTTCTGCTCATGGCAGATCTTCTTCCAATGTAAACGGTGGACCTGAGCTTGAC  
CGTTGCATAAGTCTGAAGGTGTGAATGGAAACAGATGCTCTGAATCATCAACTCTTCTT  
GAGAAATACAAAATTGGAAAGGTCAATTGGTGATGGCAATTTTGCAGTAGTCAAAGAGTGT  
ATAGACAGGTCCACTGGAAAGGAGTTTGCCCTAAAGATTATAGACAAAGCCAAATGTTGT  
GGAAAGGAACACCTGATTGAGAATGAAGTGTCAATACTGCGCCGAGTGAAACATCCCAAT  
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GTGCACAGAGACATCAAACCAGAGAATCTCTTGGTGTGTGAATATCCTGATGGAACCAAG  
TCTTTGAAACTGGGAGACTTTGGGCTTGCGACTGTGGTAGAAGGCCCTTTATACACAGTC  
TGTGGCACACCCACTTATGTGGCTCCARAAATCATTGCTGAAACTGGCTATGGCCTGAAG  
GTGGACATTTGGGCAGCTGGTGTGATCACATACATACTTCTCTGTGGATTCCACCATTC  
CGAAGTGAGAACAATCTCCAGGAAGATCTCTTCGACCAGATCTTGGCTGGGAAGCTGGAG  
TTTCCGGCCCCCTACTGGGATAACATCACGGACTCTGCCAAGGAATTAATCAGTCAAATG  
CTTCAGGTAAATGTTGAAGCTCGGTGTACCGCGGGACAAATCCTGAGTCACCCCTGGGTG  
TCAGATGATGCCTCCAGGAGAATAACATGCAAGCTGAGGTGACAGGTAAACTAAAACAG  
CACTTTAATAATGCGCTCCCCAAACAGAACAGCACTACCACCGGGTCTCCGTATCATG

## FIGURE 2R

GTGAGTGGAAGGCGGCAGGTCTGGCCTGACTGCGGAGCCGGCCTTGAAGTTTTTGAATTA  
GGTAGCCGGGAGCTGCCCTCACATGGAAGTTGGTGCCCTCCGTAAGTCTATTTTCATATGA  
AGATTGGCTTGGCATGTGGAGGGCACTCATTGCGCAACTCCCAGGCTTTGGGCACTGTGT  
GGAGGGGCTTGTGTAGGGACCAGCAGGCCTGGTGTGAGGGGTCCAGGCGTCAAGGAGCTC  
CTGGCTGGGCCCTCTGGGCAGCTGCTTCCACTCTTGTCTCTGCCTTCTCATCTAGAGAGA  
CTCCCAAGCCCTGGAGGGGTGTGTTGTGTTAGGAATTAAGTCCCTGCCTACCCCAAGGCC  
TCAGAAATAGATTATTAGAGATGTGAATTATTCTTTGAGACTTGGGATAAGAAACAGCCA  
AAGCTAAACATATTTTCAGTTTTTAAAAAATCAGTGTTTTATAAAACACAGTTTGGGGCTTT  
TAAAGGTACATAATCAAGGAAAAAATATATATTTCATTTTTTCAGGGTTGGTAACATTTTA  
TGAGATGTCAGTGACAACGATGGCCTTATTTTTTTTCAGCCTTTTCTTCTTCCAAAATGTT  
TCTTAAGGCAACTCTCCTAAATACATAAACACAACAAATTAATGAAAAGTGACATGAG  
AGTAAATGAATCAAAAGGAAAAAATATTGAACCAGAGGTGAGGGCAGCACACCCGCAGCA  
GCTGTCCAGGCCTGAGCCAATGCAACCTGGGCGGGAAGGCCAGCTCACCGTGAGCAGGT  
AGAAGCCAGCCAGCCACCCAGGCAGGGACCTTGGTTCTCCCCACACACTCCCAGGAGCAG  
GGAACAGGGGTGGAGTGGCCTTTCCAGAGCTGGAGTTGGCTGCAGCAGCTTTCGAATCA  
GACCTGCCAAGGTGATGGGCGTCTGAGTTTACATCTGGGCCCCCGTGACCCCACTGAG  
TCCTGACAGCTAAGGATGGGCCACCTCCACAGCTCCGTCACTCGTACTTGGGACAGGCCT  
CTCATCTCTGGGAAGGTCTCTCCTTGTCTTCTTACCCAAGTGAAGGGAAACAGTGGCATA  
TTCTCATGGTACATGGTTGTCTGAAAGCCTTACCTAGGAAGACGCAGGGTCTAGATAGAA  
GCTATAAGGAAGCCACACACATAACCCACATCCCCACACCCCAACATCCCCCACACTCC  
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ACCAAGTCTCCAGCTCCTCTCCAACCAGCCCGGAAGTTTCAGAGGATTGAAGATTTCT  
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CCTGAAGGTGTGAATGGAAACCGGTGCTCCGAGTCGTTCCCCCTTCTGGAGAAATACAGA  
ATAGGGAAGGTGATCGGGGACGGCAACTTCGCGGTAGTTAAGGAGTGCCTGGACAGGTAC  
ACTGGAAGAGATTTGCATTAAAGATTATAGACAAAGCCAAATGCTGTGGAAAGGAGCAT  
CTGATTGAGAACGAAGTGTCAATCCTGCGCGAGTGAAGCACCCCAACATCATCATGTTG  
GTTGAAGAGATGGAAACAGCAACTGACCTCTTCTAGTGATGGAAGTGGTCAAAGGTGGA  
GATCTCTTTGATGCGATTACCTCTTCAACCAAGTACACTGAGAGAGATGGAAGCGCCATG  
GTGTACAACCTAGCCAATGCCCTCCGGTACCTGCACAGCCTCAGCATCGTCCACAGGGAC  
ATCAAGCCTGAGAATCTGCTGGTGTGCGAATACCCAGATGGAACCAAGTCTTTGAAGCTG  
GGAGACTTTGGGCTGGCGACGGTGGTTGAAGGCCCGTTGTACACGGTCTGTGGCACGCCA  
ACTTATGTGGCACCAGAGATCATAGCTGAAACAGGTTATGGCCTGAAGGTGGATGTTTGG  
GCAGCTGGTGTGATTACATACATACTTCTCTGTGGATTCCCACCATTCGGGAGTGAGAAC  
AATCTCCAGGAAGATCTCTTTGACCAGATCTTGGCTGGAAAGCTGGAATTCACAGCCCCC  
TACTGGGACAACATTACAGACTCTCCTTGTGTGTGTTTTAGGAAATGCTTATGAAGCTGG  
CCCGTGGGCTTCCAGTGGGACGTGCAGCAGTTCTTGGCAGAGCAGGGCCAGCTCTGCTG  
TGTCATCTCCAGGGTCTCCCATCACCTCTGCTCTTTGCCATGGCAGGTCTGCTGAGACCC  
CGCGGGGACGGGGGCATGGTGTCTCCCTGATTGGCCTGTGACCAACCTTCTGGAAGGCTGC  
TGGCAGTTTTCCCTGTTTTCCACCACCCCACTCTTTTTAATAATTGTATATAACTGTACT  
TGTTCTACTTGCTTGTCTTTAAACAGGGGCCCCCACAGTTCACTCTCACTGTTAGATTT  
TGCCTTTTCCAGGTATCCCCAACCTGCAATAAACTCTTCCCTCTTCAG

SEQ ID NO: 26\_AA383293\_H

CCAGCAGCCAAGGGTAGTGGTGTACCGGAATGGGGACCCATTCTTCCCAGGCTCCCAG  
CTGGTGGTGAAGCAACGCCGCTTCCCCACCATGGAGGCCTTCTCTGCGAGGTGACATCA  
GCTGTGCAGGCCCCACTGGCTGTGCGTGGCCTCTACACACCTTGTGATGGCCACCCTGTC  
ACCAACCTGGCAGACTTGAAGAACAGAGGGCAGTATGTGGCCGCTGGATTGTAACGATTC

FIGURE 2S

CACAAGCTCCCCCTTACCAGGCTTTTTGTCTCAGTGTGTTT CAGGAATGGGGACCTGGTA  
AGTCCCCCATTTAGTCTGAAGCTGTCCCAGGCTGCCAGCCAGGACTGGGAAACTGTGTTG  
AAGCTCCTGACTGAGAAGGTCAAGTTGCAGAGTGGGGCTGTGAGACTCTGCACCCTAGAG  
GGGCTCCCACTGT CAGCAGGGAAGGAGCTGGTAACTGGCCATTACTATGTGGCTGTCCGA  
GAGGATGAGTTCAAGGACCTTCCCTATCCAGCTCTGTCCACAAGAGGGCTCCTGGCAGCA  
GGCAATGAAGCCCACCTGAGGAGTGGAGTGGGGACTGTGCTGGTTCCCCCAAGCCTCTT  
GGAAGGAAGGCTAAGAAGGAGACATGCCTAATCGTGACCCTGACCCTGAAATACCAGCAG  
TCAGAAACAAGCAGAGACGGGCAATCATTCCCATCAGGAGTTATAGGAGTATATGGAGCT  
CCCCACCGAAGGAAGGAGACAGCGGGGGCCCTGGAAGTAGCAGATGATGAAGACACTCAG  
ACAGAGGAGCCCTTGGATCAGAGGGCAGCACAGATAGTGAACAGGTTACTTGTCTGCAA  
GACTTTTTTGGTGATGACGATGTTTTTATTGTCATGTGGACCAGAAAAATTTTCGTTATGCC  
CAAGATGACTTTGTCTGGATCATAGTCGTCGACGGCTCCTGAGAGAGCACCAGGCGGGC  
TTTGAGAAGCTCCGCAGGACCCGAGGAGAAGAGAAGGAGGCAGAGAAGGAGAAAAAGCCA  
TGTATGTCTGGAGGCAGAAGGATGACTCTCAGAGATGACCAACCTGCAAAGCTAGAAAAG  
GAGCCCAAGACGAGGCCAGAAGAGAAACAAGCCAGAGCGGCCAGCGGTGCGAAGCCACGG  
CCCATGGGCATCATTGCCGCCAATGTGGAAGCATTATGAGACTGGCCGGGTGCTTGGG  
GATGGGAACTTTGCTGTGCTGAAGGAGTGCAGACACCGCGAGACCAGGCAGGCCTATGCG  
ATGAAGATCATTGACAAGTCCAGACTCAAGGGCAAGGAGGACATGGTGGACAGTGAGATC  
TTGATCATCCAGAGCCTCTCTCACCCCAACATCGTGAAATTGCATGAAGTCTACGAAACA  
GACATGGAATCTACCTGATCCTGGAGTACGTGCAGGGAGGAGACCTTTTTGACGCCATC  
ATAGAAAGTGTGAAGTTCCCGGAGCCCGATGCTGCCCTCATGATCATGGACTTATGCAAA  
GCCCTCGTCCACATGCACGACAAGAGCATTGTCCACCGGGACCTCAAGCCGGAACCTT  
TTGGTTCAGCGAAATGAGGACAAATCTACTACCTTGAAATTGGCTGATTTTGGACTTGCA  
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TATATCCTGCTGTGTGGCTTTCCCCCATTCCGCAGCCCTGAXXGAGGGGACCAGGACGAG  
CTCTTTAACATCATCCAGCTGGGCCACTTTGAGTTTCTCCCCCTTACTGGGACAATATC  
TCTGATGCTGCTAAAGATCTGGTGAGCCGGTTGCTGGTGGTAGACCCCAAAAAGCGCTAC  
ACAGCTCATCAGGTTCTTCAGCACCCCTGGATCGAAACAGCTGGCAAGACCAATACAGTG  
AAACGACAGAAGCAGGTGTCCCCCAGCAGCGATGGTCACTTCCGGAGCCAGCACAAGAGG  
GTTGTGGAGCAGGTATCATAGTCACCACCTTGGGAATCTGTCCAGCCCCCAGTTCTGCTC  
AAGGACAGAGAAAAGGATAGAAGTTTGAGAGAAAAACAATGAAAGAGGCTTCTTCACATA  
ATTGGTGAATCAGAGGGAGAGACACTGAGTATATTTTAAAGCATATTAAAAAATTAAGT  
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TGGGGGGTAAGCATTGTCTCAGTGAGGAATTTTGGTAATAATGATGTGTTTTGCTTCCC  
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SEQ ID NO: 28\_AA197883\_M

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CAGAGCAGCCTCCACTCAGTCCGCGCAGAGCACAGCCCACTGAAGCCCAGGGTGGTGACG  
GTGGTGAAGCTGGGTGGGCAGCCCCCTCCGTAAGGCCACCCCTGCTCCTCAACCGGCGCTCA  
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AAGAACGACCGTGTGCGGAAGCTGTTACCCCTCAAGGGCAGGGAGGTGAAGAGTGTGTCT  
GACTTCTTCCGGGAGGGTGATGCTTTTAGCTATGGGCAAAGAGCCGCTGACATTGAAG  
AGTATCCAGTTGGCCATGGAGGAGCTGTATCCTAAGAACCGGGCTCTTGCCCTGGCCCT  
CACAGTAGAGTCCCCTCCCCAAGGCTGAGAAGCAGACTTCCCAGCAAGCTTCTGAAAGGA

FIGURE 2T

AGTCACCGCTGTGGGGAGGCAGGAAGCTATAGCGCGGAAATGGAGAGTAAGGCAGTCTCT  
AGGCATCAGGGCAAGACTTCCACAGTGCTGGCCCCAGAAGACAAGGCGAGGGCCCAGAAG  
TGGGTAAGAGGGGAAACAGGAGTCAGAACCTGGTGGCCCGCCTTCACCCGGGGCAGCCACT  
CAGGAGGAGACTCATGCAAGTGGAGAGAAACATCTGGGGGTGGAGATCGAAAAGACCTCC  
GGGGAGATTGTGAGATGTGAGAAGTGTAAAGAGAGAAAGAGAGCTGCAGTTGGGCCTGCAG  
AGGGAGCCGTGCCCCGCTGGGAACCAAGTGCAGCTGGACCTGGGGAGAGCTCAGAAGAGGGAT  
TCCGAGAAGTTGGTGAGGACCAAGAGCTGCAGGAGGCCTTCTAAGGCAAAATTTACAGAT  
GGAGAGGAAGGGTGGAAAGGTGACAGCCATCGGGGCAGTCCCAGGGACCCCCCTCAGGAA  
ATGAGGAGGCCCAACAGCAACTCAGACAAGAAAGAGATCAGAGGCTCAGAAAGTCAGGAC  
AGTTATCCTCAGGGGGCACCCAAGGCCCAGAAGGACTTCGTGGAAGGGCCACCAGCTGTA  
GAGGAGGGGCCGATAGACATGAGGAGAGAGGACCGGCACACATGCAGGAGCAAGCATGCC  
GCCTGGCTCCGGAGAGAGCAGCAGGCCGAACCCCCACAGCTCCCCAGAACCCGAGGGGAG  
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AAGGAGTCTAAGAGGAAGCTAGAAGAGAAGAGGCCAGAACGACCCAGTGGCCGGAAGCCG  
AGGCCCAAGGGCATCATCTCAGCGGATGTGGAGAAGCACTATGACATAGGTGGGGTCATT  
GGGGATGGCAACTTTGCCACCGTGAAGGAATGCAGGCACCGAGAGACCAAGCAGGCTTAC  
GCCATGAAGATGATTGACAAGTCCCAGCTGAAGGGTAAGGAGGACATTGTGACAGTGAG  
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ACGGAGGCGGAGATCTACCTGATCATGGAGTATGTGCAGGGAGGGGACCTTTTTTGATGCC  
ATCGTTGAAAATGTGAAGTTTCCAGAGCCCCGAGGCTGCAGTTATGATCACAGACTTGTGT  
AAGGCCCTTCGTCCACATGCACGACAAGAATATCGTCCACCGGGACGTGAAACCAGAAAAC  
CTCCTGGTTCAGCGAAATGAAGACAAGTCTATCACCTTGAAGCTGGCTGATTTTGGCTTG  
GCCAAATATGTGGTGAGGCCTATATTTACTGTGTGTGGGACGCCAACATATGTAGCTCCT  
GAAATTCTTTCTGAGAAAGGTTACGGCCTGGAGGTGGACATGTGGGCGGCAGGTGTGATC  
CTATACATCCTCTTGTGTGGCTTCCCCCTTTCCGAAGTCTTGAGAGGGACCAAGACGAG  
CTCTTCAACATCATCCAAGTGGGCCAGTTTGAGTTCCCTCTCTCCTTACTGGGACAACATT  
TCTGATGCTGCCAAAGATCTGGTGAGAAATTTGCTGGAGGTGGACCTAAGAAGCGGTAC  
ACGGCCGAACAGGTCTTACAGCATCCCTGGATTGAGATGGTTGGGCATACCAACACAGGG  
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SEQ ID NO: 29\_DRAK2\_H

CTCCGCTGCTGTGCGCCAGGAGTCACTTCACGAGAAGCCAGGTCAACAACCGTCGGCCCTTG  
TCTGGAAAAGTAAAAGTGGATCCTGCCACGTTCCGAGCTCCCTGGCGCCTCGCCCGGCTG  
GAGCTAGAGAACTCGTCCTGTGGCGGCCCCCGGCGTGGGGCGGGACAGCGGCCCCCTGGA  
GGGGGCAGTCCCGGGAGAACCTGCGGCGGCGGAGCGGTAAAAATAAGTGACTAAAGAAG  
CAGACCTGGGAATCACCTAACATGTGAGGAGGAGATTTGATTGCCGAAGTATTTACAGGC  
CTACTAACTACAACCTCTCAAATTTCAATAAAAAATGGAAAACTTTAATAATTTCTATATA  
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TCTACTGGCCAAGAATATGCTGCAAAAATTTCTAAAAAAGAGAAGAAGAGGACAGGATTGT  
CGGGCAGAAAATTTTACACGAGATTGCTGTGCTTGAATTGGCAAAGTCTTGTCCCCGTGTT  
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ATTGTACACCTTGATTTAAAGCCACAGAATATATTACTGAGCAGCATATACCTCTCGGG  
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GAAATCATGGGAACACCAGAATATTTAGCTCCAGAAATCCTGAACCTATGATCCCATACC  
ACAGCAACAGATATGTGGAATATTGGTATAATAGCATATATGTTGTTAACTCACACATCA  
CCATTTGTGGGAGAAGATAATCAAGAAACATACCTCAATATTTCTCAAGTTAATGTAGAT  
TATTCGGAAGAACTTTTTCATCAGTTTACAGCTGGCCACAGACTTTATTCAGAGCCTT

## FIGURE 2U

TTAGTAAAAAATCCAGAGAAAAGACCAACAGCAGAGATATGCCTTTCTCATTCTTGGCTA  
CAGCAGTGGGACTTTGAAAACCTTGTTTCACCCTGAAGAACTTCCAGTTCCTCTCAAAC  
CAGGATCATTCTGTAAGGTCCTCTGAAGACAAGACTTCTAAATCCTCCTGTAATGGAACC  
TGTGGTGATAGAGAAGACAAAGAGAATATCCCAGAGGATAGCAGCATGGTTTCCAAAAGA  
TTTCGTTTTCGATGACTCATTACCCAATCCCATGAACCTGTTTCAGATTTGCTCTGTTAG  
CACTTTTTTCTTTGACTCATTGACTGAATTTGAAATTTTATATCCACTCCAGTGAGAT  
TATGATTTGTAGCTTCATATATGACATGTTTATATTGTAAATGCACTTTTCCATGGAATA  
ATTTAGGGAAGTGTTTAAATGTTAAATTACTAGTTGCTAGCATGTTATGATTTTCATATCC  
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GTGAAAG

SEQ ID NO: 30\_W44160\_M\_DRAK2\_M

CCAGACGCGGCTGCACCTTTCAAACCTCAACTGTAAGAAGCGTCGGTCAGCGTCTGTGCG  
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GAGTGCGAGGTAAAAGTCTGCCCTAGAGAAGCAGGTCTGGCAGTCATCAACATGTCTCGGA  
GGAGATTCGATTGCCGAAGTGCTCAGGCTTGCTAACTACAACCCCTCAAACGCCGATTA  
AAACAGAGAATTTTAATAATTTCTATACTCTTACCCCAAAGAACTTGGGAGAGGAAAAT  
TTGCTGTGGTTAGACAATGTATATCAAAATCAACTGGACAAGAGTATGCTGCCAAATCCC  
TGAAAAAGAGGAGAAGAGGGCAGGATTGCCGGGCGGAAATTCTGCATGAGATAGCTGTGC  
TGGAGCTGGCCAGGTCTTGTCCCCACGTGATTAATCTGCATGAGGTCTACGAAAATGCAA  
CGGAAATCATTTTGGTGTTAGAATATGCTGCGGGTGGAGAAATTTTCAACCTGTGTTTAC  
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AAGGAGTTCATTATCTACATCAGAATAACATTGTTTACCTTGATTTAAAGCCACAGAATA  
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GAAAAATTGGGAATGCAAGTGAGCTTCGGGAAATCATGGGAACACCTGAATACTTAGCTC  
CAGAAATCCTCAACTATGATCCCATACCACAGCAACAGATATGTGGAATATTGGCATAA  
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ATCTGAATATTTCTCAAGTGAATGTAGATTATTCAGAAGAAATGTTTTCATCAGTTTCAC  
AGCTGGCCACAGACTTCATCCAGAGCCTTCTAGTAAAGAACCAGAGAAAAGACCAACAG  
CAGAATCCTGCCTATCCCACTCATGGCTGCAGCAGTGGGACTTTGGAAGCTTGTTTCATC  
CTGAGGAAACTTCAGGCTCCTCTCAAATTCAGGATCTGACTCTCAGGTCCTCTGAAGAGA  
AGACCTCCAAGTCTCCTGTAATGGGAGCTGTGGAGCCCGGGAGGACAAGGAGAACATCC  
CTGAAGATGGCAGCTTAGTTTCTAAAAGATTTGATTGATGACTCCTTGCCAGCCCCC  
ATGAACCTGTTCCAGATTTGTTCTGTTAGCATTTTCTCTGTGACTCATCTGGACTGACT  
CGGAAATTTGAAATCTCTGGTGTGAGATTGTGTTTGTAGCTTCATATATTATGTTTATAT  
TATAAATGCACCTCTGCTTAGAAGAACCTTAAGGAACAGTTTAAATGCTAGGCTTCTGTTG  
GCTAGCATATCATTTCTTGTCCTGAAATTGTTTTGCAGAGGAAAATATTTAAGTATATGA  
CAAAAAATGTAAATTGTGTTTAAAGAGAACACATGCAACTGAAAGAACTCAAGTTCAGTCA  
GACTTATAAAATGGGTTATATTATGGTTAGTAAAAGTTGAAAAAAATGAAAACAGGAAT  
TTAGTAGGTTCTAAGGTAAGCCCTATACCATAACTCTATTACAGAGAATCTGTTTGGGGA  
AATGCTGTCAAGGGTAAACCACAACATATACTGCTTTATAAATACTCCAGAGAGAGTTTA  
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TGCAACCGAGTCAAACTCGACATCATTTCCAGCTCATGTATTTGTACGTGCATCATA  
TATCAGATCTAATAAGATCTGGAAGATGGATATGCAATAAGAGGCCTTTGTCTTCTAGA  
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TTCATAAAGGGAAATGTTAAGTTCTGGCAGCTGACTTAGTGTTGGATGTCTCCTAAGTCT  
CAGGATAGAAGCCCATCATTAGAGCATAGGCACCTCAGGAATCTTGTGTGAAATTTCTAG  
TGAGTGAGGAGGTGTGACATGCAGCTATCTTTGGGCTCCTTTTGTGTGTGTTCTGCTGGA  
CAACACATGGGAGTGTTTCAAGTGTTGTCGGTGGTCAATATCTATGTTTCAAGTCCTGATGG

## FIGURE 2V

GAGGGGCCTAGGGACTGCTTTGGAGATTTCCCACTGGTGTCCATTTTAAGGTCTGTAATA  
ATGTCATGTTAAGATAACAGATCTCATAAATATGCTACTCTATCAGACTCCGTTGCCAAA  
ACAAATTAAAAGCCTGTGTATTGAAGTGGGTGTTAGTCTAACAACCTGTAAATTCTTGAA  
ATTGTTACTAAAATTCCAAATTCCTTTAGATAAATTTAACTATTTAAATTGAGCATTGCT  
GTCTTTGTTTGATTAAAGGTTGAGTTCCTTTATATCTGTTATTTTAAAGGAAAAGTTGT  
TTGCCCTTTTGTATATGTGTGTGCATATGTGTATGTGTACAGGTATATGTATATATGTATT  
GATAGATAAAATACAGCCTTTAAACAACCTTC

SEQ ID NO: 31\_H01248\_H, DRK1\_H

ATGATCCCTTTGGAGAAGCCAGGCAGCGCGGCTCCTCCCCAGGCGCCACCTCAGGCTCG  
GGCCGGGCAGGCCGGGGTCTGAGCGGGCCGTGCCGGCCGCCGCCGCCGCCAGGCCCGC  
GGGCTGCTGACAGAGATACGCGCCGTGGTGCACCGAGCCCTTCAGGACGGCTACAGC  
CTGTGCCCGGGCCGGGAGCTGGGCAGGGGGAAATTTGCAGTGGTGAGAAAATGTATAAAG  
AAAGATTCTGGGAAAGAATTTGCTGCAAAGTTCATGAGAAAAAGAAGAAAAGGCCAAGAT  
TGTCGGATGGAAATAATTCATGAGATTGCTGTACTTGAAGTAGCACAAGACAATCCTTGG  
GTCATTAATTTACATGAAGTTTATGAGACTGCATCAGAAATGATCTTAGTTCTGGAATAT  
GCTGCTGGGGTGAAATCTTTGACCAGTGTGTTGCAGACAGAGAAGAAGCCTTTAAAGAA  
AAAGATGTTCAAAGACTTATGCGACAGATTTTAGAAGGTGTTCACTTTTTACACACTCGT  
GATGTAGTTCATCTTGATTTGAAGCCTCAGAATATCTGTTGACAAGTGAATCTCCATTG  
GGTGACATTAAGATTGTTGATTTTGGCCTTTCAAGAATATTGAAGAACAGTGAAGAGCTC  
CGAGAAATTATGGGTACCCCTGAATATGTGGCTCCTGAAATCTTAGTTATGATCCTATA  
AGCATGGCAACAGATATGTGGAGCATTGGAGTGTAAACATATGTCATGCTTACAGGAATA  
TCACCTTTCTTAGGCAATGATAAACAAGAAACATTCTTAAACATCTCACAGATGAATTTA  
AGTTATTCTGAGGAAGAATTTGATGTTTTGTCTGAGTCGGCTGTTGATTTTCATCAGGACA  
CTTTTAGTTAAGAAACCTGAAGATCGAGCCACTGCTGAAGAATGTCTAAAGCACCCCTGG  
TTGACACAGAGCAGTATTCAAGAGCCTTCTTTCAAGATGGAAAAGGCACTAGAAGAAGCA  
AATGCCCTCCAAGAAGGTCAATCTGTGCCTGAAATTAATTCGGATACCGACAAATCAGAA  
ACCGAGGAATCCATTGTAACCGAAGAGTTAATTGTAGTTACTTCATATACTCTAGGACAA  
TGCAGACAGTCTGAAAAAGAGAAAAATGGAGCAAAAGGCCATTTCAAACGATTTAAATTT  
GAGGAACCTTTGCTACAAGAAATTCAGGAGAATTTATCTACTGA

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CGGGGCTGCCGGGGCCGGGACTGGGGGAGCCGGGCCCCGCGGGCCGCTGCTGCCTCCGCC  
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CCCAGCCCCGGCCTCCCGCGGACCCATGCCCGCCCGTATCGGCTACTACGAGATCGACCG  
CACCATCGGCAAGGGCAACTTCGCGGTGGTCAAGCGGGCCACGCACCTCGTCACCAAGGC  
CAAGGTTGCTATCAAGATCATAGATAAGACCCAGCTGGATGAAGAAAACCTGAAGAAGAT  
TTTCCGGGAAGTTCAAATTATGAAGATGCTTTGCCACCCCCATATCATCAGGCTCTACCA  
GGTTATGGAGACAGAACGGATGATTTATCTGGTGACAGAATATGCTAGTGGAGGGGAAAT  
ATTTGACCACCTGGTGGCCCATGGTAGAATGGCAGAAAAGGAGGCACGTCGGAAGTTCAA  
ACAGATCGTCACAGCTGTCTATTTTTGTCACTGTGCGAACATTGTTTCATCGTGATTTAAA  
AGCTGAAAATTTACTTCTGGATGCCAATCTGAATATCAAAAATAGCAGATTTTGGTTTCAG  
TAACCTCTTCACTCCTGGGCAGCTGCTGAAGACCTGGTGTGGCAGCCCTCCCTATGCTGC  
ACCTGAACTCTTTGAAGGAAAAGAATATGATGGGCCCCAAAGTGACATCTGGAGCCTTGG  
AGTTGTCCTCTACGTGCTTGTGTGCGGTGCCCTGCCATTTGATGGAAGCACACTGCAGAA  
TCTGCGGGCCCGGTGCTGAGTGGAAAGTTCGCGATCCCATTTTATGTCCACAGAATG  
TGAGCATTTGATCCGCCATATGTTGGTGTAGATCCCAATAAGCGCCTCTCCATGGAGCA  
GATCTGCAAGCACAAGTGGATGAAGCTAGGGGACGCCGATCCCAACTTTGACAGGTTAAT  
AGCTGAATGCCAACAACTAAAGGAAGAAAGACAGGTGGACCCCTGAATGAGGATGTCTCT  
CTTGCCCATGGAGGACATGGGACTGGACAAAGAACAGACACTGCAGTCATTAAGATCAGA

## FIGURE 2W

TGCCTATGATCACTATAGTGCAATCTACAGCCTGCTGTGTGATCGACATAAGAGACATAA  
AACCCTGCGTCTCGGAGCACTTCCTAGCATGCCCGAGCCCTGGCCTTTCAAGCACCAGT  
CAATATCCAGGCGGAGCAGGCAGGTACTGCTATGAACATCAGCGTTCCCCAGGTGCAGCT  
GATCAACCCAGAGAACCAAATTGTGGAGCCGGATGGGACACTGAATTTGGACAGTGATGA  
GGGTGAAGAGCCTTCCCCCTGAAGCATTGGTGCCTATTTGTCAATGAGGAGGCACACAGT  
GGGTGTGGCTGACCCACGCACGGAAGTTATGGAAGATCTGCAGAAGCTCCTACCTGGCTT  
TCCTGGAGTCAACCCCCAGGCTCCATTCTGCAGGTGGCCCCCTAATGTGAACCTCATGCA  
CAACCTGTTGCCTATGCAAACTTGCAACCAACCGGGCAACTTGAGTACAAGGAGCAGTC  
TCTCCTACAGCCGCCCACGCTACAGCTGTTGAATGGAATGGGCCCCCTTGGCCGGAGGGC  
ATCAGATGGAGGAGCCAACATCCAACCTGCATGCCAGCAGCTGCTGAAGCGCCACGGGG  
ACCTCTCCGCTTGTCAACCATGACACCAGCAGTGCCAGCAGTTACCCCTGTGGACGAGGA  
GAGCTCAGACGGGGAGCCAGACCAGGAAGCTGTGCAGAGGTACTTGGCAAATAGGTCCAA  
AAGACATACTGGCCATGACCAACCCTACAGCTGAGATCCACCGGACCTACAACGGCA  
GCTAGGACAGCAGCCTTTCGTTCCCGGGTCTGGCCTCCTCACCTGGTACCTGATCAGCA  
TCGCTCTACCTACAAGGACTCCAACACTCTGCACCTCCCTACGGAGCGTTTCTCCCCTGT  
GCGCCGGTTCTCAGATGGGGCTGCGAGCATCCAGGCCTTCAAAGCTCACCTGGAAAAAAT  
GGGCAACAACAGCAGCATCAAACAGCTGCAGCAGGAGTGTGAGCAGCTGCAGAAGATGTA  
CGGGGGGCGAGATTGATGAAAGAACCCTGGAGAAGACCCAGCAGCAGCATATGTTATACCA  
GCAGGAGCAGCACCATCAAATTCTCCAGCAACAAATTCAAGACTCTATCTGTCTCTCTCA  
GCCATCTCCACCTCTTCAGGCTGCATGTGAAAATCAGCCAGCCCTCCTTACCCATCAGCT  
CCAGAGGTTAAGGATTAGCCTTCAAGCCCACCCCCCAACCACCCCAACAACCATCTCTT  
CAGGCAGCCCAGTAATAGTCCCTCCCCCATGAGCAGTGCCATGATCCAGCCTCACGGGGC  
TGCATCTTCTTCCAGTTTCAAGGCTTACCTTCCCGCAGTGCAATCTTTCAGCAGCAACC  
TGAGAACTGTTCTCTCTCTCCCAACGTGGCACTAACCTGCTTGGGTATGCAGCAGCCTGC  
TCAGTCACAGCAGGTACCATCCAAGTCCAAGAGCCTGTTGACATGCTCAGCAACATGCC  
AGGCACAGCTGCAGGCTCCAGTGGGCGCGGCATCTCCATCAGCCCCAGTGCTGGTCAGAT  
GCAGATGCAGCACCCTACCAACCTGATGGCCACCCTCAGCTATGGGCACCCTCCCTTGTCT  
CAAGCAGCTGAGTGCTGACAGTGACAGGCTCACAGCTTGAACGTGAATCGGTTCTCCCC  
TGCTAACTACGACCAGGCGCATTTACACCCCCATCTGTTTTTCGGACCAGTCCCGGGGTTC  
CCCCAGCAGCTACAGCCCTTCAACAGGAGTGGGGTTCTCTCCAACCCAAGCCCTGAAAAGT  
CCCTCCACTTGACCAATTCCCCACCTTCCCTCCCAGTGACATCAGCAGCCGCCACACTA  
TACCACGTCGGCACTACAGCAGGCCCTGCTGTCTCCACGCGCCAGACTATAACAAGACA  
CCAGCAGGTACCCACATCCTTCAAGGACTGCTTTCTCCCGGCATTGCTCACCGGCCA  
CTCGGACATCCGGCTGCCCCCAACAGAGTTTGCACAGCTCATTAAGGAGCAGCAGCAACA  
ACGGCAGCAGCAGCAGCAACAGCAGCAACAGCAAGAATACCAGGAACCTGTTACGGCACAT  
GAACCAAGGGGATGCGGGGAGTCTGGCTCCCAGCCTTGGGGGACAGAGCATGACAGAGCG  
CCAGGCTTTATCTTATCAAAATGCTGACTCTTATCACCATCACACCAGCCCCCAGCATCT  
GCTACAAATCAGGGCACAAGAATGTGTCTCAGAGGCTTCCTCACCCACCCCGCCCCACGG  
GTATGCTCACCCAGCCGGCACTGATGCATTAGAGAGCATGGAGGAGGACTGCTCGTGTGA  
GGGGGCCAAGGATGGCTTCCAAGACAGTAAGAGTTCAAGTACATTGACCAAAGGTTGCCA  
TGACAGCCCTCTGCTCTTGAGTACCGGTGGACCTGGGGACCCTGAATCTTTGCTAGGAAC  
TGTGAGTCATGCCAAGAATTGGGGATACATCCCTATGGTCATCAGCCAACCTGCTGCATT  
CAGTAAAAATAAGGTGCCAGCAGAGAGCCTGTCATAGGGAAGTGCATGGATAGAAGTTC  
TCCAGGACAAGCAGTGGAGCTGCCGGATCACAATGGGCTCGGGTACCCAGCACGCCCCCTC  
CGTCCATGAGCACCACAGGCCCCGGGCCCTCCAGAGACACCACACGATCCAGAACAGCGA  
CGATGCTTATGTACAGCTGGATAACTTGCCAGGAATGAGTCTCGTGGCTGGGAAAGCACT  
TAGCTCTGCCCGGATGTGCGATGCAGTTCTCAGTCAGTCTTCGCTCATGGGCAGCCAGCA  
GTTTCAGGATGGGGAAAATGAGGAATGTGGGGCAAGCCTGGGAGGTATGAGCACCAGCA  
CCTGAGTGATGGCAGCCAGCATTTAACTCCTCTTGCTATCCATCTACGTGTATTACAGA  
CATTCTGCTCAGCTACAAGCACCCCGAAGTCTCCTTCAGCATGGAGCAGGCAGGCGTGTA

## FIGURE 2X

ACAAGAAACAGAGAGTTTTGTGTACAGCTTGGGAATGAAAAGGTTGATTGTAAACCCACA  
GTATCTAGCAGCGTTGTGCCAAATTGCCCTTGTGTTTCTCTCCACCCAAAATATCACAGC  
TGCTTTTCTCACATTTGGTTCATCCGTGTGCTGTTCTTTTGGGTTCTGAGAGGGTTTTGC  
CATGTTTGCCTTGATGACCAAGTCACCAAGGAAATAAACAGGAAGGAAATCCATGTTCTC  
C

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CTGGGCGCGTGCCTGAGTCCGCGCCCTGACAGCTCCGGGAGCCTCAAGCGCGACA  
GGGCGCCCTCACCTCGGGACATCCACACACCGACCGCTCCTGCTCCAGAGGCAACAACCC  
AGCGCGCCTAGCCTGGCGCCGTGCAGCGAAGCCCAAGAGCTGGCCTCGCCACGAAGGTTG  
AACCAGCCAAAATTTTCGAGACAGCTCACGGCTTAGAGGAAGGTTTCATCTAAATAAAGGCC  
GGCTAAAGTGACATTGCAGGGATTAAATCCTTCTTTGGCTGCCTGTGTGACCAGAAGGCT  
TATTTGCAAGTTTCTTCTTTCTTGGGGTCCAGATTATTAGGCTCTCCAGCGCCCTGCAGCT  
TGACAGAAAGAGAAGCATGAAATGAAGGTCAGAGATGAGATCCCGCAGCAGGGACGTGGG  
GGCCTCCAGGGGCATTTACGCACCAGAGTGCAAGATTCTCTGGCCATCAAGGGAAATAG  
CAAACAGAAGCCTTTGTCTTGGGGCAGGCCACCTACCACAAAGCATCAGACTCCACGTC  
TGCCAGAAAAGTTCTTGAGTCCCATCAGGCCAGTGGGTATGTAACATGTGCCTAATTGT  
ACAGCTAGAGCCTGCAAGTTCAACGTGAGGGAAGGTGGGAAATGTCTTGAGTGAGGCGAG  
CAGCTCCTGGCTGGGCTGGGCAGACTCAGCTACCACGTTCACTGCCTTCTCTCACTAAA  
GCCGAGAGGGAGGCTGCTCAGCTCTCAGGAAAACCTCTTTGAACCCTGGGCACCTGCTGT  
CCTCAGTTGGCATCTCCACCCCTCTGAGCCTCTTCTGCTCCTGCACAACCTGCCTCTTCG  
CTGAGATGGAGACGTGAGCCCCGTGGACGATGACTGCAGTGTATATGAATGGAGGTGGC  
CTGGTGAACCCCCACTATGCCCGGTGGGATCGGCGCGACAGTGTAGAAAGTGGCTGTGAG  
ACCGAGAGTAGCAAGGAGGGTGAGGAGGGACAGCCCCGCCAGCTGACGCCCTTCGAGAAA  
CTGACACAGGACATGTCCAGGATGAGAAGGTGGTGAGGGAGATCACGCTGGGGAAACGG  
ATAGGCTTCTACCGAATTCGAGGGGAAATCGGAAGTGGAACCTTCTCCCAAGTGAAGCTT  
GGGATTCACCTCCCTAACCAAGAAAAGGTGGCCATTAAGATCCTGGACAAGACCAAGTTA  
GACCAGAAAACCCAGAGGCTACTATCCCAGAAAATCTCCAGCATGGAAAAGCTGCACCAT  
CCCAACATCATCCGCCTTTACGAAGTGGTGGAGACCCTATCCAAGCTGCACTTGGTGATG  
GAGTATGCAGGGGGTGGGGAGCTCTTCGAAAAAATTAGCACTGAGGGGAAGCTCTCTGAA  
CCAGAAAGCAAGCTCATCTTCTCCAGATTGTGTCTGCCGTGAAGCACATGCATGAAAAC  
CAAATTATTCATAGAGATCTGAAAGCAGAAAATGTATTCTATACCAGTAATACTTGTGTG  
AAGGTGGGCGATTTTGGATTACGACAGTAAGCAAAAAAGGTGAAATGCTGAACACTTTC  
TGTGGGTCTCCTCCCTACGCTGCGCCTGAACTCTTCCGGGACGAGCACTACATCGGCATT  
TACGTGGATATCTGGGCCTTGGGGGTGCTTTTGTACTTCATGGTGAAGTGGCACCATGCCA  
TTTCGGGCAGAAACCGTGGCCAACTAAAAAAGAGCATCCTCGAGGGCACATACAGTGTA  
CCGCCGCACGTGTGAGAGCCCTGCCACCGACTCATCCGAGGAGTCCCTTCAGCAGATCCCC  
ACGGAGAGGTACGGAATCGACTGCATCATGAATGATGAATGGATGCAAGGGGTGCCATAC  
CCTACACCTTTGGAACCTTTCCAACCTGGATCCCAACATTTGTGCGAAACACGACTCTC  
AAGGAAGAAGAAAATGAGGTCAAAAGCACTTTAGAACATTTGGGCATTACAGAAGAGCAT  
ATTGCAATAACCAAGGGAGAGATGCTCGCAGCTCAATCACAGGGGTCTATAGAATTATT  
TTACATAGAGTCCAAAGGAAGAAGGCTTTGGAAAGTGTCCCAGTCATGATGCTACCAGAC  
CCTAAAGAAAAGAGACCTCAAAAAAGGGTCCCGTGTCTACAGAGGGATAAGACACACATCC  
AAATTTTGCTCGATTTTATAAATTGCACTAGACTGCTTGTAACCTAACCAAGATGATTGTT  
GCTGCTTCTAAATTTTTTTTCAAGGACAACCTTGAGTGGAGACATTTTTTGTAATTTTTAAAT  
AAACTTAAATTTGAGATATGCAAAAAAAA

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ATGTCCACTAGGACCCCATTTGCCAACGGTGAATGAACGAGACACTGAAAACCACACGTCA  
CATGGAGATGGGCGTCAAGAAGTTACCTCTCGTACCAGCCGCTCAGGAGCTCGGTGTAGA



FIGURE 2Y

AACTCTATAGCCTCCTGTGCAGATGAACAACCTCACATCGGAAACTACAGACTGTTGAAA  
ACAATCGGCAAGGGGAATTTTGCAAAAGTAAATTTGGCAAGACATATCCTTACAGGCAGA  
GAGGTTGCAATAAAAAATAATTGACAAAACCTCAGTTGAATCCAACAAGTCTACAAAAGCTC  
TTCAGAGAAGTAAGAATAATGAAGATTTTAAATCATCCCAATATAGTGAAGTTATTCGAA  
GTCATTGAAACTGAAAAAACACTCTACCTAATCATGGAATATGCAAGTGGAGGTGAAGTA  
TTTGAATTTTGGTTGCACATGGCAGGATGAAGGAAAAAGAAGCAAGATCTAAATTTAGA  
CAGATTGTGTCTGCAGTTCAATACTGCCATCAGAAACGGATCGTACATCGAGACCTCAAG  
GCTGAAAATCTATTGTTAGATGCCGATATGAACATTAAATAGCAGATTTCCGTTTGTAGC  
AATGAATTTACTGTTGGCGGTAAACTCGACACGTTTGTGGCAGTCCTCCATACGCAGCA  
CCTGAGCTCTTCCAGGGCAAGAAATATGACGGGCCAGAAGTGGATGTGTGGAGTCTGGGG  
GTCATTTTATACACACTAGTCAGTGGCTCACTTCCCTTTGATGGGCAAAACCTAAAGGAA  
CTGAGAGAGAGAGTATTAAGAGGGAAATACAGAATTCCTTCTACATGTCTACAGACTGT  
GAAAACCTTCTCAAACGTTTCTGGTGCTAAATCCAATTAAACGCGGCACTCTAGAGCAA  
ATCATGAAGGACAGGTGGATCAATGCAGGGCATGAAGAAGATGAACTCAAACCATTGT  
GAACCAGAGCTAGACATCTCAGACCAAAAAAGAATAGATATTATGGTGGGAATGGGATAT  
TCACAAGAAGAAATTCAAGAATCTCTTAGTAAGATGAAATACGATGAAATCACAGCTACA  
TATTTGTTATTGGGGAGAAAACTTTCAGAGCTGGATGCTAGTGATTCCAGTTCTAGCAGC  
AATCTTTCACTTGCTAAGGTTAGGCCGAGCAGTGATCTCAACAACAGTACTGGCCAGTCT  
CCTCACCAAAAGTGCAGAGAAGTGTCTTCAAGCCAAAAGCAAAGACGCTACAGTGAC  
CATGCTGGACCAGCTATTCTTCTGTTGTGGCGTATCCGAAAAGGAGTCAGACAAGCACT  
GCAGATGGTGACCTCAAAGAAGATGGAATTTCTCCCGGAAATCAAGTGGCAGTGCTGTT  
GGAGGAAAGGGAATTGCTCCAGCCAGTCCCATGCTTGGGAATGCAAGTAATCCTAATAAG  
GCGGATATTCTGAACGCAAGAAAAGCTCCACTGTCCCTAGTAGTAACACAGCATCTGGT  
GGAATGACACGACGAAATACTTATGTTTGCAGTGAGAGAACTACAGCTGATAGACACTCA  
GTGATTGAGAATGGCAAAGAAAACAGCACTATTCTGATCAGAGAACTCCAGTTGCTTCA  
ACACACAGTATCAGTAGTGACGCCACCCAGATCGAATCCGCTTCCCAAGAGGCACTGCC  
AGTCGTAGCACTTTCACGGCCAGCCCCGGGAACGGCGAACCAGCAACATATAATGGCCCT  
CCTGCCTCTCCAGCCTGTCCCATGAAGCCACACCATTGTCCAGACTCGAAGCCGAGGC  
TCCACTAATCTCTTTAGTAAATTAACCTCAAACTCACAAGGAGTCGCAATGTATCTGCT  
GAGCAAAAAGATGAAAACAAAGAAGCAAAGCCTCGATCCCTACGCTTACCTGGAGCATG  
AAAACCACTAGTTCAATGGATCCCGGGGACATGATGCGGGAAATCCGCAAAGTGTTGGAC  
GCCAATAACTGCGACTATGAGCAGAGGGAGCGCTTCTTGCTCTTCTGCGTCCACGGAGAT  
GGGCACGCGGAGAACCCTCGTGAGTGGGAAATGGAAGTGTGCAAGCTGCCAAGACTGTCT  
CTGAACGGGGTCCGGTTTAAGCGGATATCGGGGACATCCATAGCCTTCAAAAATATTGCT  
TCCAAAATTGCCAATGAGCTAAAGCTGTAA

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AAAGGGCCGTCCTGGTCCAGCCGTTCCCTGGGTGCCCGTTCGCGGAACTCTATCGCTTCC  
TGCCCTGAGGAACAACCCCATGTGGGCAACTATAGGCTGCTAAGGACCATCGGGAAGGGC  
AACTTCGCCAAAGTCAAGCTGGCTCGGCATATCCTCACGGGCCGGGAGGTGCTATTAAAG  
ATCATTGATAAGACCCAGCTGAACCCAGTAGCTTGCAAGAGCTGTTGAGAGAAGTCCGA  
ATTATGAAGGGACTCAACCACCCCAACATCGTGAAGCTTTTTGAGGTGATAGAGACGGAG  
AAGACGCTATACCTGGTGATGGAATACGCTAGCGCAGGAGAAGTGTGTTGACTACCTCGTG  
TCGCACGGCCGCATGAAGGAGAAGGAGGCTCGAGCCAAGTTCCGGCAGATCGTGTACGCC  
GTGCACTACTGTATCAGAAGAACATTGTACACAGGGATCTAAAGGCTGAAAACCTGTTG  
CTGGATGCCGAGGCCAACATCAAAATCGCCGACTTCGGCTTCAGCAATGAGTTCACGCTG  
GGCTCCAAGCTGGACACCTTCTGTGGGAGCCCCCATACGCCGCCAGAGCTGTTCCAG  
GGCAAGAAGTATGATGGGCCAGAGGTGGACATCTGGAGCCTGGGTGTCATCCTGTACAG  
CTGGTCAGCGGCTCCCTGCCCTTCGATGGGCACAACCTCAAGGAGCTGCGGGAGCGAGTC  
CTCAGAGGAAAGTACCGGGTCCCTTCTACATGTCTACAGACTGCGAGAGCATTCTGCGG

## FIGURE 2Z

AGATTTCTGGTGTGAACCCCGCAAAACGCTGTACTCTGGAGCAAATCATGAAAGACAAA  
TGGATCAACATCGGCTATGAGGGTGAGGAGCTGAAGCCAGACACGGAGCTCAAAGAAGAG  
CGGATGCCGGGTTCGGAAAGCGAGCTGCAGTGCAGTGGGCAGTGGGAAGTCGAGGCTTGCCC  
CCCTCCAGCCCCATGGTCAGCAGTGGCCACAACCCCAATAAGGCAGAGATCCCTGAGCGG  
CGGAAGGACAGCACTAGCACCCCTAACAACCTCCCCCCCAGCATGATGACCCGAAGAAAC  
ACCTATGTGTGCACAGAGCGACAGGATCTGAACGCCCCGTCTTGTGTCCAAATGGCAAA  
GAAAATAGCTCCGGTACCTCGCGGGTGCCCCCTGCCTCGCCTTCAGTCATAGCCTGGCT  
CCCCCGTCAGGCGAGCGGAGCCGCTGGCTCGGGGCTCCACCATCCGCAGCACCTTCCAT  
GGGGGCCAGGTCCGAGACCGGCGGGCAGGGAGCGGGAGTGGCGGGGGTGTGCAGAATGGA  
CCCCCAGCCTCACCCACGCTTGCCACGAGGCGCACCCCTGCCCTCCGGGCGGCCTCGC  
CCCACCACCAACCTCTTACCAAGCTGACCTCCAACTGACCCGAAGGGTCACAGACGAA  
CCTGAGAGAATCGGGGGACCTGAGGTACAAGTTGCCATCTACCTTGGGATAAAACGGAA  
ACCGCCCCCAGGCTGCTCCGATTCCCCTGGAGTGTGAAGCTGACCAGCTCGCGACCTTCC  
TGAGGCCCTGATGGCTGCCCTGCGACAGGCCACA

SEQ ID NO: 36\_406786.5\_H

GTAGCCGGCTTGCGGTGACCGTCGCTGATCCAGTTGTTAGAGGTGGAAGCTTGGCAGTT  
GGCCTCCCTTCTTCCCATGGAGGTGCGGGGCTTAACAGTCTTTGAAGAGGACCAGAGATG  
CCTTTCCAGAGCCTCCCCCTTGCCAGTGTGAGCAGAGGGCCAGCTGCACAGACCACTGC  
TGAGCCCAGCAGGTGCTTTTCTCAGCCACAGACACCTGAGCAGAAGGAATGGGCTTTC  
CAGACTCTGCCAGAGCAGGACGGCGCTCTCTGAAGACAGATGGAGCTCCTATTGTCTATC  
ATCACTGGCTGCCAGAATATTTGTACAAGTAACTGCACTGCCCTGCTGCCCCCTGAGCA  
CACGGACCCGTCCGAACCGCGGGGCAGTGTGTCTGCTGCTCCCTGCTGCGGGGACTGTC  
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CACGGTGGATGCCAAGACCACAGAGATCCTCGTTGCTAACGACAAAGCTTGCGGGCTCCT  
GGGGTACAGCAGCCAGGACCTGATTGGCCAGAAGCTCACGCAGTTCTTTCTGAGGTGAGA  
TTCTGATGTGGTGGAGGCCCTCAGCGAGGAGCACATGGAGGCCGACGGCCACGCTGCGGT  
GGTGTGTTGGCACGGTGGTGGACATCATACCCGTAGTGGGGAGAAGATTCCAGTGTCTGT  
GTGGATGAAGAGGATGCGGCAGGAGCGCCGCCCTATGCTGCGTGGTGGTCTGAGCCCGT  
GGAGAGGGTCTCGACCTGGGTGCTTTCCAGAGCGATGGCACCATCACGTGATGTGACAG  
TCTCTTTGCTCATCTTCACGGGTACGTGTCTGGGGAGGACGTGGCTGGGCAGCATATCAC  
AGACCTGATCCCTTCTGTGCAGCTCCCTCCTTCTGGCCAGCACATCCCAAAGAACTCTCAA  
GATTACAGAGGTCTGTTGGAAGAGCCAGGGACGGTACCACCTTCCCTCTGAGCTTAAAGCT  
GAAATCCCAACCCAGCAGCGAGGAGGCGACCACCGGTGAGGCGGCCCCCTGTGAGCGGCTA  
CCGGGCATCTGTCTGGGTGTTCTGCACCATCAGTGGCCTCATCACCCCTCCTGCCGGATGG  
GACCATCCACGGCATCAACCACAGCTTCGCGCTGACACTGTTTGGTTACGGAAAAGACGGA  
GCTCCTGGGCAAGAATATCACTTTCTGATTCTGTTTCTACAGCTACATGGACCTTGC  
GTACAACAGCTCATTACAGCTCCCAGACCTGGCCAGCTGCCTGGACGTGCGCAATGAGAG  
TGGGTGTGGGGAGAGAACCCTTGACCCGTGGCAGGGCCAGGACCCAGCTGAGGGGGGCCA  
GGATCCAAGGATTAATGTGCTGCTTGGTGGCCACGTTGTGCCCCGAGATGAGATCCG  
GAAGCTGATGGAAAGCCAAGACATCTTACCCGGACTCAGACTGAGCTGATTGCTGGAGG  
CCAGCTCCTTTCTGCCTCTCACCTCAGCCTGCTCCAGGGGTGGACAATGTCCCAGAAGG  
AAGCCTGCCAGTGCACGGTGAACAGGCGCTGCCCAAGGACCAGCAAATCACTGCCTTGGG  
GAGAGAGGAACCTGTGGCAATAGAGAGCCCCGGACAGGATCTTCTGGGAGAAAGCAGGTC  
TGAACCAAGTGGATGTGAAGCCATTTGCTTCTGCGAAGATTCTGAAGCTCCAGTCCCAGC  
TGAGGATGGGGGCAGTGATGCTGGCATGTGTGGCCTGTGTGAGAAGGCCAGCTAGAGCG  
GATGGGAGTCAGTGGTCCCAGCGGTTACAGCCTTTGGGCTGGGGCTGCCGTGGCCAAGCC  
CCAGGCCAAGGGTCAGCTGGCGGGGGGACGCTCCTGATGCACTGCCCTTGCTATGGGAG  
TGAATGGGGCTTGTGGTGGCGAAGCCAGGACTTGCCCCCAGCCCCCTTGGGATGGCAGG  
CCTCTCGTTTGGGACACCTACTCTAGATGAGCCGTGGCTGGGAGTGGAACGACCCGAGA

## FIGURE 2AA

AGAGCTGCAGACCTGCTTGATTAAGGAGCAGCTGTCCCAGTTGAGCCTTGACAGGAGCCCT  
GGATGTCCCCACGCCGAACCTCGTTCCGACAGAGTGCCAGGCTGTCACCGCTCCTGTGTC  
GTCCTGCGATCTGGGAGGCAGAGACCTGTGCGGTGGCTGCACGGGCAGCTCCTCAGCCTG  
CTATGCCTTGGCCACGGACCTCCCTGGGGGCCCTGGAAGCAGTGAGAGGCCAGGAGGTTGA  
TGTGAATTCTGTTTTCTGGAACCTCAAGGAACTCTTTTTCAGTGACCAGACAGACCAAAC  
GTCATCAAATTGTTCTGTGCTACGTCTGAACTCAGAGAGACACCCCTCTTCTTGGCAGT  
GGGCTCCGATCCAGATGTAGGCAGTCTCCAGGAACAGGGGTCTGTGTCTTGGATGACAG  
GGAGCTGTTACTACTGACCGGCACCTGTGTTGACCTTGGCCAAGGCCGACGGTCCGGGA  
GAGCTGTGTGGGACATGATCCAACAGAAACCGCTTGAGGTTTGTGTTGGTGTCTCTGAGCA  
TTATGCAGCAAGCGACAGAGAAAGCCCAGGACACGTTCTTCCACGTTGGATGCTGGCCC  
TGAGGACACGTGCCCATCAGCAGAGGAGCCAAGGCTGAACGTCCAGGTCACCTCCACGCC  
CGTGATCGTGATGCGCGGGGCTGCTGGCCTGCAGCGGGAGATCCAGGAGGGTGCCTACTC  
CGGGAGCTGCTACCATCGAGATGGCTTACGGCTGAGTATACAGTTTGAGGTGAGGCGGGT  
GGAGCTCCAGGGCCCCACACCTCTGTTCTGCTGCTGGCTGGTGAAAGACCTCCTCCACAG  
CCAACCGGACTCAGCCGCCAGGACCCGCTGTCTTGGCAGCCTGCCCGGCTCCACCCA  
CTCTACCGCTGCTGAGCTCACCGGACCCAGCCTGGTGGAAGTGCTCAGAGCCAGACCCTG  
GTTTGAGGAGCCCCCAAGGCTGTGGAAGTGGAGGGGTTGGCGGCTGTGAGGGCGAGTA  
CTCCCCAAAGTACAGTACCATGAGCCCGCTGGGCAGTGGGGCCTTCGGCTTCGTGTGGAC  
TGCTGTGGACAAGGGAAAAACAAGGAGGTGGTGGTGAAGTTTATTAAGAAGGAGAAGGT  
CTTGAGGATTGTTGGATTGAGGATCCCAAACTTGGGAAAGTTACTTTAGAGATCGCAAT  
TCTATCCAGGGTGGAGCACGCCAATATCATCAAGGTATTGGATATATTGAAAACCAAGG  
GTTCTTCCAGCTTGTGATGGAGAAGCACGGCTCCGGCCTAGACCTCTTCGCTTTCATCGA  
CCGCCACCCAGGCTGGATGAGCCCCTGGCGAGCTACATCTTCCGACAAGTGAGAGCAGG  
CCAGAGCCGTCTAGTGTGAGCAGTGGGATACCTGCGCTTGAAGGACATCATCCACCGTGA  
CATCAAGGATGAGAACATCGTGATCGCTGAGGACTTCACAATCAAGCTGATAGACTTTGG  
CTCGGCCGCTACTTGGAAAGGGGAAAATTATTTTATACTTTTTGTGGGACCATCGAGTA  
CTGTGCACCCGAAGTTCTCATGGGGAATCCCTACAGAGGGCCGGAGCTGGAGATGTGGTC  
TCTGGGAGTCACTCTGTACACGCTGGTCTTTGAGGAGAACCCCTTCTGTGAGCTGGAGGA  
GACCGTGGAGGCTGCCATACACCCGCCATACCTGGTGTCCAAAGAACTCATGAGCCTTGT  
GTCTGGGCTGCTGCAGCCAGTCCCTGAGAGACGCACCACCTTGGAGAAGCTGGTGACAGA  
CCCGTGGGTAACACAGCCTGTGAATCTTGCTGACTATACATGGGAAGAGGTGTTTCGAGT  
AAACAAGCCAGAAAGTGGAGTTCTGTCCGCTGCGAGCCTGGAGATGGGGAACAGGAGCCT  
GAGTGATGTGGCCAGGCTCAGGAGCTTTGTGGGGCCCCGTTCCAGGCGAGGCTCCTAA  
TGGCCAAGGCTGTTTGATCCCGGGGATCCCCGTCTGCTGACCAGCTAAACACCAATTTCT  
TCTCTGCTTTTCTCCACTTGGTTTGGAAATCACACAGTTTTTCAGGCTCCATCTGTTTG

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CCACGCGTCCGCATCCCTGCTTGGATGAGCCCTGGCGAGTTTCATCTTTTCGACAACCTAG  
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ACATTGTGATTGCTGAGGACTTCACAATTAAGCTGATAGATTTTGGCTCAGCTGCCTACT  
TAGAGAGGGGCAAACTATTTTATACCTTTTGTGGAACAATCGAATACTGTGCACCTGAGG  
TTCTCATTGGAAATCCCTACAGAGGGCCAGAGCTGGAGATGTGGTCTCTGGGGGTCAACC  
TGTACACGCTCATCTTCGAGGAGAATCCCTTCTGTGAGGTGGAGGAGACCATGGAGGCAG  
TTATTTCATCCCCCATTCCTGGTTTCCCAAGAACTTATGAGTCTTCTGTCTGGACTGCTGC  
AGCCTTGGCCTGAGCAGCGGACCCTTTGGAGAAGCTGATCAGGGACCCCTGGGTGACAC  
AGCCTGTGAACCTTGCTAGCTATACTTGGGAAGAGGTGTGTAGGACCAACCAGCCAGAAA  
GTGGCCTGCTGTGAGCTGCAAGTCTGGAGATTGGGAGTAGGAGTCCAAGTGAAATGGCTC  
AGAGAGAGGGTCTCTGTGGGCCTCCTGCTCCAGGGAGACTCGTGGTGACCAGCACTGCT  
TGCATCTTAAGGACCCCTCTTTGCCAGTCAGCTGAGCAAGCTCTCCTGCTCTTTGGTTTG  
GGCAGTTGTATGGATTTTCAGGGCTTTCTACCTGGAGAAAGGAAGTTGTGAAGGATTGGGA

## FIGURE 2BB

TGACTTCTGCTTCTAGATTCTATGCAAATGCTACAAGAGCCTGCGATGCTAGTTTTCTT  
AGGTTTATGATATAGACTTGTAATTCATGTTTTTTTATAACCTTGAAAATCATTCTAATG  
TTCAGTTATACTGTACTATTAAAGGGCTTTAAGTTGTAAGCCTCAGAAAGACACAAGGAG  
TGTTTAAGTTCTCTATTTTTTGTGTTTGTGTTTTTGCTTGTAAGTTTTTGAGACAGGATCTC  
ACCATGTAACCTTTGGCTGGCCTGGAACCTCAACTATGTAGACCAGGTAGACCTTAAACTGA  
CAGATCTGCCTGCGCTTGCCCTCCCAAGCATTAGGACTGATGGTGTGTGTCACCATGCCCCA  
GTTCTTCCTGGTTTTGTGTGTAGGTTCTTTCCCACTGACTTGGTACATGTGACATGTGA  
CAGATGTATGGAGTCTATAGAAGTGGCCAGACAAAATGGCCAGAATATTTATTTATTTT  
CTTAAAAATTTTCCAAATTAAAGCTACTTAGTTAACAGTTAAACTGGCCAGGACTATATG  
AGATAAACTTGTTTTCTATTTCTTTTGT

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GGCACGAGGCGCGCTGGCTGGGCCCTGCGGAGGANGGGAAGGAGCGAAGGAGCGAAGGA  
GCAAGCGGAGCGCAGTTCGCCCAAGCCAAGCCGCGCTGCCAACCCTCCCGCCCGCCCGCG  
CTCCTGTCCGCCGTGTCTAGCAGCGGGGCCAGCATGGTCATGGCGGATGGCCCGAGGCA  
CTTGACGCGCGGGCCGGTCCGGGTGGGGTTCTACGACATCGAGGGCACGCTGGGCAAGGG  
CAACTTCGCTGTGGTGAAGCTGGGGCGGCACCGGATCACCAAGACGGAGGTGGCAATAAA  
AATAATCGATAAGTCTCAGCTGGATGCAGTGAACCTTGAGAAAATCTACCGAGAAGTACA  
AATAATGAAAATGTTAGACCACCCTCACATAATCAAACCTTTATCAGGTAATGGAGACCAA  
AAGTATGTTGTACCTTGTGACAGAATATGCCAAAAATGGAGAAAATTTTTGACTATCTTGC  
TAATCATGGCCGGTTAAATGAGTCTGAAGCCAGGCGAAAATTTCTGGCAAATCCTGTCTGC  
TGTTGATTATTGTCTATGGTCGGAAGATTGTGCACCGTGACCTCAAAGCTGAAAATCTCCT  
GCTGGATAACAACATGAATATCAAAATAGCAGATTTCCGTTTTGGAAATTTCTTTAAAG  
TGGTGAACCTGCTGGCAACATGGTGTGGCAGCCCCCTTATGCAGCCCCAGAAGTCTTTGA  
AGGGCAGCAGTATGAAGGACCACAGCTGGACATCTGGAGTATGGGAGTTGTTCTTTATGT  
CCTTGTCTGTGGAGCTCTGCCCTTTGATGGACCGACTCTTCCAATTTTGAGGCAGAGGGT  
TCTGGAAGGAAGATTCCGGATTCGGTATTTTATGTCTCAGAAGATTGCGAGCACCTTATCCG  
AAGGATGTTGGTCCTAGACCCATCCAAACGGCTAACCATAGCCCAAATCAAGGAGCATAA  
ATGGATGCTCATAGAAGTTCCTGTCCAGAGACCTGTTCTCTATCCACAAGAGCAAGAAAA  
TGAGCCATCCATCGGGGAGTTTAATGAGCAGGTTCTGCGACTGATGCACAGCCTTGGAAAT  
AGATCAGCAGAAARCCATTGAGTCTTTGCAGAACAGAGCTATAACCACTTTGCTGCCAT  
TTATTTCTTGTGTTGGTGGAGCGCCTGAAATCACATCGGAGCAGTTTCCCAGTGGAGCAGAG  
ACTTGATGGCCGCCAGCGTCGGCCTAGCACCATTGCTGAGCAAACAGTTGCCAAGGCACA  
GACTGTGGGGCTCCCAGTGACCATGCATTACCGAACATGAGGCTGCTGCGATCTGCCCT  
CCTCCCCCAGGCATCCAACGTGGAGGCCTTTTCAATTTCCAGCATCTGGCTGTGAGGCGGA  
AGCTGCATTTCATGGAAGAAGAGTGTGTGGACACTCCAAAGGTCAATGGCTGTCTGCTTGA  
CCCTGTGCCTCCTGTCTGGTGCAGGAAGGGATGCCAGTCACTGCCCAGCAACATGATGGA  
GACCTCCATTGACGAAGGGCTGGAGACAGAAGGAGAGGCCGAGGAAGACCCCGCTCATGC  
CTTTGAGGCATTTTCAGTCCACACGCAGCGGGCAGAGACGGCACACTCTGTCTCAGAAGTGAC  
CAATCAACTGGTCGTGATGCCTGGGGCAGGGAAAATTTTCTCCATGAATGACAGCCCCCTC  
CCTTGACAGTGTGGACTCTGAGTATGATATGGGGTCTGTTTCAAGGGACCTGAACTTTCT  
GGAAGACAACCTTCCCTTAAGGACATCATGTTAGCCAATCAGCCTTCACCCCGCATGAC  
ATCTCCCTTCATAAGCCTGAGACCTACCAACCCAGCCATGCAGGCTCTGAGCTCCAGAA  
ACGAGAGGTCCACAACAGGTCTCCAGTGAGCTTCAGAGAGGGCCGAGAGCATCAGATAC  
CTCCCTCACCCAGGGAATTGTAGCATTTAGACAACATCTTCAGAATCTGGCTAGAACCAA  
AGGAATTCTAGAGTTGAACAAAGTGCAGTTGTTGTATGAACAAATAGGACCGGAGGCAGA  
CCCTAACCTGGCGCCGGCGGCTCCTCAGCTCCAGGACCTTGCTAGCAGCTGCCCTCAGGA  
AGAAGTTTCTCAGCAGCAGGAAAGCGTCTCCACTCTCCCTGCCAGCGTGCATCCCCAGCT  
GTCCCCACGGCAGAGCCTGGAGACCCAGTACCTGCAGCACAGACTCCAGAAGCCCAGCCT  
TCTGTCAAAGGCCAGAACACCTGTGAGCTTTATTGCAAAGAACCACCGCGAGCCTTGA

## FIGURE 2CC

GCAGCAGCTGCAGGAACATAGGCTCCAGCAGAAGCGACTCTTTCTTCAGAAGCAGTCTCA  
ACTGCAGGCCTATTTTAAATCAGATGCAGATAGCAGAGAGCTCCTACCCACAGCCAAGTCA  
GCAGCTGCCCCCTTCCCGCCAGGAGACTCCACCGCCTTCTCAGCAGGCCCCACCGTTCAG  
CCTGACCCAGCCCCCTGAGCCCCGTCTGGAGCCTTCCCTCCGAGCAGATGCAATACAGCCC  
TTTCCTCAGCCAGTACCAAGAGATGCAGCTTCAGCCCCCTGCCCTCCACTTCCGGTCCCCG  
GGCTGCTCCTCCTCTGCCCACGCAGCTACAGCAGCAGCAGCCGCCACCGCCACCACCCCC  
TCCACCACCACGACAGCCAGGAGCTGCCCCAGCCCCCTTACAGTTCTCCTATCAGACTTG  
TGAGCTGCCAAGCGCTGCTTCCCCCTGCGCCAGACTATCCCACTCCCTGTCAGTATCCTGT  
GGATGGAGCCCAGCAGAGCGACCTAACGGGGCCAGACTGTCCAGAAGCCCAGGACTGCA  
AGAGGCCCCCTCCAGCTACGACCCACTAGCCCTCTCTGAGCTACCTGGACTCTTTGATTG  
TGAAATGCTAGACGCTGTGGATCCACAACACAACGGGTATGTCTGGTGAATTAGTCTCA  
GCACAGGAATTGAGGTGGGTCAAGTGAAGGAAGAGTGTATGTTCTTATTTTATTCAGC  
CTTTTAAATTTAAAGCTTATTTTCTTGCCCTCTCCCTAACGGGGAGAAATCGAGCCACCC  
AACTGGAATCAGAGGGTCTGGCTGGGGTGGATGTTGCTTCTCCTGGTTCTGCCCCACCA  
CAAAGTTTTCTGTGGCAAGTGTGGAACATAGTTGTAGGCTGAGGCAGGAGAATGGCGTG  
AACCCGGGAGGCGGAGCTTGCACTGAGCCAAGATCGTGCCACTGCACTCCAGCCTGGGCG  
ACTGAGCAAGACTCCACCTCAAAAAAAAAAAAAAAAAAGGACAAGAGCAGTATCATCTGCCTC  
TGTTTCTAAACTGGACAAAGAGATTTTCTTAAAGTTTCTATCATCTCCCTTCTGACAGGT  
TCTACAGTGTGGTCTGAAGCACCTGTAATGTGAGAGCCCTTGTCTGGCCCTTGGTGGCAG  
GTGAACGAAAGCAGTGGAGCCTCTCACCTTCCAGTAGCCTCTCACATTCTTATTTTACCA  
TTTTTGTCTTAATTAAGGTAGCCTAGCTGATTCTAGAAGACAGCCATCCTACGTGCACCC  
CCACCTTGTGTCCACATCTTCTCCAGGCAGGTTTCAACCTATCAGCAGACTCAGGCACAC  
ACTGGGGCACAGATAGAGAACCAGGCGGCAGCAGTGCTCGCAGACCCACCCAGGGAGAGC  
TGTGATGGGTTCTGCCCAGATACTCTGCTCGCCACCCACAAGGGAGCAATAGCTTATAT  
TTGTACATTAGTTTTTACCAAGCACTTTCTCTTCTAACCCTCACAACAATTCTATGAAATT  
AGCTGGGGAGATACTGTCCTTATTTTTTACAGCTGAAGAAACCAAAGCTTTGGGAAGTTT  
GTGACTTCTCTGAGATCACAGCTGGTGATAGAAGGAGCTGGGACACGCGCTTGGGTGAC  
TGGCTTCTGGTTTTTGGTTCTCTGGCTTCTAGTGCTGGAAGAAGCCCTCTCTTTCCCTTCT  
CTTTCTCAGTAGCATCTGACTCTTTTATAAGCAAAACAGCTGTATAAAACAAAGCCCCCA  
TTTTTGGTCAAGCACAGGTGAATGTGATATTGTTCCCAACCTTATTCTCCACTCAACA  
GCCGCCTGGCTTTGGGGAAGAGGCCGCTTCAAGTGACAGTGCAGCTGTCCAGGTGGCCG  
TGCAGTGAACCAGGCTGAGGGAGACAAAAACCCGAGACCCGCTGCCTTTTCAAGCTCC  
AGTTAACTGCAGAAGTTTAGGCTCACCTCAAAGATGTCTAGTTTTTCCAAGTTACAATAC  
AGCAGTTTCTTACAGAACACCCCTTCTCAATTGCCAAGGGGCCGATCGCACGGCATC  
AGGCCACCACTGCAGGCCAGCAGATTCCACCCAGGAACGGTCATGAACTCAGCCTTTGT  
CTCAACGAGGGGCGTAACATTTCTTACAGTCAAGCCCCATCACTAGAAGTGCTTATTA  
CTTTTAGGATTAAAAAAGTAATAACAGACTTTGACTTAATACTCTGTCTTTTCAAGGCCA  
AAGTGGGTGGGTAGAGGGGAGCTTTAAAAATAGAAGTACAAAACAACATCCTGGAAACAT  
ATGACCCAGATGGAATAATGTACATTCCCAAGTGCAGATAATGGGCTGCTGCTGGCTC  
TGTGGTGTCTGTCTGCAGAAGATTTGCTCAGTCAAGGAAATTCAAGTGGTGAGACCTTTC  
CACCATGGGTGGTAAGAGAAACCTGCCTTACCACAAATCTCTGAAGGGGAAAGAAGTGGA  
GAGAAAGGTTTGCCTTCACTTCGGGGACTGCAGTTTGAAGAAATAAAGGGATACAGAGATA  
TCTGCACTTTGTAGAAAGGGCAAGATTATTTGCTTATATCTGAAGGGAGGTGGGTGGTTT  
TGCTGGATGTTTGGTCTGAAAGAGTTACTTTTGATAAAGTTAATCTAATTGTAGTTATAT  
TTTCTGTGTGCTTTTTTTTTAATTACTAAGAAAAAAATTGGTGAGTTCAGTAGCTTTGGTA  
TTATGAGTGCAAAATCATAATAGCTCCAATGTGAAAAAAAATCAAAGTATAAAGTGTG  
ACTTAATGTTAGAAAATTGCCTAAATGCAGTGTAATAAATAATCTCTGTACCAAAATAGT  
AATTTAAATGGGGTAATTTTCTGCAAGGAAATGTACTGTTTTTATGTTTTCAACCCCTCT  
TGA

## FIGURE 2DD

SEQ ID NO: 39\_AA207220\_H

GCTGTGGCTCCCCGTCTGGTGC GG GACCTGTGCCCCGCGCTTCAGCCCTCCCCGCAAGC  
CTATTGATTCCCCTGCCGCCCTTGCTCCACCTCCTGCTCGCCATGGAGTCGCTGGTTTTTC  
GCGCGGCGCTCCGGCCCCACTCCCTCGGCCGAGAGCTAGCCCGCCGCTGGCGGAAGGG  
CTGATCAAGTCGCCCAGCCCCCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACAAG  
CACAACCTGCGGCACCGCTACGAGTTCTTGAGACCCTGGGCAAAGGCACCTACGGGAAG  
GTGAAGAAGGCGGGGAGAGCTCGGGGCGCCTGGTGGCCATCAAGTCAATCCGGAAGGAC  
AAAATCAAAGATGAGCAAGATCTGATGCACATACGGAGGGAGATTGAGATCATGTCTATCA  
CTCAACCACCCTCACATCATTGCCATCCATGAAGTGTGAGAACAGCAGCAAGATCGTG  
ATCGTCATGGAGTATGCCAGCCGGGGCGACCTTTATGACTACATCAGCGAGCGGCAGCAG  
CTCAGTGAGCGCGAAGCTAGGCATTTCTTCCGGCAGATCGTCTCTGCCGTGCACTATTGC  
CATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCTTGATGCCAAT  
GGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACCATCAAGGCAAGTTCCTG  
CAGACATTCTGTGGGAGCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTAC  
ACAGGCCCAGAGGTGGACAGCTGGTCCCTGGGTGTTCTCCTCTACATCCTGGTGCATGGC  
ACCATGCCCTTTGATGGGCATGACCATAAGATCCTAGTGAAACAGATCAGCAACGGGGCC  
TACCGGGAGCCACCTAAACCTCTGATTGCCTGNNTGGCCTGATCCGGTGGCTGTTGATG  
GTGAACCCCAACCGCGGGGCCACCCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGG  
GGCTACGCCACCCGAGTGGGAGAGCAGGAGGCTCCGCATGAGGGTGGGCACCCTGGCAGT  
GACTCTGCCCGCGCCTCCATGGCTGACTGGCTCCGGCGTTCTCCTCCGCCCCCTCTGGAG  
AATGGGGCCAAGGTGTGCAGCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAGCACCACC  
CCTGGCCTGGAGCGCCAGCATTCGCTCAAGAAGTCCCGCAAGGAGAATGACATGGCCAG  
TCTCTCCACAGTGACACGGCTGATGACACTGCCCATCGCCCTGGCAAGAGCAACCTCAAG  
CTGCCAAAGGGCATTCTCAAGAAGAAGGTGTGAGCCTCTGCAGAAGGGGTACAGGAGGAC  
CCTCCGGAGCTCAGCCCAATCCCTGCGAGCCAGGGCAGGCTGCCCCCTGCTCCCCAAG  
AAGGGCATTCTCAAGAAGCCCCGACAGCGGAGTCTGGCTACTACTCCTCTCCCGAGCCC  
AGTGAATCTGGGGAGCTCTTGAGCGCAGGCGACGTGTTTGTGAGTGGGGATCCCAAGGAG  
CAGAAGCCTCCGCAAGCTTCAGGGCTGCTCCTCCATCGCAAAGGCATCCTCAAACCTCAAT  
GGCAAGTTCTCCAGACAGCCTTGAGGCTCGCGGCCCCCACCACCTTCGGCTCCCTGGAT  
GAACTCGCCCCACCTCGCCCCCTGGCCCGGGCCAGCCGACCCTCAGGGGCTGTGAGCGAG  
GACAGCATCCTGTCTCTGAGTCTTTGACCAGCTGGACTTGCCTGAACGGCTCCAGAG  
CCCCACTGCGGGGCTGTGTGTCTGTGGACAACCTCACGGGGCTTGAGGAGCCCCCTCA  
GAGGGCCCTGGAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGACAGTGCTTT  
TCCCTGACAGACTGCCAGGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGCTCA  
AAGCTCACCTGAGTGGAGTAGGCATTGCCCCAGCCGGTCAGGCTCTCAGATGCAGCTGG  
TTGCACCCCGAGGGGAGATGCCTTCTCCCCACCTCCAGGACCTGCATCCCAGCTCAGA  
AGGCTGAGAGGGTTTGCAGTGGAGCCCTGAGCAGGGCTGGATATGGGAAGTAGGCAAATG  
AAATGCGCCAAGGGTTCAGTGTCTGTCTTCAGCCCTGCTGAACGAAGAGGATACTAAAGA  
GAGGGGAACGGGAATGCCCGGACAGAGTCCACATTGCCTGTTTCTTGTGTACATGGAGG  
GGCCACAGAGA

SEQ ID NO: 40\_AA426580\_H, MAK\_V\_H

ATGCCGGCGGCGGGGGGACGGGCTCCTGGGGGAGCCGGCGCGCCTGGGGGCGGCGGC  
GGCGCGGAGGACGCGGCCAGGCCCGCGCGGCCTGCGAGGGAAGTTTCTGCCTGCCCTGG  
GTGAGCGGCGTGCCCCGCGAGCGGCTCCGCGACTTCCAGCACCAAGCGCGTGGGCAAC  
TACCTCATCGGCAGCAGGAAGCTGGGCGAGGGCTCCTTTGCCAAGGTGCGCGAGGGGCTG  
CACGTGCTGACCGGGGAGAAGGTGGCCATAAAAGTCATTGATAAGAAGAGAGCCAAAAAG  
GACACCTATGTACCAAAAACCTGCGGCGAGAGGGTCAGATCCAGCAGATGATCCGCCAC  
CCCAATATCACTCAGCTCCTTGATATTTAGAAACGGAAAACAGCTACTACCTGGTCATG  
GAGCTGTGCCCTGGGGGCAACCTGATGCACAAGATCTATGAGAAGAAGCGGCTGGAGGAG

## FIGURE 2EE

TCCGAAGCCCCGAGATACATCCGACAGCTCATCTCTGCCGTAGAGCACCTGCACCGGGCC  
GGGGTGGTCCACAGAGACTTGAAGATAGAGAATTTGCTACTAGATGAAGACAATAATATC  
AAGCTGATTGACTTTGGTTTGAGCAACTGCGCAGGGATCCTGGGTTACTCGGATCCGTTT  
AGCACACAGTGTGGCAGCCCTGCCTACGCTGCACCTGAACTGCTCGCCAGGAAGAAATAC  
GGCCCCAAAATCGATGTCTGGTCCATAGGTGTGAACATGTATGCCATGTTGACCGGGACG  
CTGCCTTTTCACGGTGGAGCCTTTTCAGCCTGAGGGCTTTGTACCAGAAGATGGTAGACAAA  
GAAATGAACCCCCCTCCCCACTCAGCTCTCCACAGGTGCCATCAGTTTCTGCGCTCTCTC  
CTGGAACCGGATCCTGTGAAGAGGCCAAATATTTCAGCAGGCACTGGCGAATCGCTGGCTT  
AATGAGAATTACACGGGCAAAGTGCCCTGTAATGTCACCTATCCCAACAGGATTTCTCTG  
GAAGATCTGAGCCCCGAGCGTCGTGCTGCACATGACCGAGAAGCTGGGTTACAAGAACAGC  
GACGTGATCAACACTGTGCTCTCCAACCGCGCTGCCACATCCTGGCCATCTACTTCCTC  
TTAAACAAGAACTGGAGCGCTATTTGTCAGGGAAATCTGACATCCAGGACAGCCTCTGC  
TACAAGACCCGGCTCTACCAGATAGAAAAGTACAGGGCCCCCAAGGAGTCTTATGAGGCC  
TCTCTGGACACCTGGACACGAGATCTTGAATTCCATGCCGTGCAGGATAAAAAGCCCCAA  
GAACAAGAAAAAAGAGGGGATTTTCTTCATCGACCATTCTCCAAGAAGTTGGACAAGAAC  
CTGCCCTCGCACAAACAGCCCTCAGGCTCGCTTATGACACAGATTTCAGAACACCAAAGCC  
CTCCTGAAGGACCGGAAGGCCTCCAAGTCCAGCTTCCCCGACAAAGATTCCTTTGGCTGC  
CGCAATATTTTCCGCAAAACCTCAGATTCCAATTGTGTGGCTTCTTCTCCATGGAGTTC  
ATCCCCGTGCCACCGCCAGGACCCCGAGGATTGTGAAGAAACCGGAGCCCCATCAGCCA  
GGGCCCCGAAGCACTGGCATCCCCACAAGGAAGACCCCTGATGCTGGACATGGTGC GC  
TCCTTCGAGTCTGTGGATCGCGACGACCACGTAGAAGTGCTGTCTCCCTCTCATCTACTAC  
AGGATTCTGAACTCCCCGGTCAGCTTGGCTCGCAGAAATTCAGCGAGAGGACGCTGTCC  
CCGGGTCTGCCATCCGGAAGCATGTGCGCTCTCCATACTCCTTTGCATCCAACCTCTGGTC  
TCTTTTGCTCACGAAGATAAGAACAGCCCCCAAAAGAGGAGGGCCTGTGTTGCCACCT  
CCGTTTCCCAGCAATGGCCCCATGCAGCCTCTGGGGAGCCCCAATTGTGTGAAAAGCCGA  
GGCCGGTTCCCTATGATGGGCATCGGACAGATGTTAAGGAAGCGCCATCAGAGTCTGCAG  
CCATCTGCAGATAGGCCCTGGAGGCCAGCCTGCCCCACTGCAGCCCCTAGCCCCTGTG  
AACCTTGCCTTTGACATGGCCGATGGGGTCAAGACCCAGTGCTAA

SEQ ID NO: 41\_Z36720\_H

ATGGACACAAAGCTGAACATGCTGAACGAGAAGGTGGACCAGCTCCTGCACTTCCAAGAA  
GATGTCACAGAGAAGTTGCAGAGCATGTGCCGAGACATGGGCCACCTGGAGCGGGGCCTG  
CACAGGCTGGAGGCCCTCCCGGGCACCGGGCCCCGGGCGGGCTGATGGGGTTCCCCACATT  
GACACCCAGGCTGGGTGGCCCGAGGTCTTGAGCTGGTGAGGGCCATGCAGCAGGATGCG  
GCCCAGCACGGTGCCAGGCTGGAGGCCCTCTTCAGGATGGTGGCTGCGGTGGACAGGGCC  
ATCGCTTTGGTGGGGGCCACGTTCCAGAAATCAAAGGTGGCGGATTTCTCATGCAGGGG  
CGTGTGCCCTGGAGGAGAGGCAGCCAGGTGACAGCCCTGAGGAGTGGGTAAAAGAGGAG  
GAGGTCTGTTTCATGCCTCCAGTTCCCCCAGCTCCGGGGGCAGCAGGACAGAGCCTGCAG  
AAGGATAAGGGGAGCTGTCTGCCGAGCAGGGGATCTGGGCCACATTGATGACGCTGGTG  
ATCATGGTGACAGCGGCAAATAAAGAGCGAGTGGAAGAAGAGGGAGGAAAACCAAAGCAT  
GTGCTGAGCACCAGTGGGGTGCACTGTATGCCAGGGAGCCTGGGGAAGAGAGCCAGAAG  
GCGGACGTGCTGGAGGGGACAGCGGAGAGGCTGCCCCCATCAGAGCGTCAGGGCTGGGA  
GCTGACCCCGCCAGGCAGTGGTCTCACCGGGCCAGGGAGATGGTGTTCCTGGCCCAGCC  
CAGGCATTCCCTGGCCACCTGCCCCCTGCCCAAAAGGTGGAAGCCAAGGCTCCTGAGACA  
CCCAGCGAGAACCTCAGGACTGGCCTGGAATTGGCTCCAGCACCCGGCAGGGTCAATGTG  
GTCTCCCCGAGCCTGGAGGTTGCACCAGGTGCAGGACAAGGAGCATCGTCCAGCAGGCCT  
GACCCTGAGCCCTTAGAGGAAGGCACGAGGCTGACTCCAGGGCCTGGCCCTCAGTGCCCA  
GGGCCTCCAGGGCTGCCAGCCAGGCCAGGGCAACCCACAGTGGTGGAGAAACACCTCCA  
AGGGCAGCCCTGCTGAAGGGCGCTGTGGCCCCGGGCTTCTCTCGGAGGGACCTGGTGT  
CCTAGCATCTTCTGCGCCTGCCTAGGGATCTCCATCCACATACAAGAGATGGATACTCCT

## FIGURE 2FF

GGGGAGATGCTGATGACAGGCAGGGGAGCCTTGGACCCACCCTCACCACAGAGGCTCCA  
GCAGCTGCCCAGCCAGGCAAGCAGGGCCACCTGGGACCGGGCGCTGCCTCCAAGCCCCCT  
GGGACTGAGCCCGGAGAACAGACCCCTGAAGGAGCCAGAGAGCTCTCCCCGCTGCAGGAG  
AGCAGCAGCCCCGGGGGAGTGAAGGCAGAGGAGGAGCAAAGGGCTGGGGCCGAGCCTGGC  
ACGAGACCAAGCTTGGCCAGGAGTGACGACAATGACCACGAGGTTGGGGCCCTGGGCCTG  
CAGCAGGGCAAAGCCAGGGGCGGGAAACCCTGAGCCTGAGCAGGACTGTGCAGCCAGG  
GCTCCGGTGAGAGCTGAAGCAGTAAGGAGGATGCCCCAGGCGCCGAGGCTGGCAGCGTG  
GTTCTGGATGACAGTCCGGCCCCACCAGCTCCTTTTGAACACCGGGTAGTGAGCGTCAAG  
GAGACCTCCATCTCTGCGGGTTACGAGGTGTGCCAGCACGAAGTCTTGGGAGGGGGTTCGG  
TTTGGCCAGGTCCACAGGTGCACAGAGAAGTCCACAGGCCTCCCACTGGCTGCCAAGATC  
ATCAAAGTGAAGAGCGCCAAGGACCGGGAGGACGTGAAGAACGAGATCAACATCATGAAC  
CAGCTCAGCCACGTGAACCTGATCCAGCTCTATGACGCCCTTCGAGAGCAAGCACAGCTGC  
ACCCTTGTTCATGGAGTACGTGGACGGGGGTGAGCTCTTCGACCGGATCACAGATGAGAAG  
TACCACCTGACTGAGCTGGATGTGGTCTGTTCACCAGGCAGATCTGTGAGGGTGTGCAT  
TACCTGCACCAGCACTACATCCTGCACCTGGACCTCAAGCCGGAGAACATATTGTGCGTC  
AATCAGACAGGACATCAAATTAAGATCATTGACTTTGGGCTGGCCAGAAGGTACAAGCCT  
CGAGAGAAGCTGAAGGTGAACCTTCGGCACTCCTGAGTTCTTGGCCCCAGAAGTCGTCAAT  
TATGAGTTTGTCTCATTCCCCACAGACATGTGGAGTGTGGGAGTCATCACCTACATGCTA  
CTCAGTGGCTTGTCCCCATTTCTAGGGGAAACAGATGCAGAGACCATGAATTTTCATTGTA  
AACTGTAGCTGGGATTTTGTGCTGACACCTTTGAAGGGCTCTCGGAGGAGGCCAAGGAC  
TTTGTTCCTCGGTGCTGGTCAAAGAGAAGAGCTGCAGAATGAGTGCCACACAGTGCCTG  
AAACACGAGTGGCTGAATAATTTGCCTGCCAAAGCTTCAAGATCCAAAACCTCGTCTCAA  
TCCCAACTACTGCTGCAGAAATACATAGCTCAAAGAAAATGGAAGAAACATTTCTATGTG  
GTGACTGCTGCCAACAGGTTAAGGAAATTTCCAACCTTCTCCCTAA

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GGGGAGATGGCGCTGTTTGAGTGCCTGGTGGCGGGGCCCACTGACGTGGAGGTGGATTGG  
CTGTGCCGTGGCCGCTGCTGCAGCCTGCACTGCTCAAATGCAAGATGCATTTTCGATGGC  
CGCAAATGCAAGCTGCTACTTACATCTGTACATGAGGACGACAGTGCGCTCTACACCTGC  
AAGCTCAGCACGGCCAAAGATGAGCTGACCTGCAGTGCCCGGCTGACCGTGCGGCCCTCG  
TTGGCACCCCTGTTTCACACGGCTGCTGGAAGATGTGGAGGTGTTGGAGGGCCGAGCTGCC  
CGTTTCGACTGCAAGATCAGTGGCACCCCGCCCCCTGTTGTTACCTGGACTCATTTTGGC  
TGCCCCATGGAGGAGAGTGAGAACTTGGCGCTGCGGCAGGACGGGGGTCTGCACTCACTG  
CACATTGCCCATGTGGGCAGCGAGGACGAGGGGCTCTATGCGGTCACTGCTGTTAACACC  
CATGGCCAGGCCCACTGCTCAGCCAGCTGTATGTAGAAGAGCCCCGGACAGCCGCTCA  
GGCCCCAGCTCGAAGCTGGAGAAGATGCCATCCATTCCCGAGGAGCCAGAGCAGGGTGAG  
CTGGAGCGGTGTCCATTCCCGACTTCTGCGGCCACTGCAGGACCTGGAGGTGGGACTG  
GCCAAGGAGGCCATGCTAGAGTGCCAGGTGACCGGCCTGCCCTACCCACCATCAGCTGG  
TTCCACAATGGCCACCGCATCCAGAGCAGCGACGACCGGCGCATGACACAGTACAGGGAT  
GTCCATCGCTTGGTGTTCCTGCCGTGGGGCTCAGCACGCCGGTGTCTACAAGAGCGTC  
ATTGCCAACAAAGCTGGGCAAAGCTGCCTGCTATGCCACCTGTATGTCACAGATGTGGTC  
CCAGGCCCTCCAGATGGCGCCCCGAGGTGGTGGCTGTGACGGGGAGGATGGTCACACTC  
ACATGGAACCCCCCAGGAGTCTGGACATGGCCATCGACCCGGAATCCCTGACGTACACA  
GTGCAGCACCAAGTGTGGCTCGGACAGTGGACGGCACTGGTTCACAGGCCTGCGGGAG  
CCAGGGTGGGCAGCCACAGGGCTGCGTAAGGGGGTCCAGCACATCTTCCGGGTCTCAGC  
ACCACTGTCAAGAGCAGCAGCAAGCCCTCACCCCTTCTGAGCCTGTGCAGCTGCTGGAG  
CACGGCCCAACCCTGGAGGAGGCCCTGCCATGCTGGACAAACCAGACATCGTGTATGTG  
GTGGAGGGACAGCTGCCAGCGTCACCGTCACATTCAACCATGTGGAGGCCAGGTCTGTC  
TGGAGGAGCTGCCAGGGGCCCTCTAGAGGCACGGGCCGGTGTGTACGAGCTGAGCCAG  
CCAGATGATGACCAGTACTGTCTTCGATCTGCCGGGTGAGCCGCCGGGACATGGGGGCC



## FIGURE 2GG

CTCACCTGCACCGCCCCGAAACCGTACGGCACACAGACCTGCTCGGTACATTGGAGCTG  
GCAGAGGCCCCCTCGGTTTGAGTCCATCATGGAGGACGTGGAGGTGGGGGCTGGGGAAACT  
GCTCGCTTTGCGGTGGTGGTTCGAGGGAAAACCACTGCCGGACATCATGTGGTACAAGGAC  
GAGGTGCTGCTGACCGAGAGCAGCCATGTGAGCTTCGTGTACGAGGAGAATGAGTGCTCC  
CTGGTGGTGTCTCAGCACGGGGGGCCAGGATGGAGGCGTCTACACCTGCACCGCCCCAGAAC  
CTGGCGGGTGAGGTCTCTGCAAAGCAGAGTTGGCTGTGCATTACAGCTCAGACAGCTATG  
GAGGTCGAGGGGGTGGGGAGGATGAGGACCATCGAGGAAGGAGACTCAGCGACTTTTAT  
GACATCCACCAGGAGATCGGCAGGGGTGCTTTCTCTACTTGCGGCGCATAGTGGAGCGT  
AGCTCCGGCCTGGAGTTTGCGGCCAAGTTCATCCCCAGCCAGGCCAAGCCAAAGGCATCA  
GCGCGTCGGGAGGCCCCGGCTGCTGGCCAGGCTCCAGCACGACTGTGTCTCTACTTCCAT  
GAGGCCTTCGAGAGGCGCCGGGACTGGTCATTGTACCGAGCTCTGCACAGAGGAGCTG  
CTGGAGCGAATCGCCAGGAAACCCACCGTGTGTGAGTCTGAGATCCGGGCCTATATGCGG  
CAGGTGCTAGAGGGAATACACTACCTGCACCAGAGCCACGTGCTGCACCTCGATGTCAAG  
CCTGAGAACCTGCTGGTGTGGGATGGTGTCTGCGGGCGAGCAGCAGGTGCGGATCTGTGAC  
TTTGGAATGCCAGGAGCTGACTCCAGGAGAGCCCCAGTACTGCCAGTATGGCACACCT  
GAGTTTGTAGACCCCGAGATTGTCAATCAGAGCCCCGTGTCTGGAGTCACTGACATCTGG  
CCTGTGGGTGTTGTTGCCTTCTCTGTCTGACAGGAATCTCCCCGTTTGTGGGGAAAAT  
GACCGGACAACATTGATGAACATCCGAAACTACAACGTGGCCTTCGAGGAGACCACATTC  
CTGAGCCTGAGCAGGGAGGCCCGGGGCTTCTCATCAAAGTGTTGGTGCAGGACCGGCTG  
AGACCTACCGCAGAAGAGACCCTAGAACATCCTTGTTTCAAAACTCAGGCAAAGGGCGCA  
GAGGTGAGCACGGATCACCTGAAGCTATTCTCTCTCCCGCGGAGGTGGCAGCGCTCCAG  
ATCAGCTACAAATGCCACCTGGTGTCTGCGCCCCATCCCCGAGCTGCTGCGGGCCCCCCCCA  
GAGCGGTGTGGGTGACCATGCCAGAAGGCCACCCCCAGTGGGGGGCTCTCATCCTCC  
TCGATTCTGAAGAGGAAGAGCTGGAAGAGCTGCCCTCAGTGCCCCGCCACTGCAGCCC  
GAGTTCTCTGGCTCCCGGTGTCCCTCACAGACATTCCCACTGAGGATGAGGCCCTGGGG  
ACCCAGAGACTGGGGCTGCCACCCCCATGGACTGGCAGGAGCAGGGAAGGGCTCCCTCT  
CAGGACCAGGAGGCTCCAGCCCAGAGGCCCTCCCCCTCCCCAGGCCAGGAGCCCCGAGCT  
GGGGCTAGCCCCAGGCGGGGAGAGCTCCGCAGGGGCAGCTCGGCTGAGAGCGCCCTGCCC  
CGGGCCGGGCCGCGGGAGCTGGGCGGGGCTGCACAAGGCGGCGTCTGTGGAGCTGCCG  
CAGCGCCGAGCCCCGGCCCCGGGAGCCACCCGCTGGCCCGGGGAGGCCTGGGTGAGGGC  
GAGTATGCCAGAGGCTGCAGGCCCTGCGCCAGCGGCTGCTGCGGGGAGGCCCCGAGGAT  
GGCAAGGTGAGCGGCCTCAGGGGTCCCTGCTGGAGAGCCTGGGGGGCCGTGCTCGGGAC  
CCCCGATGGCACGAGCTGCCCTCAGCGAGGCAGCGCCCCACCACAGCCCCCACTCGAG  
AACCGGGCCTGCAAAAGAGCAGCAGCTTCTCCAGGGTGAGGCGGAGCCCCGGGGCCGG  
CACCGCCGAGCGGGGGCGCCCCCTCGAGATCCCCGTGGCCAGGCTTGGGGCCCCGTAGGCTA  
CAGGAGTCTCCTTCCCTGTCTGCCCTCAGCGAGGCCAGCCATCCAGCCCTGCACGGCCC  
AGCGCCCCCAAACCCAGTACCCCTAAGTCTGCAGAACCTTCTGCCACCACACCTAGTGAT  
GCTCCGAGCCCCCGCACCCAGCCTGCCCAAGACAAGGCTCCAGAGCCCAGGCCAGAA  
CCAGTCCGAGCCTCCAAGCCTGCACCAACCCCCAGGCCCTGCAAACCTAGCGCTGCCC  
CTCACACCTATGCTCAGATCATTCAGTCCCTCCAGCTGTGAGGCCACGCCAGGGCCCC  
TCGAGGGCCCTGCCGCGCCGCTTCAGAGCCCAAGCCCCACGCTGCTGTCTTTGCCAGG  
GTGGCTCCCCACCTCCGGGAGCCCCCGAGAAGCGCGTGCCTCAGCCGGGGGTCCCCCG  
GTGCTAGCCGAGAAAGCCCCGAGTTCCACGGTGCCCCCAGGCCAGGCAGCAGTCTCAGT  
AGCAGCATCGAAACTTGAGTTCGGAGGCCGTGTTTCGAGGCCAAGTTCAAGCGCAGCCGC  
GAGTCGCCCCCTGTGCTGGGGCTGCGGCTGCTGAGCCGTTTCGCGCTCGGAGGAGCGCGC  
CCCTTCGTGGGGCCGAGGAGGAGGATGGCATATACCGGCCAGCCCCGGCGGGGACCCCG  
CTGGAGCTGGTGCACGGCCTGAGCGCTCACGCTCGGTGCAGGACCTCAGGGCTGTCCGA  
GAGCCTGGCCTCGTCCGCCGCTCTCGCTGTCACTGTCCCAGCGGCTGCGGCGGACCCCT  
CCCGCGCAGCGCCACCCGGCCTGGGAGGCCCGCGCGGGGACGGAGAGAGCTCGGAGGGC  
GGGAGCTCGGCGGGGGCTCCCCGGTGTGGCGATGCGCAGGCGGCTGAGCTTACCCCTG

FIGURE 2HH

GAGCGGCTGTCCAGCCGATTGCAGCGCAGTGGCAGCAGCGAGGACTCGGGGGGCGCGTCG  
GGCCGCGAGCACGCCGCTGTTTCGGACGGCTTCGACGGGCCACGTCCGAGGGCGAGAGTCTG  
CGGCGCCTTGCGCTTCCGCAACAACAGTTGGCCGCCAGGCCGGCGCCACCACGCCTTCC  
GCCGAGTCCCTGGGCTCCGAGGCCAGCGCCACGTTCGGGCTCCTCAGCCCCAGGGGAAAGC  
CGAAGCCGGCTCCGCTGGGGCTTCTCTCGGCCGCGGAAGGACAAGGGGTATATCGCCACCA  
AACCTCTCTGCCAGCGTCCAGGAGGAGTTGGGTACACAGTACGTGCGCAGTGAGTCAGAC  
TTCCCCCAGTCTTCCACATCAAACCTCAAGGACCAGGTGCTGCTGGAGGGGGAGGCAGCC  
ACCTTGCTCTGCCTGCCAGCGGCCCTGCCCTGCACCGCACATCTCCTGGATGAAAGACAAG  
AAGTCCTTGAGGTCAGAGCCCTCAGTGATCATCGTGTCTTGCAAAGATGGGCGGCAGCTG  
CTCAGCATCCCCCGGGCGGGCAAGCGGCACGCCGGTCTCTATGAGTGCTCGGCCACCAAC  
GTACTGGGCAGCATCACCAGCTCCTGTACCGTGGCTGTGGCCCCGAGTCCAGGAAAGCTA  
GCTCCTCCAGAGGTAACCCAGACCTACCAGGACACGGCGCTGGTGCTGTGGAAGCCGGGA  
GACAGCCGGGCACCTTGCACGTATACGTGGAGCGGCAGTGAGTGGGAGTCTGTGTGG  
CACCTGTGAGCTCAGGCATCCCCGACTGTTACTACAACGTGACCCACCTGCCAGTTGGC  
GTGACTGTGAGGTTCCGTGTGGCCTGTGCCAACCCTGCTGGGCAGGGGGCCCTTCAGCAAC  
TCTTCTGAGAAGGTCCTTGTTCAGGGGTACTCAAGATTCTTCAGCTGTGCCATCTGCTGCC  
CACCAAGAGGCCCCCTGTACCTCAAGGCCAGCCAGGGCCCCGGCCTCCTGACTCTCCTACC  
TCACTGGCCCCACCCCTAGCTCCTGCTGCCCCACACCCCGTCAGTCACTGTAGCCCC  
TCATCTCCCCCACACCTCCTAGCCAGGCCCTGTCTCTCGCTCAAGGCTGTGGGTCCACCA  
CCCCAAACCCCTCCACGAAGACACAGGGGCCCTGCAGGCTGCCCCGGCCAGCGGAGCCCACC  
CTACCCAGTACCCACGTACCCCCAAGTGAGCCCAAGCCTTTCGTCTTTCGACTGGGACC  
CCGATCCAGCCTCCACTCCTCAAGGGGTAAACCAGTGCTTCTCCTACTCCTGTGTAT  
GTGGTGACTTCTTGTGTCTGCACCACAGCCCCCTGAGCCCCCAGCCCCCTGAGCCCCCT  
CCTGAGCCTACCAAGGTGACTGTGCAGAGCCTCAGCCCCGCCAAGGAGGTGGTCAGCTCC  
CCTGGGAGCAGTCCCCGAAGCTCTCCAGGCCCTGAGGGTACCACTCTTCGACAGGGTCCC  
CCTCAGAAACCCCTACACCTTCTTGAGGAGAAAGCCAGGGGGCCGCTTTGGTGTTGTGCGA  
GCGTGCCGGGAGAAATGCCACGGGGCGAACGTTTCGTGGCCAAGATCGTGCCCTATGCTGCC  
GAGGGCAAGCCGCGGGTCTTCAGGAGTACGAGGTGCTGCGGACCCTGCACCACGAGCGG  
ATCATGTCCCTGCACGAGGCCTACATCACCCCTCGGTACCTCGTGCTCATTGCTGAGAGC  
TGTGGCAACCGGGAACCTCCTCTGTGGGCTCAGTGACAGGTTCCGGTATTCTGAGGATGAC  
GTGGCACTTACATGGTGAGCTGCTACAAGGCCTGGACTACCTCCACGGCCACCACGTG  
CTCCACCTAGACATCAAGCCAGACAACCTGCTGCTGGCCCCCTGACAATGCCCTCAAGATT  
GTGGACTTTGGCAGTGCCAGCCCTACAACCCCCAGGCCCTTAGGCCCTTGGCCACCGC  
ACGGGCACGCTGGAGTTCATGGCTCCGGAGATGGTGAAGGGAGAACCCATCGGCTCTGCC  
ACGGACATCTGGGGAGCGGGTGTGCTCACTTACATTATGCTCAGTGGACGCTCCCCGTTT  
TATGAGCCAGACCCCCAGGAAACGGAGGCTCGGATTGTGGGGGGCCGCTTTGATGCCTTC  
CAGCTGTACCCCAATACATCCCAGAGCGCCACCTCTTCTTGCGAAAGGTTCTCTCTGTA  
CATCCCTGGAGCCGGCCCTCCCTGCAGGACTGCCTGGCCCCACCCATGGTTGCAGGACGCC  
TACCTGATGAAGCTGCGCCGCCAGACGCTCACCTTCACCACCAACCGGCTCAAGGAGTTC  
CTGGGCGAGCAGCGGCGGCGCCGGGCTGAGGCTGCCACCCGCCACAAGGTGCTGCTGCGC  
TCCTACCCCTGGCGGCCCTTAGAGGCACGGACCACAGCCAGGCCCTCGGGCTTCAACTGGGG  
TTCCCACCAATGCCACGGGACATTCCAGGGGCCACGCTGAGCCAGGCGGGCCTGGGGCTT  
CGGTTACCACCAGCAGCAACATCTGGCTGGGCTCTTACCTCATAGACCTTCAAGGACAGA  
GACCCAGGGCCTGGACCTGATGCCACCCACAGGCCAAAGCCAGAGTGGGAGACCCATTGG  
TCAGGCTCAGCAGGGTGGGAACAGGCAGAGGACAAGAGGGGAATGGAGAAGTGGAGAGG  
AAAAGGAATCGAGGGACAGGAAGGGGGAGGCTCTAGGAAGGTTCTGGGTTGGGGGTGAGT  
GCATCTCAGGGAGAACCAAGGAAGGTGGGCATGGCTGGAGAGGAGGAAAAGGAAGGAGCC  
CCAGGTGTCAGGGCAGTAGGCTGGGAGTCAGTGTGGCAAAGCGGGGGCAGGACACAGATA  
CAGTGGCAGGGGGCCAGGGCTGGGACATGAGAGAAGGCAGCGAGCGGCAGAGGGAGAAG  
AGAGGACTCAGGTGGAGGTGGGGTGGGTGAGCTGTAGCATCCCTCAGAGGAGAAATGTG

## FIGURE 2II

GAGAGCTGGAGGCCAGCAGTCACTCACACTCGCTCTGTCTCCTGTCCAGTGGATACAGC  
CCTGGGCGCTCTGCTGGCCCAAGGATGTCCCCACTGCCCCTCCATGGCCTTTGGCCTTCT  
TCCCATTCATATTTATTTATTTATTGACTTTTATGAAGTTTCCCCTTCCATCCGATCCCT  
ACTGCCCATGTTGTCTGACCATCCCTCCCAGCCATCCAGCTGTCTGTCTGTCTGCCACA  
AGGAAATAAAAATGGCAAGCAGCAAAAAA

SEQ ID NO: 43\_AA542015\_M SGK088\_M

GCCACGGACATCTGGGGAGCGGGTGTGCTCACTTACATCATGCTTAGTGGGTACTCCCCA  
TTCTATGAGCCAGACCCCCAGGAAACAGAGGCTCGGATTGTTGGGGGTCTGCTTTGATGCC  
TTCCAGTTGTATCCTAACACATCCCAGAGTGCCACCCCTCTTCTTGAGAAAGGTCTCTCA  
GTACATCCCTGGAGCCGGCCCTCTCTGCAGGACTGCTTGGCCCAACCATGGCTGCAAGAT  
GCCTACCTGATGAAGCTGCGCCGCCAGACACTCACCTTACCACCAACCGGCTCAAGGAA  
TTCCTGGGCGAGCAGCGGGCAGCTCGGGCTGAGGCTGCTACCCGTCACAAGGTGCTGCTC  
CGCTCCTACCCCTGGCAGCCCCCTAGGTGGCACAGACCGCAGCCCGGCCACGGGCTTCAACT  
TGGGTTCTCACTCGCGCTGCCAAGGGACATTCCAGAGCCCATGCTGAGCTGGACAGGCAG  
GGGCTTCAGATACCAGCAGCAGCAGCAGCAGCAGCAGCAACATCTGGCTGGGCTATT  
ACCTCATGGACCTAAGAGGACAAGGCCCTGGGGCTTCAGCCGAATGTCACCCCGGCCATA  
ACCAGAGCAGGAGACCCACTGGCCAGGCTGGGCAAGGGTGAGAGCAGAAAGAGGCAAGA  
GGGAGTTGGGAAGTGAAGAATGAGACGGAGGATAGAGAGGGAGGAGTTTGAGGAAGGTTT  
TAGGCTGGAGTGAATGCTATATCTCAGGGAGAAGCCAGAAGGGGACATGGCTGAAGAGG  
AAGAAGGACCTGTGATGTGGGAATGTGGTGGAGAGGAGGACTGGACATAGAGAGTGTGC  
CAGGAGCCAGAGCAGAGACATAAGGGAGGGCAGAAGGGTAGAAGGCAACAGGAGTGGGCT  
CAGGGGTGGCAGGGCAGGCCAGCAGCTGCATCTTCAGAAAGAGAGAGGAGAAAGGCAAAAG  
AGACGAAAGGCCGCTCCAGCTGGTCTCCTGTCCCAGCCGATGCAGTTCTGGGCGTTCTCC  
ACTGGCCAGGGATGTCTCACTGCTCCTCCATGGCCTTTGCCCTCCTTCCCATTGTAT  
TTATTTATTTATTGCCTTTTGTGGAGTTTCTTTCTATCCAGTCCCTAGTGCCTATGTTG  
TCCCGACCATCCCCCTTCAGTCACCCAGCTGTCTGTGCAGCTGTCTGTCTGTCTGTCTCACA  
AGGAAATAAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAGC

SEQ ID NO: 44\_R19772\_H

ATGAAGGGCGGCGACAGGGCTTACACCCGAGGTCCCTCTTTGGGGTGGCTCTTTGCTAAG  
TGCTGCTGTTGCTTCCCGTGTAGAGATGCATACTCTCATTCCCTCAAGCGAGAATGGAGGC  
AAGTCCGAGTCCGTAGCCAACCTGCAGGCCCAGCCCTCCCTGAACCTTCATCCACAGTTCC  
CCGGGTCCCAAGCGCTCCACCAACACTCTTAAGAAAGTGGCTGACGAGTCTGTGCGTCGG  
CTCAACAGCGGGAAGGCAGATGGAAACATCAAAAAGCAGAAGAAAGTTCGCGATGGTCGG  
AAGAGCTTTGACCTGGGATCTCCCAAGCCTGGGGATGAAACAACCCCTCAGGGAGACAGC  
GCTGATGAGAGCAAGAAAGGTTGGGGTGAAGATGAGCCGGATGAAGAGTCACACACACCC  
CTCCCACCACCTATGAAGATTTTGAACAACGACCCTACACAGGATGAAATGTCCTCCTCT  
TTGCTAGCAGCCCGGCAGGCTTCCACTGAAGTACCTACTGCTGCAGACCTTGTCAATGCA  
ATAGAAAAGTTGGTCAAAAACAAGCTGAGTCTAGAAGGAAGCTCATAACGGGGGAGCTTG  
AAAGACCCTGCAGGCTGCCTGAATGAGGGGATGGCCCCACCCACACCTCCTAAAAATCCA  
GAAGAAGAACAGAAAGCCAAGGCCCTGAGAGGCAGGATGTTTGTCTGAATGAGCTGGTA  
CAGACAGAGAAAGACTATGTCAAGGATCTGGGCATTGTGGTGGAGGGCTTCATGAAGAGA  
ATAGAAGAAAAGGTTGTCCCTGAGGATATGCGAGGAAAGGACAAAATCGTGTTTGGAAAT  
ATTCATCAGATTTATGACTGGCATAAGGATTTTTTCTGGCGGAACTGGAAAAGTGTATC  
CAGGAGCAAGACAGATTGGCACAGCTCTTTATTAAGCACGAGCGGAAGCTGCACATCTAC  
GTGTGGTATTGTGAGAATAAGCCGCGCTCAGAGTACATCGTTGCTGAGTATGACGCCTAC  
TTTGAGGAGGTAAAACAGGAGATAAATCAGAGGCTGACACTGAGTGAAGTTCCTCATCAAG  
CCCATTTCAGAGAATAACAAAATACCAAGTTGCTCCTCAAGGACTTCCTGAGATACAGTGAG  
AAGGCTGGTTTGGAGTGTTTCAGATATCGAGAAAGCAGTGGAGTTAATGTGCCTTGTTC

FIGURE 2JJ

AAACGCTGCAATGACATGATGAATCTAGGACGTCTGCAGGGCTTTGAGGGCACTCTGACT  
GCTCAGGGGAAGCTACTGCAGCAGGACACATTCTATGTGATCGAGCTGGATGCAGGCATG  
CAGTCCCGGACCAAAGAGAGGGCGGTGTTCTCTTCGAGCAGATTGTCATCTTCAGTGAA  
CTGCTCAGGAAGGGATCCCTCACCCCTGGCTACATGTTCAAAGGAGCATCAAGATGAAT  
TACTTGGTCCTGGAGGAGAATGTGGACAATGATCCCTGCAAGTTTGCACTCATGAACAGA  
GAGACTTCTGAGAGGGTTGTTCTGCAAGCCGCCAACGCTGACATCCAGCAGGCCTGGGTG  
CAGGACATCAATCAAGTCTTAGAAACACAGCGAGACTTTTTGAATGCACTGCAATCGCCC  
ATTGAGTATCAACGGAAAGAAAGGAGCACAGCTGTGATGAGGTCTCAACCTGCCAGGCTT  
CCCCAAGCCAGCCCCAGGCCCTACTCCTCTGTTCTGCGGGCTCAGAGAAGCCCCCAAAG  
GGCTCCAGCTATAACCCACCTCTGCCCTCCCCTGAAGATATCTACCTCCAATGGCAGTCCA  
GGGTTTGAATACCACCAGCCTGGGGACAAGTTCGAAGCCAGCAAGAACGACCTGGGAGGC  
TGCAATGGGACCTCGTCCATGGCCGTGATCAAAGATTACTATGCACTGAAGGAGAATGAA  
ATCTGTGTGAGCCAAGGTGAGGTGGTCCAGGTCTCGCCGTCAACCAGCAGAACATGTGT  
CTGGTGTACCAGCCTGCCAGCGACCATTCCCCCGCCGCCGAGGGCTGGGTCCCAGGCAGC  
ATCCTGGCGCCCCCTACCAAAGCCACAGCAGCAGAAAGTAGTGACGGGAGCATCAAGAAG  
TCATGTTTATGGCATACTCTACGCATGAGAAAGCGGGCGGAAGTGGAGAACACGGGTAAA  
AATGAAGCCACAGGGCCTCGTAAACCCAAGGATATTCTGGGCAACAAAGTCTCTGTAA  
GAGACGAACAGTTCCGAGGAATCAGAGTGTGATGATCTTGACCCTAATACTAGCATGGAG  
ATCTTAAATCCAAATTTTATCCAAGAAGTGGCCCCAGAATTCTTGTGCCCTTGGTGGAT  
GTGACCTGCTTGCTTGGGGACACAGTGATACTGCAGTGCAAAGTCTGTGGGCGGCCAAAG  
CCCACCATCACTTGGGAAGGTCCAGACCAGAACATCCTTGACACTGATAACAGCTCAGCC  
ACATACACGGTCTCCTCTTGTGATTCTGGAGAAATCACCTGAAGATCTGTAATCTGATG  
CCCCAAGACAGTGGGATTTTATACCTGCATAGCAACAAATGACCACGGGACCACATCAACG  
TCTGCAACAGTCAAAGTGCAAGGTGTTCCAGCAGCCCCCTAACCGCCCCATTGCCCAGGAG  
AGAAGCTGCACCTCCGTGATTCTCCGCTGGCTGCCCCCTCCAGCACAGGAACTGCACT  
ATTTCTGGTTTACACTGTGGAGTACAGAGAGGAAGGTTCTCAGATCTGGCAGCAGTCAGTG  
GCTTCGACCTTGGACACTTACCTCGTCATCGAAGACCTTAGTCCCGGGTGCTCTTATCAG  
TTCAGAGTCAGTGCCAGTAACCCCTGGGGAATCAGCCTTCCCAGCGAGCCCTCGGAGTTT  
GTGCGACTTCCAGAATACGATGCTGCTGCTGATGGTGCCACCAATTTCTTGGAAGGAAAAAT  
TTTGACTCAGCTTACACTGAGCTGAATGAAATTGGAAGAGGCGGTTTCTCTATAGTAAAG  
AAATGCATTACAAAGCTACCCGCAAAGATGTGGCTGTGAAATTTGTAAACAAAAAATG  
AAGAAGAAAGAACAGGCTGCCCACGAGGCTGCCCTGCTTCAGCACCTACAGCACCCCCAG  
TACATCACTCTCCATGACACCTATGAGTCCCCCACATCCTACATCCTGATCTTGGAAGTG  
ATGGATGATGGCCGGCTCTTAGACTACCTTATGAATCATGATGAACTGATGGAGGAAAAA  
GTAGCTTTCTATATCCGAGACATCATGGAGGCTCTGCAGTACCTTCACAACTGCAGGGTT  
GCACATTTGGACATAAAGCCTGAAAACTGCTCATTGACCTACGGATTCCAGTGCCTCGA  
GTGAAGCTCATTGACTTGGAGGATGCTGTCCAGATCTCGGGTCACTTCCACATTCACCAC  
CTGCTGGGGAACCCCTGAGTTTGCTGCCCCAGAAGTCATTCAAGGCATCCCCGTCTCCCTG  
GGGACAGACATCTGGAGCATCGGGGTTCTGACATATGTCATGCTGAGTGGGGTCTCCCC  
TTCTTGATGAGAGCAAAGAGGAGACATGTATCAACGTATGCAGGGTGGATTTAGCTTC  
CCCCATGAATACTTCTGTGGTGTGAGCAATGCTGCCAGAGATTTTATCAATGTGATCTTA  
CAGGAAGATTTTCGAGGCGGCCACAGCAGCCACATGCTTGAGCATCCATGGCTGCAG  
CCCATAATGGCAGCTACTCTAAGATCCCCCTGGACACCTCCCGCTAGCATGCTTCATA  
GAACGTCGCAAGCACCAGAATGATGTGCGGCCATCCCCAATGTCAAGAGCTACATTGTCT  
AACC GGTTGAACCAAGGGACGTAG

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CGCCGCTGTTTGTCTCGCGCGGCCCGTCCACTGCCCTGCGGTTGCTCTGCGGGCTGAA  
AAGTTTCTCCCGGTGCAGAATTCGGGGCTCAGCGACAGCCTGCGCCGAGTGTGCGCACCT  
GTCGGAGACCCGCCAGTCCGCGGGCCCCGGCTTTGTTGCTGCGGAAGTGTAGTGGTGAGA

## FIGURE 2KK

AAAACCTCCATGTCTGGGCACGCCTGGCTGATCTTCACCTCTTTCTTCTAGGACCTTCCTC  
TGGGCTGTACGTGTGAATATGTGTCTAGTGCATCCTTAACCTGAGGACTTCACCAGTTC  
GAAATTACAGTTTTCACCATCAACTACCTTATCCTTTTGGCCTGGTTTTCTTCCTCAAA  
CAGTGGAACATTTTTAAAGTTGCTTTTGTTCAGAGTTAAACAAATGGCTGATAGTGGC  
TTAGATAAAAAATCCACAAAATGCCCCGACTGTTTCATCTGCTTCTCAGAAAAGATGTACTT  
TGTGTATGTTCCAGCAAAACAAGGGTTCCTCCAGTTTGGTGGTGGAAATGTCACAGACA  
TCAAGCATTGGTAGTGCAGAATCTTTAATTTCACTGGAGAGAAAAAAGAAAAAATATC  
AACAGAGATATAACCTCCAGGAAAGATTTGCCCTCAAGAACCTCAAATGTAGAGAGAAAA  
GCATCTCAGCAACAATGGGGTCGGGGCAACTTTACAGAAGGAAAAGTTCCTCACATAAGG  
ATTGAGAATGGAGCTGCTATTGAGGAAATCTATACCTTTGGAAGAATATTGGGAAAAGGG  
AGCTTTGGAATAGTCATTGAAGCGACAGACAAGGAAACAGAAACGAAGTGGGCAATTAAA  
AAAGTGAACAAAGAAAAGGCTGGAAGCTCTGCTGTGAAGTTACTTGAACGAGAGGTGAAC  
ATTCTGAAAAGTGTAACCATGAACACATCATACATCTGGAACAAGTATTTGAAACGCCA  
AAGAAAATGTACCTTGTGATGGAGCTTTGTGAGGATGGAGAACTCAAAGAAATTTCTGGAT  
AGGAAAGGGCATTTCTCAGAGAATGAGACAAGGTGGATCATTCAAAGTCTCGCATCAGCT  
ATAGCATATCTTCACAATAATGATATTGTACATAGAGATCTGAAACTGGAAAAATATAATG  
GTTAAAAGCAGTCTTATTGATGATAACAATGAAATAAACTTAAACATAAAGGTGACTGAT  
TTTGGCTTAGCGGTGAAGAAGCAAAGTAGGAGTGAAGCCATGCTGCAGGCCACATGTGGG  
ACTCCTATCTATATGGCCCCGTAAGTTATCAGTGCCACGACTATAGCCAGCAGTGTGAC  
ATTTGGAGCATAGGAGTCGTAATGTACATGTTATTACGTGGAGAACCACCTTTTTGGCA  
AGCTCAGAAGCGAAGCTTTTTGAGTTAATAAGAAAAGGAGAACTACATTTTGAAAATGCA  
GTCTGGAATTCATAAGTGACTGTGCTAAAAGTGTTTTGAAACAACCTTATGAAAGTAGAT  
CCTGCTCACAGAATCACAGCTAAGGAACTACTAGATAACCAGTGGTTAACAGGCAATAAA  
CTTTCTTCGGTGAGACCAACCAATGTATTAGAGATGATGAAGGAATGGAAAAATAACCCA  
GAAAGTGTGAGGAAAAACAACAGAAGAGAAGAATAAGCCGTCCACTGAAGAAAAGTTG  
AAAAGTTACCAACCTTGGGGAATGTCCCTGAGACCAATTACACTTCAGATGAAGAGGAG  
GAAAAACAGTCTACTGCTTATGAAAAGCAATTTCTTGCAACCAGTAAGGACAACTTTGAT  
ATGTGCAGTTCAAGTTTCACATCTAGCAAACTCCTTCCAGCTGAAATCAAGGGAGAAATG  
GAGAAAACCCCTGTGACTCCAAGCCAAGGAACAGCAACCAAGTACCCTGCTAAATCCGGC  
GCCCTGTCCAGAACCAAAAAGAACTCTAAGGTTCCCTCCAGTGTTGGACAGTACAAAAA  
CAAAGCTGCTCTTGTAGCACTTTGATGAGGGGGTAGGAGGGGAAGAAGACAGCCCTATG  
CTGAGCTTGTAGCCTTTTAGCTCCACAGAGCCCCGCCATGTGTTTGCACCAGCTTAAAT  
TGAAGCTGCTTATCTCAAAGCAGCATAAGCTGCACATGGCATTAAGGACAGCCACCAG  
TAGGCTTGGCAGTGGGCTGCAGTGGAAATCAACTCAAGATGTACACGAAGGTTTTTTAGG  
GGGGCAGATACCTTCAATTTAAGGCTGTGGGCACACTTGCTCATTTTTACTTCAAATTTCT  
TATGTTTAGGCACAGCTATTTATAGGGGAAAAACAAGAGGCCAAATATAGTAATGGAGGTG  
CCAAATAATTATGTGCACTTTGCACTAGAAGACTTTGTTAGAAAATTACTAATAAACTTG  
CCATACGTATTACAGCAGAAGTGCTTCAGTCATTCACATGTGTTTCGTGAGATTTTAGGTT  
GCTATAGATTGTTTAAGACAGCTTATTTTAAATGTAGAAAAATAGGAGATTTTGTAAGTG  
CTTGCCATTAACTTGCTGCTAAATTCCCAATGTATTGATTAAATCAATAAAAAACAGATG  
TTACTC

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GGGTCCGCAGCCCCGCCCTCACAGGCCCTCCTCACTCCCCCTAGGTAGATGGCCCCCTCAGG  
GCAGGCCCGGCGGACACCCCTCCCTCTGGCTGGCGGATGCAGTGCCTAGCGGCCCGCCCTT  
AAGGACGAAACCAACATGAGTGGGGGAGGGGAGCAGGCCGACATCCTGCCGGCCAACTAC  
GTGTTCAAGGATCGCTGGAAGGTGCTGAAAAAGATCGGGGGCGGGGCTTTGGTGAATC  
TACGAGGCCATGGACCTGCTGACCAGGGAGAATGTGGCCCTCAAGGTGGAGTCAGCCAG  
CAGCCCAAGCAGGTCTCAAGATGGAGGTGGCCGTGCTCAAGAAGTTGCAAGGTTCCGGC  
CTCGGGCAGGGGGATGGGAAGGAAGAGATGATGAAGCCAGGGGCTAAGAGAGGGAAGGAC

## FIGURE 2LL

CATGTGTGCAGGTTTCATTGGCTGTGGCAGGAACGAGAAAGTTTAACTATGTAGTGATGCAG  
CTCCAGGGCCGGAACCTGGCCGACCTGCGCCGTAGCCAGCCGCGAGGCACCTTCACGCTG  
AGCACCACATTGCGGCTGGGCAAGCAGATCTTGGAGTCCATCGAGGCCATCCACTCTGTG  
GGCTTCCTGCACCGTGACATCAAGCCTTCAAACCTTTGCCATGGGCAGGCTGCCCTCCACC  
TACAGGAAGTGCTATATGCTGGACTTCGGGCTGGCCCGGCAGTACACCAACACCACGGGG  
GATGTGCGGCCCCCTCGGAATGTGGCCGGGTTTCGAGGAACGGTTTCGCTATGCCTCAGTC  
AATGCCCCACAAGAACCAGGAGATGGGCCGCCACGACGACCTGTGGTCCCTCTTCTACATG  
CTGGTGGAGTTTGCAGTGGGCCAGCTGCCCTGGAGGAAGATCAAGGACAAGGAACAGGTA  
GGGATGATCAAGGAGAAGTATGAGCACCAGGATGCTGCTGAAGCACATGCCGTCAGAGTTC  
CACCTCTTCTGGACCACATTGCCAGCCTCGACTACTTCACCAAGCCCCGACTACCAGTTG  
ATCATGTGAGTGTGAGAACAGCATGAAGGAGAGGGGCATTGCCGAGAATGAGGCCTTT  
GACTGGGAGAAGGCAGGCACCGATGCCCTCCTGTCCACGAGCACCTCTACCCCCGCCCCCA  
GCAGAACACCCGGCAGACGGCAGCCATGTTTGGGGTGGTCAATGTGACGCCAGTGCCCTGG  
GGACCTGCTCCGGGAGAACACCCGCGGATGTGCTACAGGGAGAGCACCTGAGTGACCAGGA  
GAATGCACCCCCAATTCTGCCCGGGAGGCCCTCTGAGGGGCTGGGCCACAGTCCCCACCT  
TGTCCCCACCCCGGGGTCTGAGGCTGAAGTCTGGGAGGAGACAGATGTCAACCGGAA  
CAAACCTCCGGATCAACATCGGCAAAGTAAGTCCCGCCAGGGCGAAGGGCGTGGGTGGCCT  
TTTCTCTCACCCCCGATTCCAGCCTTGTGCCCTGCCCTGTTCTCTAAGCACCCCTGT  
CCCCGCCAATCTCCCTGCTTGCCCGGCCTCTGTTTCCGGTCCCCTCCCCGGCACTAGCC  
TCGCTGTGTCTTCCATCATCATCATCCTCTGTCTCCTTCACACTGAGGAGACCATCCGCC

SEQ ID NO: 47\_AA234451\_H

GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCGGCGGCGGCGGCAGGAGGGG  
GAGCAGGTGCTGGCACAAGAGCAGCGGCTTGGGGGAGCCGGCAGCAGCAGTAACAGCAGC  
AGCAGCCGCCGCCGCCGCCAGTAAACGCGGACCGTACCCAGGGGACTACCCAGCCG  
GCCGGCCCTGGAAGCCGCGCTCGGGTCCCGCCGCGAGTCGGCGGTGGGGGATGGGCAGGCA  
GTGGCGGTCCCGCCTGCCGAGGGTTAACCCCGCCGGTCCCGGTCTGAGCTGGACCAGA  
GCCCTCCTCCAGAAACCCCTGCGTCCGCCACGGCCAGGTTAAATGGAAACCACCCTTGG  
GAACTGGATGCCTGTGTAGCTGTTCTACCATATCAGTGTATTGCAATGAGTGGGGGAGGA  
GAGCAGCTGGATATCCTGAGTGTGGAATCCTAGTGAAAGAAAGATGGAAAGTGTGAGA  
AAGATTGGGGGTGGGGGCTTTGGAGAAATTTACGATGCCTTGGACATGCTCACCAGGGAA  
AATGTTGCACTGAAGGTGGAATCAGCTCAACAACCAAAACAAGTTCTGAAAATGGAAGTT  
GCTGTTTTGAAAAGCTGCAAGGGAAAGACCATGTTTGTAGATTTATTGGCTGTGGGAGG  
AATGATCGATTCAACTATGTGGTCATGCAGTTGCAGGGTCGGAATCTGGCAGATCTTCGC  
CGTAGCCAGTCCCGAGGCACATTACCATTAGTACCACTCTCCGGCTGGGTAGACAGATT  
TTGGAGTCTATTGAAAGCATTCAATTCTGTGGGATCTTGNCATCGAGACATCAAACCGTCG  
AACTTCGCTATGGGTCGCTTTCTAGTACATGTAGGAAATGTTACATGCTTGATTTTGGC  
TTGGCTCGACAATTTACCAATTCCTGTGGTGACGTGAGACCACCTCGAGCTGTGGCAGGT  
TTTCGAGGGACAGTTCGTTATGCATCAATCAACGCACATCGGAACAGGGAAATGGGAAGA  
CATGATGACCTTTGGTCCTTATTCTACATGTTGGTGGAGTTTGTGGTTGGTCAGCTGCCC  
TGGAGAAAAATAAAGGACAAGGAGCAAGTAGGCTCTATTAAGGAGAGATATGACCACAGG  
CTCATGTTGAAACATCTCCCTCCAGAATTCAGCATCTTTCTAGACCATATCTCTTCTTG  
GATTATTTTACAAAACCAAGACTACCAGCTTCTTACATCCGTGTTTGACAATAGCATCAAG  
ACTTTTGGAGTAATTGAGAGTGACCTTTTGGACTGGGAGAAGACTGGAAATGATGGCTCC  
CTAACAACCACCACTACTTCTACCACCCCTCAGTTGCACACTCGCTTGACCCCTGCTGCA  
ATTGGAATTGCCAATGCTACTCCCATCCCTGGAGACTTGCTTCGAGAAAATACAGATGAG  
GTATTTCCAGATGAACAGCTTAGCGATGGAGAAAATGGCATCCCTGTTGGTGTGTACCA  
GATAAATTGCCTGGATCTCTGGGACACCCCCGTCCCCAGGAGAAGGATGTTTGGGAAGAG  
ATGGATGCCAACAAAAACAAGATAAAGCTTGGAAATTTGTAAGGCTGCTACTGAAGAGGAG  
AACAGCCATGGCCAGGCAAATGGTCTTCTCAATGCTCCAAGCCTTGGGTACCAATTCTGT

## FIGURE 2MM

GTCCGCTCAGAGATTACTCAGCCAGACAGAGATATTCCACTGGTGCGAAAGTTACGTTCC  
ATTCACAGCTTTGAGCTGGAAAAACGTCTGACCCTGGAGCCAAAGCCAGACACTGACAAG  
TTCCTTGAGACCTGGTATAAAATAGTGATTTTTCTTTTAAAGCTTCTAAGGTACCATT  
ATTATTGTTGTCATTGTTGTTATTATTATTGTATATTTCTGTTACATAAAGTCTTTCAAA  
TAAGAAATCCTTGCATTTTTGTAACTGAGTCTATTGAGCTCCAATTTTCATCCATGTT  
TTTAATTATTATTATCCTGATTCTTAATTATTATAAATTCTATAGCATATCCTTTGGCTT  
TGGAAGCTGAGCAGTAAGAGCTGATGACTTCCTAACACTAGGTACAAGTTAAATGAACAT  
TTTTACAGTAACTTTGTGTTAGAAAGTAATCTCTTCCACACAACAGTGTAGTGCTGGAGAG  
GGCATGATAAAGATGGCATTAGGCAGAGATGAGGGGAATACATAAAGGAGGGGAAAAAGT  
AATTCATACACAAGGGACGGTGAGTTCATTCACCTTTAGTGAAGACCCTCTAGGAGTAAG  
ATACTGTGGGAAAACAGATACCAATAAGTATATCATGCTTGCCCTAGAGAGTTTGCAATC  
TACCTAGAGAGAAAGGAAGGTGAACTTGAGAGATCTATATACATAGGTAAAGATTGTAG  
TGCATGGTTTTGAGGCACATTATCCCTACAACAATTTTGATAACAGAAGAC

SEQ ID NO: 48\_AA435956\_H

ACTTTTACTATATCTTTGAGATGACTGTTTTTGATTAGAGGCGAAATCAGCACGTGGT  
GGCTCAAATCTCCTTATGGATAGTGTTCCTCCTTCCAGCTTTTCATGTTTCAACTTTTG  
CGGGGCTGGCGTACATCCACCACCAACACGTTCTTACAGGGACCTGAAACCTCAGAAC  
TTACTCATCAGTCACCTGGGAGAGCTCAAACCTGGCTGATTTTGGTCTTGCCCCGGGCCAAG  
TCCATTCCCAGCCAGACATACTCTTCAAGAGTCGTGACCCTCTGGTACCGGCCCCCTGAT  
GCTTTGCTGGGAGCCACTGAATATTCTCTGAGCTGGACATATGGGGTGCAGGCTGCATC  
TTTATTGAAATGTTCCAGGGTCAACCTTTGTTTCTGGGGTTTCCAACATCCTTGAACAG  
CTGGAGAAAATCTGGGAGGTGCTGGGAGTCCCTACAGAGGATACTTGGCCGGGAGTCTCC  
AAGCTACCTAACTACAATCCAGAATGGTTCCCACTGCCTACGCCTCGAAGCCTTCATGTT  
GTCTGGAACAGGCTGGGCAGGGTCTCTGAAGCTGAAGACCTGGCCTCCCAGATGCTAAAA  
GGCTTTCCCAGAGACCGCGTCTCCGCCCAGGAAGCACTTGTTTCATGATTATTTTCAGCGCC  
CTGCCATCTCAGCTGTACCAGCTTCTCTGATGAGGAGTCTTTGTTTACAGTTTTCAGGAGTG  
AGGCTAAAGCCAGAAATGTGTGACCTTTTGGCCTCCTACCAGAAAGGTCAACCCAGCC  
CAGTTTGTAGCAAATGCTGGTGAAAAGAAAGGGCGAGATCACCAGGTTCTTCCAGGGCTGT  
ATTTCTGCAGTTTTCGGTTTTTCATTTGCTTTCAGCTTACTAAGAAGCTTCAAATCTAACTCC  
ATACTGAACAAGGGGCTTTATGTCCTCACCTATGACCTGGAATAGTTTAAATATGGTGTT  
CAAGGCAATAGTACATAATAGTGGAAGAAAATTCAGTGGAAGGTTATTGCTATTGTGATT  
TGCATAGAATTTAAGTGATTGATTTAAAAAACTGGACATAAACTAAGTCTAAGAAG

SEQ ID NO: 49\_AA626859\_H

AAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAA  
TTTCTGTATATACATAACTGTATTACAGAGATATAAAACCTGAAAATATTCTAATAAC  
TAAGCAAGGAATAATCAAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGA  
TGCCTACACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAACCTCTTGTTGGGAGA  
TACTCAGTATGGTTCTTTCAGTCGATATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCCT  
GACAGGCCAGCCACTGTGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAG  
AACACTAGGAAAATTAATCCCAAGACATCAATCAATCTTTAAAAGTAACGGGTTTTTCCA  
TGGCATCAGTATACCTGAGCCAGAAGACATGGAACTCTTGAGGAAAAGTTCTCAGATGT  
TCATCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT  
AACCTGTTCCCAACTCCTGGAGAGCTCCTACTTGTATTCTTTCAAGAGGCCCAAATTA  
AAGAAAAGCACGTAATGAAGGAAGAAACAGAAGACGCCAACAGAATCAACTGTTGCCTCT  
CATACCAGGAAGCCACATCTCCCCACACCTGATGGAAGAAAACAAGTCTCCAGTTAAA  
ATTTGATCACCTTCCAAACATTTAGGAAAATGTTCTTTCAAGTGCAAAGTAATTTAATAT  
GTACACATTTTGTACAAGTGAGATAGGAATTCAGTGTTTTCAAATGCAAATGAGCCATA

## FIGURE 2NN

TGAAAATTAAGATGCCTTCTAGAATTGGTTTGCTCTGATCATTGCTGATTCTTTCCCCA  
TGCTTTTACAT

SEQ ID NO: 50\_AA061797 M

GAAAATAGCCCTGCGGAAATCCGTATGCTGAAGTTGAAACACCCAAACCTCGTGAAACCT  
CATCGAGGTGTTTCAAGAAAAGAGAAAGATGCATCTAGTTTTTTGAGTACTGTGATCACAC  
ACTGTTAAACGAGCTGGAGAGAAACCCAAACGGAGTTTCTGATGGAGTGATTAAAAAGTGT  
GCTATGGCAAACCTTCAAGCCCTTAACCTTCTGTCACAAGCACAATTGTATTTCATCGGGA  
TGTAACACCTGAAAACATCCTAATAACCAAGCAAGGGATGATAAAGATTTGTGACTTTGG  
ATTTGCACGAATTCTAATTCCAGGAGACGCCTACACAGACTATGTTGCCACCAGGTGGTA  
CCGAGCCCCCGAACTTCTCGTGGGAGACACGAAGTACGGTTCCTCTGTAGACGTGTGGGC  
CGTCGGCTGTGTTTTTGCAGAGCTCCTGACGGGTGAGCCACTCTGGCCGGGAAATCCGA  
CGTGGACCAGCTTTACCTGATCATCAGGACGTTGGGGAAGCTGATTCCAAGACACCAGTC  
TATCTTTAGGAGTAACCAGTTTTTCCGCGGCATCAGCATACCTGAACCAGAGGACATGGA  
GACTCTTGAAAGAAAAATTCTCAAAATGTTTCAAGCTGTGGCTTTAAGTTTCATGAAGGGATG  
CCTGAAGATGAATCCTGATGAGAGGCTGACCTGTGCCAGCTGCTGGACAGTGCCTACTT  
TGAGTCTTTTCAAGAGGATCAAATGAAAAGAAAAGCCCGCAGTGAGGGGAGAAGCCGAAG  
GCGCCAGCAGAATCAACTGCTGCCTCTTATTCTGGAAGCCACATCTCCCCACACCTGA  
TGGAAGGAAACAAGTCGTCCAGTTAAAGTTTCGATCATCTTCCAAACATTTAGGGGACTCA  
TCCTTCCCAGCACATCCTTTTAATATTGTCTACATAGGAATAAGACGGGAATCCTCAGCA  
TCTCAAATACAGTGAGCGACGTGAACACCAGGGCACCTCTAATCACCACGGGCTCCTCCC  
CTGTGCTTTTTTCCACGCCAGCTCCATCTCCTTAAACATTTCTCTTTAAATGTTGCAGTATC  
AAAATGGCACATCCGAAAGAGATGCTTCCAGTTTACCAGAGCCGGGCTTCTCAGGCAA  
TCGGTACTGTGCATCTGTGGACTTATGCTCCGACCTAGGGAAAGATTTCCACGTAGCCGT  
CTCACTTCAGCCGACCAGTGGTGTCTCTGAAGCAGACCCAGATCTGCTGGCTGCTGTTTGT  
GGAGGGGATGGCCCTGAGCCCTCTCACTGGAGTTTCTTCTCCGTGCAGCCAGGTCTTACT  
TTAGACTACATTTGTGTTATTGTGGCATGGCAATCGTGAAAGGTGGTCTAGGTTTACCCT  
TGACTCCACAGCAGATGCTAGTCTCCTTCTCGTGAGGAGCTGACAAGTCTGCTTCTAAAA  
CGAACTAGAGAAAAATTCCAAACGTGACCAGTTAGTGGACAGACTACAAGGAATCGACCAC  
CATACCACAGTAACGCCCTGGATCCCTGGCTGCCACCCACTCTAAGGCTATCCTGGTT  
CACCATGGTTTTCTCTTTCTTTCTTTTCTTTTAAATCTATTGTACATATGAGAAAGAGGC  
AGAGGGGCGAGAGAAACCTCGTGTGTGAAAATCAAAGACAAGCAGGAGGCCAGCCTAAG  
CTACATAGCAAGGCCTTTTCTCTACACCCATTCTCTAAGGTTGCTTAAACCAAGTCCCT  
GCTGCTGATTGTATAAACTATGAATAAGTCTACATATGTAGGACATATTGTTGTCATTG  
TTGAAATATCTAAGGATCTTGGTAGAAGCAGAAGTGTTCTAAATATTCTCCACACTGGTG  
AGTATCTTGGCATTTCATTTCTGACCTCATCACAGATGAACACATCAAAGGATGAGTATG  
TATCACTTTGCATCTTAGAATTCTACCTGTTTTAGCTGCGTTAAACCTTGTGAAAGGGCG  
GGGCCATAACTGAACCTGTGGAGTTCTTGCTGTGTGCAGGAAACCTCTGGTTTTGTCT  
CCAGCATGGAAGAAAACAGCTATAGTCACACCTACCTGAAAGTAGAAATTCAAAGTCACT  
GTCCTTGACTACATATGCAGTCCAAGGCCACGCTGGGCTACACTTCTCCAGGCATGAAGG  
TCCGTGTTTGTATCAAGGGGCAGGAAAGGAGAGTCCAAGGTCAAGGCCAGCCGAGGCTGC  
ATAGTGAGTTGAGGCTCTTCAGCAAAAGAAAAGCAAACCTAATAGGAGTCGTTGAAGGTAG  
CCACCGGCCATTTCTCTAAATATCATTCTGCTGAAAAGGGGGCTTAGTTTAGTTTGAAT  
GCATTAATGTATGTAGAAGCTGGGCTATTTTCAGATTATTTGAAATTGTAGCTATTGTTAA  
TTAGCACTTAATAACTAACTAGCATTATGGTAGTCTAAACTATTAGAGTTTACTACAAAG  
AGGTTTTGATTGAATTATATTAACATATAATATGGATTTTAAAAATTTAAGATGTTTAA  
GAAAGCTATATAAAGATTAAACATTTTTTGTGGCTGTATATTTGTGTATATACCTTGGTTG  
TTCTTTAAATTATTTTAAATAAAAGCCAGAAACATT



FIGURE 200

SEQ ID NO: 51\_AA397553\_H

ATGCCCAATTCAGAGAGACATGGGGGCAAGAAGGACGGGAGTGGAGGAGCTTCTGGAAC  
TTGCAGCCGTCATCGGGAGGCGGCAGCTCTAACAGCAGAGAGCGTCACCGCTTGGTATCG  
AAGCACAAGCGGCATAAGTCCAAACACTCCAAAGACATGGGGTTGGTGACCCCCGAAGCA  
GCATCCCTGGGCACAGTTATCAAACCTTTGGTGGAGTATGATGATATCAGCTCTGATTCC  
GACACCTTCTCCGATGACATGGCCTTCAAACCTAGACCGAAGGGAGAACGACGAACGTCGT  
GGATCAGATCGGAGCGACCGCCTGCACAAACATCGTCACCACCAGCACAGGCGTTCCCGG  
GACTTACTAAAAGCTAAAACAGACCGAAAAAGAAAAAGCCAAGAAGTCTCCAGCAAGTCG  
GGATCGATGAAGGACCGGATATCGGGAAGTTCAAAGCGTTTGAATGAGGAGACTGATGAC  
TATGGGAAGGCGCAGGTAGCCAAAAGCAGCAGCAAGGAATCCAGGTCATCCAAGCTCCAC  
AAGGAGAAGACCAGGAAAGAACGGGAGCTGAAGTCTGGGCACAAAGACCGGAGTAAAAAGT  
CATCGAAAAAGGGAAACACCCAAAAGTTACAAAACAGTGGACAGCCAAAACGGAGATCC  
AGGAGCCCCACAGGAAGTGGTCTGACAGCTCCAAACAAGATGATAGCCCCCTCGGGAGCT  
TCTTATGGCCAAGATTATGACCTTAGTCCCTCACGATCTCATACCTCGAGCAATTATGAC  
TCCTACAAGAAAAGTCCCTGGAAGTACCTCGAGAAGGCAGTCGGTCAGTCCCCCTTACAAG  
GAGCCTTCGGCCTACCAGTCCAGCACCCGGTCACCGAGCCCCCTACAGTAGGCGACAGAGA  
TCTGTGAGTCCCTATAGCAGGAGACGGTCGTCCAGCTACGAAAGAAGTGGCTCTTACAGC  
GGGCGATCGCCAGTCCCTATGGTGAAGGCGGTCCAGCAGCCCTTTCTGAGCAAGCGG  
TCTCTGAGTCGGAGTCCACTCCCCAGTAGGAAATCCATGAAGTCCAGAAGTAGAAGTCCCT  
GCATATTCAAGACATTTCATCTTCTCATAGTAAAAAGAAGAGATCCAGTTCACGCAGTCGT  
CATTCCAGTATCTCACCTGTGAGGCTTCCACTTAATTCCAGTCTGGGAGCTGAACTCAGT  
AGGAAAAAGAAGGAAAGAGCAGCTGCTGCTGCTGCAGCAAAGATGGATGGAAAGGAGTCC  
AAGGGTTCACCTGTATTTTTGCCTAGAAAAAGAGAACAGTTCAGTAGAGGCTAAGGATTCA  
GGTTTGGAGTCTAAAAAGTTACCCAGAAGTGTAATAATTGGAAAAATCTGCCCCAGATACT  
GAACTGGTGAATGTAAACATCTAAACACAGAGGTAAAAAATTCTTCAGATACAGGGAAA  
GTAAAGTTGGATGAGAACTCCGAGAAGCATCTTGTTAAAGATTTGAAAGCACAGGGGAACA  
AGAGACTCTAAACCCATAGCACTGAAAGAGGAGATTGTTACTCCAAGGAGACAGAAACA  
TCAGAAAAGGAGACCCCTCCACCTCTTCCCACAATTGCTTCTCCCCACCCCTCTACCA  
ACTACTACCCCTCCACCTCAGACACCCCTTTGCCACCTTTGCCTCCAATACCAGCTCTT  
CCACAGCAACCACCTCTGCCTCCTTCTCAGCCAGCATTTAGTCAGGTTCCCTGCTTCCAGT  
ACTTCAACTTTGCCCCCTTCTACTCACTCAAAGACATCTGCTGTGTCCTCTCAGGCAAT  
TCTCAGCCCCCTGTACAGGTTTCTGTGAAGACTCAAGTATCTGTAACAGCTGCTATTCCA  
CACCTGAAAACTTCAACGTTGCCTCCTTTGCCCTCCCACCTTATTACCTGGAGGTGAT  
GACATGGATAGTCCAAAAGAACTCTTCCTTCAAACCTGTGAAGAAAGAGAAGGAACAG  
AGGACACGTCACTTACTCACAGACCTTCCTCTCCCTCCAGAGCTCCCTGGTGGAGATCTG  
TCTCCCCAGACTCTCCAGAACCAGGCAATCACACCACCTCAGCAACCATATAAAAAG  
AGACCAAAAATTTGTTGTCCTCGTTATGGAGAAAGAAGACAAACAGAAAGCGACTGGGGG  
AAACGCTGTGTGGACAAGTTTGACATTATTGGGATTATTGGAGAAGGAACCTATGGCCAA  
GTATATAAAGCCAGGGACAAAGACACAGGAGAACTAGTGGCTCTGAAGAAGGTGAGACTA  
GACAATGAGAAAGAGGGCTTCCCAATCACAGCCATTTCGTGAAATCAAATCCTTCTGTCAG  
TTAATCCACCGAAGTGTGTTAACATGAAGGAAATTGTACAGATAAAACAAGATGCACTG  
GATTTCAAGAAGGACAAAGGTGCCTTTTACCTTGTATTGTAGTATATGGACCATGACTTA  
ATGGGACTGCTAGAATCTGGTTTGGTGCACTTTTCTGAGGACCATATCAAGTCGTTTCATG  
AAACAGCTAATGGAAGGATTGGAATACTGTACAAAAAGAAATTTCTGCATCGGGATATT  
AAGTGTCTTAACATTTTGCTGAATAACAGTGGGCAATCAAACCTAGCAGATTTTGGACTT  
GCTCGGCTCTATAACTCTGAAGAGAGTCGCCCTTACACAAACAAAGTCATTACTTTGTGG  
TACCGACCTCCAGAACTACTGCTAGGAGAGGAACGTTACACACCAGCCATAGATGTTTGG  
AGCTGTGGATGTATTCTTGGGGAATATTACAAAGAAGCCTATTTTCAAGCCAATCTG  
GAACTGGCTCAGCTAGAATGATCAGCCGACTTTGTGGTAGCCCTTGTCCAGCTGTGTGG  
CCTGATGTTATCAAACCTGCCCTACTTCAACACCATGAAACCGAAGAAGCAATATCGAAGG

## FIGURE 2PP

CGTCTACGAGAAGAATTCTCTTTTCATTCCTTCTGCAGCACTTGATTTATTGGACCACATG  
CTGACACTAGATCCTAGTAAGCGGTGCACAGCTGAACAGACCCTACAGAGCGACTTCCTT  
AAAGATGTGGAACCTCAGCAAAATGGCTCCTCCAGACCTCCCCCACTGGCAGGATTGCCAT  
GAGTTGTGGAGTAAGAAACGGCGACGTCAGCGACAAAGTGGTGTGTAGTCGAAGAGCCA  
CCTCCATCCAAAACCTTCTCGAAAAGAACTACCTCAGGGACAAGTACTGAGCCTGTGAAG  
AACAGCAGCCCAGCACCACCTCAGCCTGCTCCTGGCAAGGTGGAGTCTGGGGCTGGGGAT  
GCAATAGGCCTTGCTGACATCACACAACAGCTGAATCAAAGTGAATTGGCAGTGTTATTA  
AACCTGCTGCAGAGCCAAACCGACCTGAGCATCCCTCAAATGGCACAGCTGCTTAACATC  
CACTCCAACCCAGAGATGCAGCAGCAGCTGGAAGCCCTGAACCAATCCATCAGTGCCCTG  
ACGGAAGCTACTTCCCAGCAGCAGGACTCAGAGACCATGGCCCCAGAGGAGTCTTTGAAG  
GAAGCACCCCTCTGCCCCAGTGATCCTGCCTTCAGCAGAACAGATGACCCTTGAAGCTTCA  
AGCACACCAGCTGACATGCAGAATATATTGGCAGTTCTCTTGAGTCAGCTGATGAAAACC  
CAAGAGCCAGCAGGCAGTCTGGAGGAAAACAACAGTGACAAGAACAGTGGGCCACAGGGG  
CCCCGAAGAACTCCCACAATGCCACAGGAGGAGGCAGCAGCATGTCCTCCTCACATTCTT  
CCACCAGAGAAGAGCCCCCTGAGCCCCCGGACCTCCACCGCCGCCACCTCCACCCCTT  
CTGGTTGAAGGCGATCTTTCCAGCGCCCCCAGGAGTTGAACCCAGCCGTGACAGCCGCC  
TTGCTGCAACTTTTATCCCAGCCTGAAGCAGAGCCTCCTGGCCACCTGCCACATGAGCAC  
CAGGCCTTGAGACCAATGGAGTACTCCACCCGACCCCGTCCAAACAGGACTTATGGAAAC  
ACTGATGGGCCTGAAACAGGGTTTCACTGCCATTGACACTGATGAACGAACTCTGGTCCA  
GCCTTGACAGAATCCTTGGTCCAGACCCTGGTGAAGAACAGGACCTTCTCAGGCTCTCTG  
AGCCACCTTGGGGAGTCCAGCAGTTACCAGGGCACAGGGTCAGTGCAGTTTCCAGGGGAC  
CAGGACCTCCGTTTGGCAGGGTCCCCTTAGCGTTACACCCGGTGGTGGGCAACCATTCT  
CTGAAGGCTGAGGGAAGCAGCAATTCTGTGGTACATGCAGAGACCAAATTGCAAAACTAT  
GGGGAGCTGGGGCCAGGAACCACTGGGGCCAGCAGCTCAGGAGCAGGCCTTCACTGGGGG  
GGCCCAACTCAGTCTTCTGCTTATGGAAGAACTCTATCGGGGGCCTACAAGAGTCCCACCA  
AGAGGGGGAAGAGGGAGAGGAGTTCTTACTAA

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TGAAAATGGAGATGTATGAAACCCTTGGAAGTGGGAGAGGGAAGTTACGGAACAGTCA  
TGAAATGTAAACATAAGAATACTGGGCAGATAGTGGCCATTAAAGATATTTTATGAGAGAC  
CAGAACAATCTGTCAACAAAATTGCGATGAGAGAAATAAAGTTTCTAAAGCAATTTTCATC  
ACGAAAACCTGGTCAATCTGATTGAAGTTTTTAGACAGAAAAAGAAAATTCAATTTGGTAT  
TTGAATTTATTGACCACACAGTATTAGATGAGTTACAACATTATTGTCTATGGACTAGAGA  
GTAAGCGACTTAGAAAAATACCTCTTCCAGATCCTTCGAGCAATTGACTATCTTCACAGTA  
ATAATGTAATCATTTCGAGATATAAAACCTGAGAATATTTTAGTATCCAGTCAGGAA  
TTACTAAGCTCTGTGATTTTGGTTTTGCACGAACACTAGCAGCTCCTGGGGACATTTATA  
CGGACTATGTGGCCACACGCTGGTATAGAGCTCCCGAATTAGTATTAAGATACTTCTT  
ATGGAAAGTATGTGCCTGTGGATATCTGGGCTTTGGGCTGTATGATCATTGAGATGGCCA  
CTGGAAATCCCTATCTTCTAGTAGTTCTGATTTGGATTTACTCCATAAAATTGTTTTGA  
AAGTNGATTTCATGCCAGAACTGAAAGCTAAATTACTGCAGGAAGCAAAGTCAATTCAT  
TAATAAGCCAAAAGAGAGTTCTAAAGAAAATGAACTCAGGAAAGATGAAAGAAAACAG  
TTTATACCAATACACTGCTAAGTAGTTTCACTTTTGGGAAAGGAAATAGAAAAAGAGAAA  
AGCCCAAGGAGATCAAAGTCAGAGTTATTAAGTCAAAGGAGGAAGAGGAGATATCTCAG  
AACCAAAAAAGAAAGAGTATGAAGGTGGACTTGGTCAACAGGATGCAAATGAAAATGTTC  
ATCCTATGTCTCCAGATACAAAACCTTGTAACCATTTGAACCAACCAACCTATCAATCCCA  
GCACTAATGTAATGGCTTGAAAGAAAATCCACATTGCGGAGGTCTGTGACAAATGCCAC  
CCATCAATCTAATAACAGTAATTTGATGGCTGCAAATCTCAGTTCAAATCTCTTTTACC  
CCAGTGTGAGGTTAACTGAAAGAGCAAAAAAGAGACGCACTTCTTCACAATCTATTGGAC  
AAGTTATGCCTAATAGCAGGCAAGAGGATCCAGTCTTATTCAAAGCCAAATGGAGAAGG  
GTATATTTAATGAGCGAACAGGTACAGTGACCAATGGCAAATGAGAACAAAAGGAAGC

## FIGURE 2QQ

TGAATTTTTCCAGATCTGACAGGAAAGAATTCATTTTCCAGAATTGCCTGTCACAATAC  
AGTCAAAAGATACAAAAGGAATGGAAGTTAAACAGATAAAAATGCTGAAGAGGGAGTCAA  
AGAAAACAGAGTCATCTAAGATACCAACTTTACTTAACGTGGATCAAAATCAAGAAAAAC  
AAGAGTTTATTCCCTTATCTCTGCTGTCTGCCTGCTGTCTTATTTTCACAAATATTTGCT  
CTCAGCTAACTATCAGGGTGGAGATGGCCATTGCGAGGGGAAGAATTTGAAGAGAAACAG  
GTTTTTTTTCTGGTAGTGTCTTTTCTTTTACATAGTCCAAAAAATACAAGATGACAACCTC  
TTCCCGTTTTTATTTATCTACAATAGAAAGTGTGATGTGAGTTGTTGTTAAGACAGCCATCC  
ATGTGCATGAGCATCATCCAGCTTTTTTTTGTAGCAAAACATTTACTGTTTTCTTTTCCC  
TTTTAAGACTCTGTTGATGTGATAATTTGATTTGGAATTATAAAGTCATCTCTTCTCTGC  
CTTGAA

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CTGGCAGATATAGTTTCATGCTTGTTTACAAATTGATCCTGCTGAGAGGACATCATCTACT  
GATCTTTTTCGCTCACGATTACTTTACTAGAGATGGATTTATTGAGAAATTCATACCAGAG  
CTGAGAGCTAAATTATTACAGGAAGCAAAGGTTAATTCATTTATAAAGCCAAAAGAGAAT  
TTTAAAGAAAATGAACCTGTGAGAGATGAGAAGAAATCAGTTTTTACCAACACCCTGCTC  
TATGGAAATCCATCCTTTATGGCAAGGAAGTGGACAGAGACAAAAGGGCCAAGGAGCTC  
AAAGTCAGAGTCATTAAGGCCAAAGGGGGCAAAGGAGATGTCCCAGACCAGAAGAAGCCA  
GAGTATGAAGGCGACCACCGCCAGCAGGGCACAGCTGATGACACACAGCCCTCATCACTG  
GACAAGAAGCCTTCTGTCTTGGAACTGACAAACCCTCTCAATCCCAGTGAGAATTCTGAC  
GGTGTCAAAGAAGACCCACACGCTGGGGGTTGTATGATAATGCCACCTATCAACCTGACA  
AGCAGTAATTTGTTGGCCGCAAATCTCAGTTTCAAACCTTTCCCACCCCAATTCACGGTTA  
ACTGAAAGAACAAAAAGAGACGCACTTCTTCACAACTATTGGACAGACTTTGTCTAAT  
AGCAGACAAGAGGACACAGGTCCCACACAAGTCCAACAGAGAAAGGTGCATTTAATGAG  
CGAACAGGTGAGAAATGACCAAATATCGAGTGGGAACAAAAGAAAGCTGAATTTTCCCAA  
TGCGACAGGAAAGAATTCATTTCCCTGAACCTGCCATTACAGTGCAGGCGAAGGAGATG  
AAAGGGATGGAAGTTAAACAGATAAAAGTGCTGAAGAGAGAATCAAAGAAAACAGATTCA  
TCTAAAATACCAACTTTACTTAGTATGGACCCAAATCAAGAAAAACAAGAGGGTGGAGAT  
GGCGATTGTGAGGGGAAGAATTTGAAGAGGAACAGATTTTTTTTTTCCCGATAGTGCTTT  
GTCTTTTAAAGTAATCTTAAAAATACAAGCTTGACAATTCCTTCCTTTTTATTTATATAC  
ACTAGAATGTACATAGGTTGCTGCTAAGATAGCCACCCATCCCATCTGCATCAACATCAT  
CTATTTTTTTGGTTTTGCTAGCAAAATTTTCACAATTTTCTCTATCTTCCAAAAACTGT  
TATTTTGATGCTGTGATTTGAAATTATAAAGTCACCTCCTCTGTCTGCTTCCTTCCTTGC  
CATGATTACTGAGTGGGTAGTCACATGATGTGCCCTGCTCGCACTGCTCTCAGACTGCTG  
AGACTCAAACCTCATAAGCCAGGGGTCTCCTGGGAAGCACTGGCCTCTTCAAGTGGATGC  
TCGATGAACCTTCTTATCTGTTGTCTTAGTAACCACTCGTTGCCATCACATGATGAAAGA  
CATTCATTGTCCCCAGTGAAGCATTTATAGTACTTACATAACATGTTACAGTGATATGA  
TGTTCTAGGFTAAACTCCTTGAGATGAAACTATTTCTGCACTCTCTGACTCCCTAGT  
CTAATAGTTCTCTTCATTTAGCCAGAAGAATTTCTGGAAGCGATGCACAACCTGGGA  
AAGGTTTACTTTCTATCCTGGGCTGTTTTCTGTTGCTAAATAATATAGACTGGGTAGTTA  
GTTAACAT

SEQ ID NO: 54\_AA575635\_M CCRK\_M

AGCGCCTCAGGCCAGCTCAAGATAGCTGACTTTGGCCTGGCCCCGGTCTTCTCTCCGGAT  
GGTGGTGCCTCTACACACATCAGGTGGCCACCAGGTGGTACCGAGCTCCTGAACTCCTG  
TATGGCGCTCGGCAGTATGACCAGGGCGTTGACCTATGGGCTGTGGGCTGCATCATGGGA  
GAGCTGTTGAATGGGTCCCCCTGTTCCCGGGCGAAAACGACATTGAACAACTGTGCTGT  
GTGCTTCGCATCCTGGGTACCCCGAGTCTCGAGTCTGGCCGGAGATCACAGAGCTGCCT  
GACTACAACAAGATCTCCTTCGAGGAGCAGGCACCAGTGCCCTGGAGGAGGTGCTGCCT  
GATGCCTCTCCCCAGGCCTTGACCTGCTGGGCCAGTTCTCTCTACCTCCACGACAG

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## FIGURE 2RR

CGTATTGCAGCCTCCCAGGCCCTTCTGCATCAGTACTTCTTCACAGCGCCTCTGCCTGCC  
CATCCATCCGAGCTGCCAATTCCTCAGCGCCCAGGGGGACCTGCACCCAAGGCTCACCCA  
GGGCCCCCCCCATGTCCACGACTTCCATGTGGATCGACCTATTGAGGAGTCACTGTTGAAC  
CCAGAACTGATTTCGGCCCTTCATCCCAGAGGGGTGAGATGCTGGTCCAGGCCTTCCTGCT  
CGCCCTAGGAGCACCTCTTTCTGATTTGCCCTCCATGGCCTCCCCACGGCTATATATACCA  
CACCTGGTCTGCTCCTGAGTGTGCTTGAGGGCTGGGCTCTGGGAGGCAGAACCGTGAGA  
TGTTTCATCCCAGCAGAGAAAGAGACTCACGTCTACAGACAAAGCCTCCAGAACTGCTA  
GCTGTGTCTTCTCCAGGGCCACCCCTCAGTGGTGCCACCCGGCCTTAGAGATGATTGTC  
AGGCTCTGTCCCTCTTCAAGGACATTGGTACTACAGCACCACTGGTGGAAGCACAGAG  
TATAAGCTGTCTTCATACTGGGGACACAGCTGGGAAGTCAGACATGTTTTAGTTTTGGTT  
CCACTGGGTGAGGATTTGAGGTTTCATATAAAAGCCCTGGGTGTTTCTGTCTAATTGCACC  
TTGTCTGTTGCTGTTAGGGAAAGGACAATGGTGGGCCTTGATTACAGGGGTGAGGTACT  
CAGAAGGGGCTCCTGTGAAGGCCATTTGGGTCTCAGGCTTCCCATGCTATTACGGGA  
CTTGAGTGCTCATTTGGGAGCGAGGGTCCAGAAGCTGAGGCCAGGGATGGACAGTCCAG  
TTCCCGAAGCCCACTTCCACATGTGGGTGGGTGAGTCACTGAGCCTGAGGCTGCCTTG  
CAGATGCGGAAGCAGGCATTCCTGGAATCCACTCAGTAAATAAATTCCAGTGTGACTCAG

SEQ ID NO: 55\_AA631990\_H

GAACAACAATAACAGAATAAGGAAGAAAATCTCATGATTACCTCAATAAGTACAGAGAAA  
TCTGGTCACACTCACTATCCATTTCATGATTACAACCTCTTCAATACTATCGCGGCCGAGGA  
GGGAAGACGGCAGTTTGGCGACATTTCTCGGCCGAAGGGCCATTTGCTTTTGCGGAGATG  
CGGCATTCCAAAAGAACTCACTGTCTGATTGGGATAGCAGAGAAAGCTGGGGACATGAA  
AGCTATCGTGGAAGTCACAAGCGGAAGAGGAGATCTCATAGTAGCACACAAGAGAACAGG  
CATTGTAAACCACATCACCAGTTTAAAGAATCTGATTGTGCTATTATTTAGAAGCAAGGTCC  
TTGAATGAGCGAGATTATCGGGACCGGAGATACGTTGACGAATACAGGAATGACTACTGT  
GAAGGATATGTTTCTAGACATTATCACAGAGACATTGAAAGCGGGTATCGAATCCACTGC  
AGTAAATCTTCAGTCCGCAGCAGGAGAAGCAGTCTTAAAGGAAGCGCAATAGACACTGT  
TCAAGTCATCAGTCACGTTTCGNATGAAATCGTGACACTTTGGGTGAAGGAGCCTTTGGC  
AAAGTTGTAGAGTGCATTGATCATGGCATGGATGGCATGCATGTAGCAGTGAAAATCGTA  
AAAAATGTAGGCCGTTACCGTGAAGCAGCTCGTTTCAAGAAATCCAAGTATTAGAGCACTTA  
AATAGTACTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGCTAGAATGGTTTGATCAT  
CATGGTCATGTTTGTATTGTGTTTGAACACTGAGGACTTAGTACTTACGATTTTCATTAAA  
GAAAACAGCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGC  
CAGTCAATAAATTTTTTACATCATAATAAATTAACCCATACAGATCTGAAGCCTGAAAAT  
ATTTTGTGTTGTGAAGTCTGACTATGTAGTCAAATATAATTCTAAAATGAAACGTGATGAA  
CGCACACTGAAAAACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGAT  
GAACATCACAGTACTTTGGTGTCTACCCGGCACTACAGAGCTCCCGAGGTCATTTTGGCT  
TTAGGTTGGTCTCAGCCTTGTGATGTTTGGAGCATAGGTTGCATTCTTATTGAATATTAC  
CTTGGTTTTCACAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGA  
ATATTAGGACCCATACCACAACACATGATTGAGAAAACAAGAAAACGCAAGTATTTTCAC  
CATAACCAGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGC  
AAACCGTTGAAGGAATTTATGCTTTGTTCATGATGAAGAACATGAGAACTGTTTGACCTG  
GTTTCAAGAATGTTAGAATATGATCCAACCTCAAAGAATTACCTTGGATGAAGCATTGCAG  
CATCCTTTCTTTGACTTATTAATAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATA  
CTTCTCTAGAAGAGATTACTTAAGACTGTGTGAGTCAACTAAACATTCTAATATTTTGT  
AAACATTAAATTATTTTGTACAGTTAAGTGTAATATTGTATGTTTTGTATCAATAGCAT  
AATTAACCTGTTAAGCAAGTATGGTCTTGATAATGCATTAGAAAAATTAATAATTTT  
TCTTTTGAATTACCATTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTGATAAAT  
GTGATTGATCTTGCTTTTGTACATGGAGGTCACCTCTGAAGTGATTTTTTTTGTAGTAA  
AGGAAATCTTGACTACTTTATATTCTTAAAGGAATATTCTTATATACTTCAAATTTAGA

## FIGURE 2SS

ACTTAACTTTAAAAGTTTTCTTCTGTAATTGTTGAACGGGTGATTATTATTAAGTCTAG  
ATAAGCAGGTACTAGAAAACCAAACTCAGAAAATGTTTACTGTTAGAATTCTATTAAATT  
TTAAGTGTGTGATTCTTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTCATGGAA  
AGGCATGCAGTTTGTCCATTGTGACAGTTTGTTTAATAAAACCACATACACACTTTATTT  
AAGATTAAAATCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGT  
GAGTCACAGATATAAAAATAGAAATTCTGATGAGAGGTTTCAGTTTTTAATACCAAGTCC  
TTAGGAGTCTTAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAAACCTAT  
AAGAATTAAGTTTATTAATTAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAG  
GATTTGATTGGAAAGCAGTTTGGGAAGAAAGTGCTGCTGAAATTTCCAGAATTTAATTGA  
TTGGTTACATAAACTTTTGGACTTCAAT

SEQ ID NO: 56\_AA557536\_H

AGTAAGGCCCCGCGGGCGTCCCTGGCCGCCATGTGCACCGTAGTGGACCCTCGCATTTGTCC  
GGAGATACCTACTCAGGCGGCAGCTCGGGCAGGGGAGAACATTCCGGGAAATCACGCTCC  
TCCAGGTGAGTGGCCTGGGCCCTCCAGTCCAATCCCCTTGCCCAGGTACAGATCTCTCCA  
GACAGGAGAGAACTGGCCTTCTTGGGCCCCAGAGCACAGCCCCCTCCTGGCCTTCCAGCC  
GCCTCCGACTCTCTCCCCAGGAGTTTGGGGACCATCCCAACATCATCAGCCTCCTTGACG  
TGATCCGGGCAGAGAACGACAGGGACATTTACCTGGTGTGTTGAGTTTATGGACACTGACC  
TGAACGCAGTCATCCGGAAGGGCGGCCTGCTGCAGGACGTCCACGTGCGCTCCATCTTCT  
ACCAGCTCCTGCGGGCCACCCGGTTCCTCCACTCGGGGCACGTTGTGCACCGGGACCAGA  
AGCCGTCCAATGTGCTCCTGGATGCCAACTGCACAGTGAAGCTGTGTGACTTTGGCCTGG  
CCCGCTCCCTGGGCGACCTCCCTGAGGGGCCTGAGGACCAGGCCGTGACAGAGTACGTGG  
CCACACGCTGGTACCGAGCACCGGAGGTGCTGCTCTCTTCGCACCGCTACACCGCTTCCT  
GCCCCAGATACACCTTGGGGTGGACATGTGGAGTCTGGGCTGTATCCTGGGGGAGATGC  
TGCGGGGGAGACCCCTGTTCCCCGGCACGTCCACCCTCCACCAGCTGGAGCTGATCCTGG  
AGACCATCCACCGCCATCTGAGGAGXXXAGGCCACGACAGACGCTGGATGCCCTCCTAC  
CGCCAGACACCTCCCCAGAGGCCTTGGACCTCCTTAGGCGACTCCTGGTGTTCGCCCCGG  
ACAAGCGGTTAAGCGCGACCCAGGCACCTGCAGCACCCCTACGTGCAGAGGTTCCACTGCC  
CCAGCGACGAGTGGGCACGAGAGGCAGATGTGCGGCCCCGGGCACACGAAGGGGTCCAGC  
TCTCTGTGCCTGAGTACCGCAGCCGCTCTATCAGATGATCCTGGAGTGTGGAGGCAGCA  
GCGGCACCTCGAGAGAGAAGGGCCCGAGGGTGTCTCCCCAAGCCAGGCACACCTGCACA  
AACCCAGAGCCGACCCCTCAGCTGCCTTCTAGGACACCTGTGCAGGGTCCCAGACCCAGGC  
CCCAGAGCAGCCAGGCCATGACCCTGCCGAGCACGAGTCCCCCGTGCAGCCAAGAACG  
TTCCCAGGCAGAACTCCGCTCCCTGCTCCAAACTGCTCTCCTAGGGAATGGGGAAAGGC  
CCCCTGGGGCGAAGGAAGCGCCCCCTTGACACTCTCGCTGGTGAAGCCAAGCGGGAGGG  
GAGCTGCGCCCTCCCTGACCTCCCAGGCTGCGGCTCAGGTGGCCAACCAGGCCCTGATCC  
GGGGTGACTGGAACCGGGGCGGTGGGGTGAGGGTGGCCAGCGTACAACAGGTCCCTCCCC  
GGCTTCCTCCGGAGGCCCGGCCCGGCCGAGGATGTTTCAGCACCTCTGCCTTGACGGGTG  
CCCAGGGGGGTGCCAGGGCTTTGCTTGGAGGCTACTCCCAAGCCTACGGGACTGTCTGCC  
ACTCGGCACTGGGCCACCTGCCCCTGCTGGAGGGGCACCATGTGTGAGCCGCCCTACTCC  
CTTCACCTGGCCCTCTGTTCCCTGCCCCAGCNCCTTCCCCAGACCCCTCTCCAGTCTCCTG  
CACCCCTTAGCCCTCCCTGCTTTGCCTGGCCCCGTTGAAGTTCAGGGAGCTTGCCCGGGT  
CTCCTCGGGGGAGCAGATGAGGGCCCTGCCC

SEQ ID NO: 57\_N28606\_H, MOK\_H

ATGAAGAACTATAAAGCAATTGGCAAAATAGGAGAGGGAACGTTTTCTGAAGTTATGAAG  
ATGCAAAGCCTGAGAGATGGAACTACTATGCATGTAAACAAATGAAGCAGCGCTTTGA  
AGTATTGAGCAAGTCAACAACCTACGAGAGATCCAAGCACTGAGGCGCCTGAATCCGCAC  
CCAAACATTCTTATGTTGCATGAAGTGGTTTTTGACAGAAAATCTGGTTCTCTTGCACTA  
ATATGTGAACCTATGGACATGAATATTTATGAGCTAATACGAGGGAGAAGATACCCATTA

FIGURE 2TT

TCAGAAAAAAAAATTATGCACTATATGTACCAGTTATGTAAGTCCCTGGATCATATTTCAC  
AGAAATGGAATATTTACAGAGATGTAAAACAGAAAATATACTAATAAAGCAGGATGTC  
CTGAAATTAGGGGACTTTGGCTCCTGCCGGAGTGTCTATTCCAAGCAGCCGTACACGGAA  
TACATCTCCACCCGCTGGTACCGGGCCCCGGAGTGTCTCCTCACTGATGGGTTCTACACG  
TACAAGATGGACCTGTGGAGCGCCGGCTGTGTGTTCTACGAGATCGCCAGTCTGCAGCCCC  
CTCTTTCTGGAGTAAATGAACTGGACCAAATCTCAAAAATCCACGATGTTCATCGGCACA  
CCCGCTCAGAAGATCCTCACCAAGTTCAAACAGTCGAGAGCTATGAATTTTGATTTTCCT  
TTTAAAAAGGGATCAGGAATACCTCTACTAACAACCAATTTGTCCCCACAATGCCTCTCC  
CTCCTGCACGCAATGGTGGCCTATGATCCCGATGAGAGAATCGCCGCCCCACAGGCCCTG  
CAGCACCCCTACTTCCAAGAACAGAGGAAAACAGAGAAGCGGGCTCTGGGCAGCCACAGA  
AAAGCTGGCTTTCCGGAGCACCTGTGGCACCAGGAACTCAGTAACAGCTGCCAGATT  
TCCAAGGAGGGCAGAAAGCAGAAACAGTCCCTAAAGCAAGAGGAGGACCGTCCCAAGAGA  
CGAGGACCGGCTATGTCATGGAAGTCCCAAACCTAAAGCTTTCGGGAGTGGTCAGACTG  
TCGTCTTACTCCAGCCCCACGCTGCAGTCCGTGCTTGGATCTGGAACAAATGGAAGAGTG  
CCGGTGCTGAGACCTTGAAGTGCATCCCTGCGAGCAAGAAGACAGATCCGCAGAAGGAC  
CTTAAGCCTGCCCCGAGCAGTGTGCCTGCCACCATAGTGCGGAAAGGCGGAAGATAA

SEQ ID NO: 58\_AB023153\_H, ICK\_H

ATGAATAGATACACAACAATCAGGCAGCTCGGGGATGGAACCTACGGTTCCGTCTGCTG  
GGAAGAAGCATTGAGTCTGGGGAGCTGATCGCTATTAAAAAATGAAAAGAAAATTTTAT  
TCCTGGGAGGAATGCATGAACCAACGGGAGGTTAAGTCTTTAAAGAAGCTCAACCATGCC  
AATGTAGTCAAATTTAAAGAAGTTATCAGGGAAAATGATCATCTTTATTTTATCTTCGAG  
TACATGAAGGAAAATCTTTACCAGCTCATTAAGAGAGAAATAAGTTGTTTCCTGAGTCT  
GCTATAAGGAATATCATGTATCAGATATTACAAGGACTCGCATTTATTACAAACTCGGC  
TTCTTTTCATCGAGACTTAAAGCCTGAGAACCTCCTCTGCATGGGACCAGAACTTGTGAAA  
ATTGCAGACTTTGGTTTGGCCCCGAGAAATACGATCAAAACCTCCATATACAGATTATGTA  
TCTACCAGATGGTACAGGGCTCCAGAAGTACTCCTGAGGTCTACCAACTACAGCTCCCCC  
ATTGACGTCTGGGCGGTGGGCTGCATCATGGCAGAAGTTTACACCCTCAGGCCACTCTTC  
CCTGGAGCCAGTGAAATTGACACAATATTCAAAATTTGCCAAGTGCTGGGGACACCAAAA  
AAGACTGACTGGCCTGAAGGCTATCAACTTTCAAGTGCAATGAACTTCCGTTGGCCACAG  
TGTGTACCCAATAACTTTAAAGACCTTGATTCCCAATGCTAGCAGTGAAGCAGTCCAGCTC  
CTGAGAGACATGCTTCAGTGGGATCCCAAGAAACGACCAACAGCTAGTCAGGCACTTCGA  
TATCCTTACTTCCAAGTTGGACACCCACTAGGCAGCACCACACAAAACCTTCAGGATTCA  
GAAAAACCACAGAAAGGCATCCTGGAAAGGGCAGGCCACCTCCTTATATTAAGCCAGTC  
CCACCTGCCCAGCCACCAGCCAAGCCACACACGAATTTCTTCACGACAGCATCAAGCC  
AGCCAGCCCCCTCTGCATCTCACGTACCCCTACAAAGCAGAGGTCTCCAGGACAGATCAC  
CCAAGCCATCTCCAGGAGGACAAGCCAAGCCCCGTTGCTTTTCCCATCCCTCCACAACAAG  
CATCCACAGTCGAAAATCACAGCTGGCCTGGAGCACAAAATGGTGAGATAAAGCCAAAG  
AGTAGGAGAAGGTGGGTCTTATTTCCAGGTCAACAAAGGATTGAGATGATTGGGCTGAC  
TTGGATGACTTGGATTTTCAGTCCATCCCTCAGCAGGATTGACCTGAAAAACAAGAAAAGA  
CAGAGTGATGACACTCTCTGCAGGTTTGGAGAGTGTTTTGGACCTGAAGCCCTCTGAGCCT  
GTGGGCACAGGAAACAGTGCCCCCACCAGACGTCATATCAGCGGCGAGACACGCCCCACC  
CTGAGATCTGCAGCCAAGCAGCACTATTTGAAGCACTCTCGATACTTGCCTGGGATCAGT  
ATAAGAAATGGCATACTCTCGAATCCAGGCAAGGAATTTATTCACCTAATCCATGGTCT  
AGTTCTGGCTTGTCTGGAATCTTCAGGGACAATGTGAGTAATCAGCAAAGTAAATTCA  
GTTGGTTCCAGCTCTACAAGTTCTAGTGGACTGACTGGAACTATGTCCCTTCCTTTCTG  
AAAAAAGAAATCGGTTCTGCTATGCAGAGGGTACACCTAGCACCTATTCCAGACCCTTCC  
CCTGGTTATTCCTCCCTGAAGGCCATGAGACCTCATCCTGGGCGACCATTCTTGGACACC  
CAGCCTAGAAGCACTCCTGGGTTGATACCACGGCCTCCAGCCGCCAGCCAGTGCATGGC  
CGGACAGACTGGGCTTCCAAGTACCCATCCCGGCGGTGA

FIGURE 2UU

SEQ ID NO: 59\_AA839940\_M

AGCAGCAACAATGGTGGCATGAGTGCAGAGGAGGAGATAGGGCCTGGGGCTGAGCCTATG  
AGAGGACCAAGCTTGGCTACAAGGGACTGGAGAGATGAGACTGTTGGGACCACAGACCTG  
CAGCAAGGCATAGACCCAGGAGCAGTGAGCCCTGAGCCTGGGAAGGACCACGCAGCCCAG  
GGCCCAGGAAGAACTGAAGCTGGAAGGGTATCTTCTGCTGCAGAGGCTGCCATTGTGGTT  
CTAGATGACAGCGCAGCACCCCCAGCCCCCTTTTGAACACCCGGGTAGTGAGCATCAAAGAT  
ACCCTGATCTCAGCAGGCTACACGGTATCCCAACATGAAGTCTTAGGAGGGGGTCCGTTTT  
GGCCAGGTGCACAGGTGTACAGAGAGGTCTACAGGCCTTGCACTGGCAGCCAAGATCATC  
AAAGTGAAGAACGTAAAGGACCGGGAGGATGTGAAGAATGAGGTCAACATCATGAACCAG  
CTCAGCCACGTAAACTTGATCCAACCTTTATGATGCGTTTGAGAGCAAGAACAGCTTCACT  
CTGATCATGGAGTATGTGGATGGAGGCGAACTCTTGACCGGATCACGGATGAGAAGTAC  
CACCTCACTGAGTTGGATGTGGTCTTGTTACGAGGCAGATCTGTGAGGGTGTGCATTAC  
CTGCATCAGCACTATATCCTGCACCTGGACCTCAAGCCTGAGAACATATTGTGTGTCAGC  
CAGACAGGGCATCAAATTAAGATCATTGACTTTGGGCTGGCTAGAAGATACAAGCCTCGG  
GAGAAGCTAAAGGTGAACCTTTGGTACTCCGGAGTTCCCTGGCCCCAGAGTTGTTAACTAT  
GAGTTTGTGTCAATTTCCAACAGACATGTGGAGTGTGGGAGTTATCACCTACATGCTACTC  
AGTGGTTTGTCCCCATTTCTAGGGGAGACAGATGCAGAGACCATGAATTTTATTGTGAAC  
TGCAGCTGGGATTTTCGATGCTGATACCTTCAAAGGGCTGTCGGAGGAAGCCAAGGACTTT  
GTTTCCCGGTTACTGGTCAAAGAGAAGAGCTGTAGGATGAGCGCCACACAGTGCCTGAAA  
CACGAGTGGTTAAATCACCTGCCTGCCAAAGCCTCGGGCTCCAACGTTCCGCTCAGATCC  
CAACAACCTGCTGCAGAAATATATGGCTCAGAGTAAATGGAAGAAACATTTCCACGTGGTG  
GCTGCAGTCAACAGGCTACGGAAATTTCCAACGTGTCCCTAATCTTCAACTCTGGTGTTC  
CACTGGGCCTGGGAATTCTTGAGGCAACACGAAGTGGTAATATGAAGAGATTACTCAAGA  
TTTTATGTAGATTGGCGCTTTGCTATTATTGATTTTTCTTATTTTGCAAAGAAATGATGGA  
AGGAAGCAAGAAAGAAAGAAAGAAAGAGGGAAGAAAGGAAAGGCAAGAAAGCAA  
GGAAACAGGCTACGTTGTTGCTCTTCTTGTTAGGTGAAAGTGTTTTTATTAAAGCCCTAG  
GAATGTTTTTCTGCCTCGTAAGGTGAGCAGGTCTCATATGCTGCTTGCTACCCCGCACCC  
TTCCTTTTGGTAATAAGAGCAGGCACGCTCAGGATGGGCAGGGAAATCCTACTTGCTTT  
TGGTCAAATTTGAATTTCTAACTTGTCTATGATTAAAGAAGCCAGTAGGGAGGGAGGTATG  
GAAGAGGGAGGAATTAGGTCCAACAGTGGGGGATGAATTTGACCGAAACATTGTATAAAA  
TTCTTAAAGAATTAATAAAATATATTTTTTAAAGGAG

SEQ ID NO: 60\_AA460132\_H

GGAACTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGTAACCACTTACAGGCCGGAAAG  
TGTCGGGGGTGGACGCATTCGGGTAGCCGAAGAAGTCCAGGATTGCCGAAGAAGTCCCA  
GGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTTCAGAGACAGCTGATCGGTTGGAG  
CTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTACGCCGCGCGATGGCGAGGAG  
CCCGCCCCGGAGGCTGAGGCTCTGGCCGCAGCCCGGGAGCGGAGCAGCCGCTTCTTGAGC  
GGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCGTGTTCGTGGCCGCTTCCAGGGC  
CGCGCGGCGGTGATCAAGCACCGCTTCCCAAGGGCTACCGGCACCCGCGCTGGAGGCG  
CGGCTTGGCAGACGGCGGACGGTGCAGGAGGCCGCGGCGCTCCTCCGCTGTGCGCGCGT  
GGAATATCTGCCCCAGTTGTCTTTTTTTGTGGACTATGCTTCCAACCTGCTTATATATGAA  
GAAATTGAAGGCTCAGTGACTGTTTCGAGATTATATTAGTCCACTATGGAGACTGAAAAA  
ACTCCCAGGGTCTCTCCAACCTTAGCCAAGACAATTGGGCAGGTTTTGGCTCGAATGCAC  
GATGAAGACCTCAATTCATGGTGATCTCACCACCTCCAACATGCTCCTGAAACCCCCCTG  
GAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTTTCATTTTCACTTCCAGAG  
GATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCTCAGTACCCATCCCAACACT  
GAAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCTCCTCCAAAAAGGCCAGGCCA  
GTGCTAAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAAAGAGGTCCATGGTTGGGTAG  
AAGAATGTGTATGACAACCACACACAGTGAAGCTCTTTTTTCAAAGTAAATTTGAAGAAA

## FIGURE 2VV

TGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAGATATTTTAAAGTGGTATGTG  
ATCGTGTCTATTATCATCTGCACTTCACTCAAGAGCTTACTATGTGTCTAAGTCATGTTCT  
AGGCAGAATTGGGTATTTAAAGTAAATTGAGGACAGGCTTCTCCAGATTGTGACATGTA  
TATCTCAGATACATGGGTGTGGCATTGAACCACATAATGAGAACATTATTCTCTTTTATG  
TCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTCGCTGAGCTTACTGGCCCTCT  
AACCCAGTGTTTTTTTTTTGTGTGTGTGTGTGTACATGTTATATTTATTTTGAAACCAGTTT  
AATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATACAGCATGG

SEQ ID NO: 61 SGK034\_H

CAGAGAGAGAAGGTAAACCAAGGGAACATGCCAGGGCTTCAGAGCACCTTCCTAGCCATG  
GACACGGAGGAGGGGGTAGAGGTGGTGTGGAACGAGCTCCACTTCGGAGACAGGAAGGCC  
TTCGCGGCGCACGAGGAGAAGATCCAGACCGTGTTCGAGCAGCTGGTGTGTGGTGGACCAC  
CCGAACATCGTGAAGTTGCACAAGTACTGGCTGGATACCTCTGAGGCCTGCGCGAGGGTC  
ATCTTCATCACAGAGTACGTGTCTCAGGCAGCCTCAAGCAATTCCTCAAAAAGACCAAG  
AAGAACCACAAGGCCATGAACGCCCCGGGCCTGGAAGCGCTGGTGCACGCAGATCCTGTCT  
GCGCTCAGCTTCCTGCACGCCTGCAGCCCCCAATCATCCACGGGAACCTGACCAGCGAC  
ACCATCTTCATTTCAGCACACCGGCCTCATCAAGATCGGCTCCGTGTGGCACCGAATCTTC  
TCCAATGCACTTCAGATGATCTCCGAAGCCCCATCCGCGCTGAGCGAGAGGAACTTCGG  
AACCTGCACTTCCTCCCCCAGAGTATGGAGAGGTGGCCGATGGGACCGCTGTGGACATC  
TTCTCCTTTGGGATGTGTGCGCTGGAGATGGCTGTACTGGAAATCCAGACCAATGGGGAC  
ACCCGGGTACAGAGGAGGCCATTGCTCGCGCCAGGCACTCGCTGAGTGACCCCAACATG  
CGGGAGTTCATCCTTTGCTGCCTGGCCCCGGGACCTGCCCGCCGGCCCTCTGCCACAGC  
CTCCTCTTCCACCGCGTGTCTTTCGAGGTGCACTCGCTGAAGCTCCTGGCAGCCCACTGC  
TTCATCCAGCACCAAGTACCTCATGCCTGAGAATGTGGTGGAGGAGAAGACCAAGGCCATG  
GACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCGAGGCCCCCGCTGCAGTGGCGG  
TACTCGGAAGTCTCCTTCATGGAGCTGGACAAATTCTTGAGGATGTGAGGAATGGAATC  
TACCCACTGATGAACTTTGCAGCCACTCGACCCCTGGGGCTGCCCCGTGTGCTGGCCCCA  
CCCCCGGAGGAGGTCCAAAAGGCCAAGACCCCGACGCCAGAGCCCTTTGACTCTGAGACC  
AGAAAGGTATCCAGATGCAGTGCAACCTGGAGAGAAGCGAGGACAAGGCGCGCTGGCAT  
CTCACTCTGCTTCTGGTGTGGAAGACCGGCTGCACCGGCAGCTGACCTACGACCTGCTC  
CCAACGGACAGCGCCAGGACCTCGCCTCGGAGCTCGTGCACTATGGCTTCCTCCACGAG  
GACGACCGGATGAAGCTGGCCGCCTTCTTGAGAGCAGCTTCCTCAAGTACCGTGGGACC  
CAGGCCTGACCCGGAGCCCCAGCCCCAGGGGACCATGCCGGGGTGTGCCCCGGGCAGGCC  
ATGTTGGGGAGACTCCAGCACCGTGGGGCTGCCCTCCTCCATGCGCCTGGGAGCACAAAG  
GCCCCGGTAGTGAAGGAACCCCCGTCTCCTGAGAGTGGGGCTGACCTGCCCTTGGGCGC  
CGAGGGGTGGGGGTGGGTGTGGGGGAGCCGTTAGGCCTCCAGGTCTTAGGATCAGG  
GTTGCCCCCAGAACCCCTTCCATATCTCCATTCTCCGCCCTGAGTTCTTACCCAGGCT  
GCCTGGCTGGGGCCACTGCCTCCTCAGCATGCAGGAGGCTGCCCTGTAGGGAACCCACAGC  
TCTGGGGCTTGGGGGTGAGGGTCAGCCCTGGACAGACCTCTGCCCAGGGAACCTGCTCCAT  
GGGGTCTGGGAGAGCAGCCATCCCCTGCTGGCACCATAGACCCACACAAGGAGCCTGCAC  
AGCAAGCCAGCGGTGACACACCTGCAGGTGTCAGGCATGGCACTGGGCACAACAGGGACC  
TGGCAGGAGAAACAGACCACAGAGAGGTCTGGAGTTGAGGCTGTTGTGAGCAAAGCCCCCT  
GGTCCACACAGCTCTGCCCTAGAGCCACCTCTTTGACCCCTTACCCACCCTGAGACCAG  
AACTTGACGCCCCCTCTGCAGATCTCCTCTGGCCACTGCAGCCCCCTCCAATGGGCTTTTTTC  
TCTCATGCATTCCCTGGCCTGGAGGCGTCAGGGACCCACATCCTCCCTGCTCCTCAGAC  
TCACAGCCCCCTCCATGTTACCTCCCGCACCTCCTCCCTGGGGCAGCTGCTCCCTGGGCCT  
CTGAGGATGTGAGCTCCTGGCTCCCTGCCTCTCTCCCACTCCACTCCTGGCTCAGTCTTA  
GAGATTTCTATGCCCTCATGGATTCTACCCCTGCCTTCTGGCCTCTTGATTCTTGGCTT  
GCCTCTCCTCCAATTCCAACTTAGTGAAATGGCCTTAAGCATTTTAACTGTATGTATA  
CATTAGCGCATTTCATGCCCTTTCTAAACGCATTTCAAATGTCAACCAGGAAGGCACACCAC



## FIGURE 2WW

TGTATTAGTTTTTATACTGCCGCTGTAAAATTTACCACAACTTAGTGACTTAACACAAAT  
TTATTGCAATTCTGTAGGCTGGAAGTCTGACTATGGGTCTCACTGGACTAGAATCAAGGC  
TGGCAGGCTGCCTTCCTTCCTGGAGGTTCTAGGGGAGACTCTGTCTCCTGCTCCTTCAGG  
CTGCTGGCAGAATCCACATCCTTTTCGGTGGCAGGGCCAAGGTCCCCACTTTCTTGCTGAC  
TGTAACCTAAGGCCACTTCCAGCTTGTAGAGGCTGCCTACATTCCCTGGCTCTTGCCCCC  
CTCCTCCATCTTCAGAGCTAGCAGGTTTCACTGTGTGTACGAACCATTTCTCTGGTTCCC  
TGCAGACAGGAAAGGTTGTCCCTAAGGACTCATGAGATTAGGTTGGGCCCAGCCAGATAA  
TACATGATAATCTCCCTCCTCAAGGTTTTTAATATTAAACACATCTGCAGGACACATTTT  
GCCATGTAACTAACATTCAGTGGTTCCAGGGATTAAGGAATGAACCTCTTTTGTGGGG  
AAGGCTGGCATTCTGCTGACCACAGCACTCCAACCAAAGCCAAAAACCAAAGCAAGACT  
TACTAACGCATATCAAAATAATTAAAGGTACAAAATCGTGAATCTCAGTTATCTTAAATA  
TTCCAATACTATTTACAAAATTATTCAAATTTCTCAGCCTTCCAACCTCAAAATTAGCAAT  
CTAAAGTAATTTCCATATCCTAGATGGAAACCCTCATGCTAACTGTCTGATTATGCATG  
GTTCTAAATGGTTTCAGTGGCAAATACATAACATTGTACTACTGATTAACTGAACCTAA  
AAGC

SEQ ID NO: 62\_AA103218\_M SGK034\_M

CCACGCGTCCGCACCAGAGTATGGCGAAGTCAATGATGGGACTGGCTTTGTGGACATCTT  
CTCCTTCGGGATGTGTGCACTGGAGATGGCTGTACTCGAGATCCAAGCCAACGGGGATAC  
CAGAGTCACAGAAGAGGCCATCGCTCGAGCCAGGCACTCACTGAGTGACCCCAACATGCG  
GGAATTCATCCTCTCCTGCCTGGCCCCGGGACCCTGCCCGCCGACCCTCAGCCCCAACCT  
CCTCTTCACCGAGTGCTCTTTGAGGTGCACTCGCTGAAGCTGCTGGCAGCTCACTGCTT  
CATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTAGAGGAAAAGACCAAGGCCATGGA  
CCTCCATGCAGTTTTTGGCTGAGATGCCGAGCCCCATGGACCCCCAATGCAGTGGCGSTA  
CTCAGAGGTCTCCTTCTTGGAGCTGGACAAATTCCTAGAGGATGTCAGGAACGGGATCTA  
TCCACTGATGAACTTTGGGCTGCTCGGCCCTTGGGGCTTCCCCGTGTGTTGGCCCCACC  
CCCAGAGGAAGCCCCAAAAGGCCAAAACCTCCAACGCCAGAACCCCTTGACTCGGAGACCAG  
GAAGGTGGTCCAGATGCAGTGCAACCTGGAAAGAAGCGAGGACAAGGCTCGGTGGCACCT  
TACTCTGCTCTTGGTGTGAGGACCGGCTACATCGGCAGCTGACCTATGATCTGCTCCC  
AACGGACAGTGCCAGGACCTCGCTGCTGAAGTAGTGATTATGGCTTCCTGCACGAGGA  
TGACAGGACAAAGCTAGCAGCCTTTCTGGAGACCACTTTTCTCAAGTACCGAGGGACGCA  
AGCGTGACCTTCCAGTCTGACGGCCCAGCAGAGATACAGGGGCTCAGGGTTGTCCACT  
TGGCAAAGAGCCCCCACACTGCTCAAAGCTGCCTTCTGCCTGTGTTCCCTGGAACCTGAAC  
ACAGGCCCTGCTAGTGAAGACACCCCCACCCCCAGCTTTCTGCAGCAGTGTGGGACCCT  
GGGGTGGTGTGAGGCCCTGAGCCTGGACGAGAGTGGATACAGGTCAGTTAGGGGAACCG  
CTCCATCTGGTACTAGACAACAGCCATGCCTTCAGGTGGCATAGAAACCTAGGGAAGGAG  
CCTGAACTCAGGTGTACAGTGCTGGGCATCAGGCAGACCAGACCTGACCTGATTGGAGA  
ACTGTAGACTAGATAGCTTGGAGTTGAACCCATGGCCAGGGAATTCCTTGGTCTGCTCA  
GACCAGTCTGATCCCTTGACAGCTGCCTTGAGCCCTCTTTCTGATCTTCCACACTCTT  
GAGACCAGGACCTGTGTCTCCCCAAAGCCCTTGGGAAGGATCTTTCTATTTCATCATCCC  
TCTGGCCTAGGGGCTCAGGGGTCAGGCATCCTCCACATTCCTCCCTGGGGAAGTTGTGT  
GTTTGAGTTGAGGATGTGGGTTTCTGGCTCCCTCTTTCTCCCCAGCCCAACTTGTCTCTT  
TCTTACTGGTTTCAAAGTCCTGATGAACGCTTCCCCCTCAGAGCCACCCTGGTTTTCTTG  
TTCTTGAAGTGCCTCTCTCCCAACTTCAAACCAGGTCTTAAACGTTTTTTAAATGCATAT  
ATAAATGTAATGCAGTCACGGTCCCTTTTTAAACACTTTGTGTATGAAACCAGGAAAGCTC  
ACTATTGTATTAGGAATAGTTCCACATTGCTGCTGTTAACAGATATCATAAACCCAGTGG  
TTTGAGACGACACACACACACACACACACACACAGAGAGAGAGAGAGATTCTGTA  
CATCAAGTGTGATCCAGGCTCTCACTAGATTAATACCCAGGCTAAGTTCCTTTCTGGAAG  
CTGGGACTTACCTCCTGCTCCTTCAAGCTATTGGCAGAACTCACTTCCCTGCAATGGTAA  
GGCAGAAATCCCTATTTTCTCAACAGCTGCCAACTAAGAACCCTCTCAGCTTCTAGAGG

## FIGURE 2XX

CCACCAACTTTTCTTAGTTCTTCTTTCTCCCCCTCAAGACCAGCAGCGTCAAGTTGAAT  
CTTTGTCTGGGCTAGCTGACTGGCTTGCCACTGCTGGGAAGAGTTGGGGCCTTTTGTGA  
GTAGGTTGGACCCACCAGGATAACCGAGGATGATCCCCTTCTCAGGGTCTATAGATGAAC  
CACACCTGCGCAGTTCCTTCTGCTGTATCCTGGGCTTTGGTGCTTGGAGAACAGCCGTG  
GGCGGTGGGTGTTGTTACTGTGGTACCTACCATGCCATCTTAACCGAAACCAAGACCTAA  
AATAAACAGATTTGTTCATGGGACATCTAATAAATTAATGAAGTCTG

SEQ ID NO: 63\_NEK7\_H, N34132\_H

CACGAATCCGAGCCCGCTCGCCTCTCTCCAGCGAACCAGCCATGTCTGGCGGCGCCGCAG  
AGAAGCAGAGCAGCACTCCCGGTTCCCTGTTCTCTCGCCGCCGGCTCCTGCCCCAAGA  
ACGGCTCCAGCTCCGATTCTCCGTGGGGGAGAACTGGGAGCCGCGGCCGCCGACGCTG  
TGACCGGCAGGACCGAGGAGTACAGGCGCCGCCGCCACACTATGGACAAGGACAGCCGTG  
GGGCGGCCGCGACCACTACCACCACTGAGCACCGCTTCTTCCGCCGGAGCGTCATCTGCG  
ACTCCAATGCCACTGCACTGGAGCTTCCCGGCCTTCTCTTTCCCTGCCCCAGCCAGCA  
TCCCCGCGGCTGTCCCGCAGAGTGCTCCACCGGAGCCCCACCGGGAAGAGACCGTGACCG  
CCACCGCCACTTCCAGGTAGCCAGCAGCCTCCAGCCGCTGCCGCCCTGGGGAACAGG  
CCGTGCGGGGCCCTGCCCCCTCGACTGTCCCGAGCAGTACCAGCAAAGACCGCCAGTGT  
CCCAGCCTAGCCTTGTGGGGAGCAAAGAGGAGCCGCCGCCGGCGAGAAGTGGCAGCGGCG  
GCGGCAGCGCCAAGGAGCCACAGGAGGAACGGAGCCAGCAGCAGGATGATATCGAAGAGC  
TGGAGACCAAGGCCGTGGGAATGTCTAACGATGGCCGCTTTCTCAAGTTTGACATCGAAA  
TCGGCAGAGGCTCCTTTAAGACGGTCTACAAAGGTCTGGACACTGAAACCACCGTGGAAG  
TCGCCTGGTGTGAAGTGCAGGATCGAAAATTAACAAAGTCTGAGAGGCAGAGATTTAAAG  
AAGAAGCTGAAATGTTAAAGGTCTTCAGCATCCCAATATTGTTAGATTTTATGATTCTT  
GGGAATCCACAGTAAAAGGAAAGAAGTGCATTGTTTGGTGACTGAACTTATGACGTCTG  
GAACACTTAAACGTATCTGAAAAGGTTTAAAGTGATGAAGATCAAAGTTCTAAGAAGCT  
GGTGCCGTGAGATCCTTAAAGGTCTTCAGTTTCTTCATACTCGAACTCCACTTATCATTC  
ACCGCGATCTTAAATGTGACAACATCTTTATCACCGGCCCTACTGGCTCAGTCAAGATTG  
GAGACCTCGGTCTGGCAACCCTGAAGCGGGCTTCTTTTGCCAAGAGTGTGATAGGTACCC  
CAGAGTTTATGGCCCCGTGAGATGTATGAGGAGAAATATGATGAATCCGTTGACGTTTATG  
CTTTTGGGATGTGCATGCTTGAGATGGCTACATCTGAATATCCTTACTCGGAGTGCCAAA  
ATGCTGCGCAGATCTACCGTCCGCTGACCAGTGGGGTGAAGCCAGCCAGTTTTTGACAAAG  
TAGCAATTCCTGAAGTGAAGGAAATTATTGAAGGATGCATACGACAAAACAAAGATGAAA  
GATATTCCATCAAAGACCTTTTGAACCATGCCTTCTTCCAAGAGGAAACAGGAGTACGGG  
TAGAATTAGCAGAAGAAGATGATGGAGAAAAAATAGCCATAAAATTATGGCTACGTATTG  
AAGATATTAAAGAAATTAAAGGAAAAATACAAAGATAATGAAGCTATTGAGTTTTGTTTG  
ATTTAGAGAGAGATGTCCAGAAGATGTTGCACAAGAAATGGTAGAGTCTGGGTATGTCT  
GTGAAGGTGATCACAAGACCATGGCTAAAGCTATCAAAGACAGAGTATCATTAATTAAGA  
GGAAACGAGAGCAGCGGCAGTTGGTACGGGAGGAGCAAGAAAACAAAAGCAGGAAGAGA  
GCAGTCTCAAAACAGCAGGTAGAACAATCCAGTGCTTCCCAGACAGGAATCAAGCAGCTCC  
CTTCTGCTAGCACCGGCATACCTACTGCTTCTACCACTTCAGCTTCAGTTTCTACACAAG  
TAGAACCTGAAGAACCCTGAGGCAGATCAACATCAACAACCTACGTACCAGCAACCCAGTA  
TATCTGTGTTATCTGATGGGACGGTTGACAGTGGTCAGGGATCCTCTGTCTTACAGAAT  
CTCGAGTGAGCAGCCAACAGACAGTTTCATATGGGTTCCCAANNCATGAACAGGCACATT  
CTACAGGCACAGTCCCAGGGCATATACCTTCTACTGTCCAAGCACAGTCTCAGCCCCATG  
GGGTATATCCACCCTCAAGTGTGCAGCAGGGAATACAGCAGACAGCCCCCTCCTCAACAGA  
CAGTGCAAGTATTCACTTTACAGACATCAACCTCCAGTGAGGCCACTACTGCACAGCCAG  
TGAGTCAGCCTCAAGCTCCACAAGTCTTGCCCTCAAGTATCAGCTGGAAAACAGAGTACTC  
AGGGAGTCTCTCAGGTTGCTCCTGCAGAGCCAGTTGCAGTAGCACAGCCCCAAGCTACCC  
AGCCGACCACTTTGGCTTCTCTGTAGACAGTGCACATTGAGATGTTGCTTCAGGTATGA  
GTGATGGCAATGAGAACGTCCCATCTTCCAGTGGAAGGCATGAAGGAAGAACTACAAAAC

## FIGURE 2YY

GGCATTACCGAAAATCTGTAAGGAGTCGCTCTCGACATGAAAAAACTTCACGCCCAAAAT  
TAAGAATTTTGAATGTTTCAAATAAAGGAGACCGAGTAGTAGAATGTCAATTAGAGACTC  
ATAATAGGAAAATGGTTACATTCAAATTTGACCTAGATGGTGACAACCCCGAGGAGATAG  
CAACAATTATGGTGAACAATGACTTTATTCTAGCAATAGAGAGAGAGTCTGTTTGTGGATC  
AAGTGCGAGAAAATTATTGAAAAAGCTGATGAAATGCTCAGTGAGGATGTCAGTGTGGAAC  
CAGAGGGTGATCAGGGATTGGAGAGTCTACAAGGAAAGGATGACTATGGCTTTTCAGGTT  
CTCAGAAATTGGAAGGAGAGTTCAAACAACCAATTCCTGCGTCTTCCATGCCACAGCAAA  
TAGGCATTCTTACCAGTTCTTTAACTCAAGTTGTTTCAATCTGCGGGAAGGCGGTTTATAG  
TGAGTCCTGTGCCAGAAAGCCGATTACGAGAATCAAAAAGTTTTCCCCAGTGAAATAACAG  
ATACAGTTGCTGCCTCTACAGCTCAGAGCCCTGGAATGAACTTGTCTCACTCTGCATCAT  
CCCTTAGTCTACAACAGGCCTTTTCTGAACCTTAGACGTGCCCAAATGACAGAAGGACCCA  
ATACAGCACCTCCAACTTTAGTCATACAGGACCAACATTTCCAGTAGTACCTCCTTTCT  
TAAGTAGCATTGCTGGAGTCCCAACCACAGCAGCAGCCACAGCACCAGTCCCTGCAACAA  
GCAGCCCTCCTAATGACATTTCCACATCAGTAATTCAGTCTGAGGTTACAGTGCCCACTG  
AAGAGGGGATTGCTGGAGTTGCCACCAGCACAGGTGTGGTAACCTTCAGGTGGTCTCCCA  
TACCACCTGTGTCTGAATCACCAGTACTTTCCAGCGTAGTTTCAAGTATCACAATACCTG  
CAGTTGTCTCAATATCTACTACATCCCCGTCACTTCAAGTCCCCACATCCACATCTGAGA  
TCGTTGTTTCTAGTACAGCACTGTATCCTTCAGTAACAGTTTCAGCAACTTCAGCCTCTG  
CAGGGGGCAGTACTGCTACCCCAAGTCTTAAGCCTCCAGCTGTAGTATCTCAGCAGGCAG  
CAGGCAGCACTACTGTGGGAGCCACATTAACATCAGTTTCTACCACCACCTTCATTCCCAA  
GCACAGCTTCACAGCTGTCCATTAGCTTAGCAGCAGTACTTCTACTCCTACTTTAGCTG  
AAACCGTGGTAGTTAGCGCACACTCACTAGATAAGACATCTCATAGCAGTACAACCTGGAT  
TGGCTTTCTCCCTCTCTGCACCATCTTCCTCTTCTCCTGAGCAGGAGTGTCTAGTT  
ATATTTCTCAGCCTGGTGGGCTGCATCCTTTGGTCATTCCATCAGTGATAGCTTCTACTC  
CTATTCTTCCCAAGCAGCAGGACCTACTTCTACACCTTTATTACCCCAAGTACCTAGTA  
TCCCACCCTTGGTACAGCCTGTTGCCAATGTGCCTGCTGTACAGCAGACACTAATTCATA  
GTCAGCCTCAACCAGCTTTGCTTCCCAACCAGCCCCATACTCATTGTCCTGAAGTAGATT  
CTGATACACAACCCAAAGCTCCTGGAATTGATGACATAAAGACTCTAGAAGAAAAGCTGC  
GGTCTCTGTTTCACTGAACACAGCTCATCTGGAGCTCAGCATGCCTCTGTCTCACTGGAGA  
CCTCACTAGTCATAGAGAGCACTGTACACCAGGCATCCCACTACTGCTGTTGCACCAA  
GCAAACTCCTGACTTCTACCACAAGTACTTGCTTACCACCAACCAATTTACCACTAGGAA  
CAGTTGCTTTGCCAGTTACACCAGTGGTCACACCTGGGCAAGTTTCTACCCCACTCAGCA  
CTACTACATCAGGAGTGAAACCTGGAAGTCTCCTCCAAGCCACCTCTAACTAAGGCTC  
CGGTGCTGCCAGTGGGTACTGAACTTCCAGCAGGTACTCTACCCAGCGAGCAGCTGCCAC  
CTTTTCCAGGACCTTCTCTAACCAGTCCCAGCAACCTCTAGAGGATCTTGATGCTCAAT  
TGAGAAGAACACTTAGTCCAGAGATGATCACAGTGAATCTGCGGTTGGTCTGTGTCCA  
TGGCGGCTCCAACAGCAATCACAGAAGCAGGAACACAGCCTCAGAAGGGTGTCTTCAAG  
TCAAAGAAGGCCCTGTCTAGCAACTAGTTTCAAGAGCTGGTGTTTTAAAGATGGGACGAT  
TTCAGGTTTCTGTTGCAGCAGACGGTGCCAGAAAGAGGGTAAAAATAAGTCAGAAGATG  
CAAAGTCTGTTTCAATTTGAATCCAGCACCTCAGAGTCTCAGTGCTATCAAGTAGTAGTC  
CAGAGAGTACCTTGGTGAAACCAGAGCCGAATGGCATAACCATCCCTGGTATCTCTTCAG  
ATGTGCCAGAGAGTGCCCAAAAATACTGCCTCAGAGGCAAGTCAGACACTGGGCAGC  
CTACCAAGGTTGGACGTTTTTCAGGTGACAACTACAGCAAAACAAAGTGGGTCTGTTCTCTG  
TATCAAAAATACTGAGGACAAGATCACTGACACAAAGAAAGAGGACCAGTGGCATCTCCTC  
CTTTTATGGATTTGGAACAAGCTGTTCTTCTGCTGTGATACCAAGAAAGAGAAGCCTG  
AACTGTCAGAGCCTTCACATCTAAATGGGCCGTCTTCTGACCCGAGGCGCTTTTTTAA  
GTAGGGATGTGGATGATGGTTCCGGTAGTCCACACTCGCCCCATCAGCTGAGCTCAAAGA  
GCCTTCTAGCCAGAATCTAAGTCAAAGCCTTAGTAATTCATTAACTCCTCTTACATGA  
GTAGCGACAATGAGTCAGATATCGAAGATGAAGACTTAAAGTTAGAGCTGCGACGACTAC  
GAGATAAACATCTCAAAGAGATTGAGGACCTGCAGAGTCGCCAGAAGCATGAAATTGAAT

## FIGURE 2ZZ

CTTTGTATACCAAACCTGGGCAAGGTGCCCCCTGCTGTTATTATTCCCCCAGCTGCTCCCC  
TTTCAGGGAGAAGACGACGACCCACTAAAAGCAAAGGCAGCAAATCTAGTCGAAGCAGTT  
CCTTGGGGAATAAAAGCCCCCAGCTTTTCAGGTAACCTGTCTGGTCAGAGTGCAGCTTCAG  
TCTTGACCCCCCAGCAGACCCCTCCACCCTCCTGGCAACATCCCAGAGTCCGGGCAGAATC  
AGCTGTTACAGCCCCCTTAAGCCATCTCCCTCCAGTGACAACCTCTATTTCAGCCTTCACCA  
GTGATGGTGGCATTTCAGTACCAAGCCTTTCTGCTCCAGGTCAAGGTAATAAAGCAACCA  
TCATCGTCCAAAACAATAAAATGGAGATGTTGCCATACCTGGGACAAAAGCCTGTAAAG  
GCGGGTTGGGAGACTAGCTGACCAGAACACAGCCTGTGTGTTGTACACTGAAGAATCTGG  
GTGAAAAGGGAAGTGGAGTGATAATGAGAATCGGTGGGCTCACTGCTCCCATTAGGTGAA  
ATTACTTTTTTTCAAGGAATTACAGTGAAAAGTTACATCTGTGTGGCCTATATGACTTGC  
TCATTTGGGATTTGGAACCTTAGGCTTTAATATTAGGCTGAGATTTCTGGATGAAATCT  
AAGGTGTTTTAGCAGTTTCTGAAGCTAATACATTTTCTTAGCCATTGTAGAATTTTGTTA  
CTTTTAAGTATGGGAGTGGCATACTAAAATGAATAACCTTACAATTTCAGTTTTTTATCCA  
TAATCTACTTTCCAAATATAGCTCTGTTTATTAGTGATTGCTGAAAAAATTCCCACAGAG  
GAAAGAGCTTTTAGTCATATTAGAACAAGAATTGAAAAGACTTGGGCATCTGGGTGAGAA  
GAATGAAAAAATATAGGTACTGGCTTATGTGCCTTTGCCACAGTTTCACAGAAATTAGA  
GATCAGTCTCTTCACAGGAAGAATGCACTTGATTGGTAAGGAGGGCAAACCTAGCTAGCAT  
TATTCGAACTAAGAAAAGCTTCCGCATTTTGCAGATGGGTAGAATTAAGACCTAATATTT  
CATCTCTTACATATCTGACCTTCCCCCAGAAGCTTGTTCTTCTGTGTGCCATCTTAGTG  
CATTTACCACTCCAGCCTCAAGTTTCTAACATCTTGTAGTTGTGTTCTGTCTCTTCTCC  
TCTCTGTCTTACCCTGTTTTTCCCCCTCTCACAGGCTGTGCGAAGTTTAACTGTGCATC  
TGAACAGGTGACATTCAAACCTGGTGGCAGGAGGACCCGATTTCTGAGTACGCCCTGCTT  
GGCTCTTTGTGTGTAACACCTTTACTCCTTCTTGTCTTGTGTTTCTGCTGCTTGGATC  
TGATGTTTCACGCAGTCCATTTTCATTTGTCTCTTTTGTATATCATCTACTCAGTGGCT  
TGGCTGAATTACTGTTACCCTCAGAAGTTTGGGCCCCCACATTAATTATGATAAAAAATG  
TCAAAATAACAAGTTATCTACAAATTTCAATGTAACTTTCTGGTAGAAGTGCTTCTTCAT  
GGATCTGTGACAGAGAGTGGATATGGTATCTAGGCAATAGATTGCTGGGTCATTTAGAAT  
AATGAAGACTGAACTCCACAGTCGTAGTCAGTGCTGTCTGTCTGCCCTAGCATTAGAAAT  
GAGAGAAATCAGCCAGACACGGTGGCGTACACCTGTAATCCCAGCACTTTGGGAGGCCGA  
GGCGGGAAGATTGCTTGAGGCCAGGAGCTCGAGACCAACCCTGGGCAACATGGTGATACC  
CCATCTCT

SEQ ID NO: 64\_BCON3\_H

GCGGAGCGCAGCTGTGAGGGAGTCGCTGTGATCCGGGGCCCCGGAACCCGAGCTGGAGCT  
GAAGCGCAGGCTGCGGGGCGGGAGTCGGGAGGCCTGAGTGTTCTTCCAGCATGTCCGA  
GGGGGAGTCCCAGACAGTACTTAGCAGTGGCTCAGACCCAAAGGTAGAATCCTCATCTTC  
AGCTCCTGGCCTGACATCAGTGTCACCTCCTGTGACCTCCACAACCTCAGCTGCTTCCCC  
AGAGGAAGAAGAAGAAAGTGAAGATGAGTCTGAGATTTTGGAAGAGTCGCCCTGTGGGCG  
CTGGCAGAAAGAGGCGAGAAGAGGTGAATCAACGGAATGTACCAGGTATTGACAGTGCATA  
CCTGGCCATGGATACAGAGGAAGGTGTAGAGGTTGTGTGGAATGAGGTACAGTTCTCTGA  
ACGCAAGAAGTACAAGCTGCAGGAGGAAAAGGTTCTGTGCTGTGTTTGATAATCTGATTCA  
ATTGGAGCATCTTAACATTGTTAAGTTTCACAAATATTGGGCTGACATTAAAGAGAACAA  
GGCCAGGGTCATTTTTATCACAGAATACATGTCATCTGGGAGTCTGAAGCAATTTCTGAA  
GAAGACCAAAAAGAACCAAGACGATGAATGAAAAGGCATGGAAGCGTTGGTGCACACA  
AATCCTCTCTGCCCTAAGCTACCTGCACCTCCTGTGACCCCCCATCATCCATGGGAACCT  
GACCTGTGACACCATCTTCATCCAGCACAACGGACTCATCAAGATTGGCTCTGTGGCTCC  
TGACACTATCAACAATCATGTGAAGACTTGTGAGAAGAGCAGAAGAATCTACACTTCTT  
TGCACCAGAGTATGGAGAAGTCACTAATGTGACAACAGCAGTGGACATCTACTCCTTTGG  
CATGTGTGCACTGGAGATGGCAGTGCTGGAGATTTCAGGGCAATGGAGAGTCCTCATATGT  
GCCACAGGAAGCCATCAGCAGTGCCATCCAGCTTCTAGAAGACCATTACAGAGGGAGTT

## FIGURE 2AAA

CATTCAAAAGTGCCTGCAGTCTGAGCCTGCTCGCAGACCAACAGCCAGAGAACTTCTGTT  
CCACCCAGCATTGTTTGAAGTGCCCTCGCTCAAACCTCCTTGCGGCCCACTGCATTGTGGG  
ACACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACCAAAAACATGGATACTAG  
TGCCGTACTGGCTGAAATCCCTGCAGGACCAGGAAGAGAACCAGTTCAGACTTTGTACTC  
TCAGTCACCAGCTCTGGAATTAGATAAAATTCCTTGAAGATGTCAGGAATGGGATCTATCC  
TCTGACAGCCTTTGGGCTGCCTCGGCCCCAGCAGCCACAGCAGGAGGAGGTGACATCACC  
TGTCGTGCCCCCTCTGTCAAGACTCCGACACCTGAACCAGCTGAGGTGGAGACTCGCAA  
GGTGGTGCTGATGCAGTGCAACATTGAGTCGGTGGAGGAGGGAGTCAAACACCACCTGAC  
ACTTCTGCTGAAGTTGGAGGACAACTGAACCGGCACCTGAGCTGTGACCTGATGCCAAA  
TGAGAATATCCCCGAGTTGGCGGCTGAGCTGGTGCAGCTGGGCTTCATTAGTGAGGCTGA  
CCAGAGCCGTTGACTTCTCTGCTAGAAGAGACCTTGAACAAGTTCAATTTTGCCAGGAA  
CAGTACCCCTCAACTCAGCCGCTGTCAACGCTCTCTCTTAGAGCTCACTCGGGCCAGGCCC  
TGATCTGCGCTGTGGCTGTCCCTGGACGTGCTGCAGCCCTCCTGTCCCTTCCCCCAGTC  
AGTATTACCCCTGTGAAGCCCCCTCCCTCCTTTATTATTACAGGAGGGCTGGGGGGCTCCC  
TGGTTCTGAGCATCATCCTTCCCCCTCCCCCTCTCTCTCCCCCTCTGCACTTTGTTTACT  
TGTTTTGCACAGACGTGGGCTGGGCCTTCTCAGCAGCCGCCTTCTAGTTGGGGGCTAGT  
CGCTGATCTGCCGGCTCCCGCCAGCCTGTGTGGAAAGGAGGCCACGGGCACTAGGGGA  
GCCGAATTCTACAATCCCGCTGGGGCGGCCGGGGCGGGAGAGAAAGGTGGTGCTGCAGTG  
GTGGCCCTGGGGGGCCATTGATTGCGCTCAGTTGCTGCTGTAATAAAAGTCTACTTTTT  
GCT

SEQ ID NO: 65\_AA711829\_M

CTTAAGCAGTTTCTGAAGAAGACCAAAAAGAACCACAAGACTATGAATGAAAAGGCTTGG  
AAACGCTGGTGTACACAGATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCTCCC  
ATCATCCATGGGAACCTGACCTGTGACACCATCTTCATCCAGCACAAACGGACTCATCAAG  
ATTGGCTCTGTGGCTCCTGACACTATCAACAATCACGTGAAGACTTGCCGGGAAGAACAG  
AAGAACCTACACTTTTTTGCACCAGAGTATGGAGAAGTCACAAACGTGACAACAGCAGTG  
GACATCTACTCCTTTGGCATGTGTGCACTGGAGATGGCAGTGCTGGAGATTAGGGCAAT  
GGCGAGTCCTCATATGTGCCACAGGAAGCCATCAGCAGTGCCATCCAGCTACTAGAAGAC  
TCATTACAGAGGGAGTTTATTCAAAGTGCCTGCAGTCTGAGCCTGCTCGGAGACCAACA  
GCCAGAGAACTTCTGTTCCACCCAGCACTGTTTGAAGTGCCCTCACTCAAGCTTCTTGCT  
GCTCACTGTATCGTGGGGCACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACC  
AAGAACATGGATACCAGTGCTGTACTAGCTGAAATTCCTGCAGGGCCAGGACGAGAACCA  
GTTACAGACTTTGTACTCTCAGTCACCAGCCCTAGAATTAGACAAATTCCTTGAAGATGTC  
AGGAATGGGATCTACCCTCTGACAGCCTTTGGGCTACCTCGGCCTCAGCAGCCACAGCAG  
GAGGAGGTGACATCACCTGTTGTGCCCCCTCTGTCAAGACTCCAACCTCCTGAGCCAGCT  
GAAGTGGAGACACGAAAGGTGGTGCTGATGCAGTGCAACATCGAATCTGTGGAGGAGGGA  
GTCAAACACCATCTAACACTTCTGCTGAAGCTGGAGGACAAATTGAACCGGCACCTGAGC  
TGTGACCTGATGCCAAATGAGAGCATCCCGGACTTGGCAGCTGAGCTGGTGCAGCTGGGC  
TTCATTAGTGAGGCTGATCAGAGCCGCTGACTTCTCTGCTGGAGGAGACGCTCAACAAG  
TTCAACTTCACCAGGAACAGTACACTCAACACAGCCACTGTACCGTCTCCTCGTAGAGC  
TCACTTGAGCCAGGCCCCCTAGCCAGGCTGTGGCTGTCCCTGGGCATGCTGCAGTCTCTCT  
GTCCCTTCTCCCCAGTCAGTATTACCCTTCGCGCCCATATTATTTAGGAGGGCTTTAGGG  
GCTCCCTGTTGAGTATCACCTGCCCCCTTCCCCCTCTCTTCCCTCCCCCTCTGCACTTTGTT  
TACTTGTTTTGCACAGACGTGGGCCTGGGCCTTCTCAGCAGCCACCTTCTAGCTGGGGGC  
TAGTAGCTGACCTGCTGCCTCCTGCCCTACTTGTGTGGACAGGAGGCCACGGGCACTGG  
GGAAGCTGAGTTCTACAATCCCGCTGGGGCGCATGGGCAGGAGAGAAAGGTGGTGCTGCA  
GGGGTGGCCCCCGGGGGGGGCATTGCAATCACCTCAGTTGCTGCTGTAATAAAGTCTAC  
TTTTTGCT

## FIGURE 2BBB

SEQ ID NO: 66\_AA099102\_H

ATGTCATCATGTGTCTCTAGCCAGCCAGCAGCAACCGGGCCGCCCCCAGGATGAGCTG  
GGGGGCAGGGGCAGCAGCAGCAGCGAAAGCCAGAAGCCCTGTGAGGCCCTGCGGGGCCTC  
TCATCCTTGAGCATCCACCTGGGCATGGAGTCCTTCATTGTGGTCACCGAGTGTGAGCCG  
GGCTGTGCTGTGGACCTCGGCTTGGCGCGGGACCGGCCCTGGAGGCCGATGGCCAAGAG  
GTCCCCCTTGACACCTCCGGGTCCCAGGCCCCGCCCCACCTCTCCGGTCGCAAGCTGTCT  
CTGCAAGAGCGGTCCCAGGGTGGGCTGGCAGCCGGTGGCAGCCTGGACATGAACGAGCGC  
TGCATCTGCCCGTCCCTGCCCTACTCACCCGTCAGCTCCCCGAGTCCTCGCCTCGGCTG  
CCCCGGCGGGCCGACAGTGGAGTCTCACCACGTCTCCATCACGGGTATGCAGGACTGTGTG  
CAGCTGAATCAGTATACCTGAAGGATGAAATTGGAAAGGGCTCCTATGGTGTCTGCAAG  
TTGGCCTACAATGAAAATGACAATACCTACTATGCAATGAAGGTGCTGTCCAAAAAGAAG  
CTGATCCGGCAGGCCGCTTTTCCACGTGCCCCCTCACCCGAGGCACCCGGCCAGCTCCT  
GGAGGCTGCATCCAGCCCAGGGGCCCATTTAGCAGGTGTACCAGGAAATTGCCATCCTC  
AAGAAGCTGGACCACCCCAATGTGGTGAAGCTGGTGGAGGTCTGGATGACCCCAATGAG  
GACCATCTGTACATGGTGTTCGAACTGGTCAACCAAGGGCCCGTGATGGAAGTGCCACC  
CTCAAAACCACTCTCTGAAGACCAGGCCCGTTTCTACTTCCAGGATCTGATCAAAGGCATC  
GAGTACTTACACTACCAGAAGATCATCCACCGTGACATCAAACCTTCCAACCTCCTGGTC  
GGAGAAGATGGGCACATCAAGATCGCTGACTTTGGTGTGAGCAATGAATTCAAGGGCAGT  
GACGCGCTCCTCTCAAACCTACGTGGGCACGCCCGCCTTCATGGCTCCCGAGTCGCTCTCT  
GAGACCCGCAAGATCTTCTCTGGGAAGGCCAAGGATGTTTGGGCCATGGGTGTGACACTA  
TACTGCTTTTGTCTTTGGCCAGTGCCCATTCATGGACGAGCGGATCATGTGTTTACACAGT  
AAGATCAAGAGTCAGGCCCTGGAATTTCCAGACCAGCCCGACATAGCTGAGGACTTGAAG  
GACCTGATCACCCGTATGCTGGACAAGAACCCCGAGTCGAGGATCGTGGTGCCGGAATC  
AAGCTGCACCCCTGGGTACGAGGCATGGGGCGGAGCCGTTGCCGTCCGAGGATGAGAAC  
TGCACGCTGGTTCGAAGTGACTGAAGAGGAGGTGAGAACTCAGTCAAACACATTCCCAGC  
TTGGCAACCGTGATCCTGGTGAAGACCATGATACGTAAACGCTCCTTTGGGAACCCATTC  
GAGGGCAGCCGGCGGGAGGAACGCTCACTGTCAGCGCCTGGAACTTGCTACCAAAAAA  
CCAACCAGGGAATGTGAGTCCCTGTCTGAGCTCAAGGAAGCAAGGCAGCGAAGACAACCT  
CCAGGGCACCGACCCGCCCCCGTGGGGGAGGAGGAAGTGCTCTTGTGAGAGGCAGTCCC  
TGCGTGGAAAGTTGCTGGGGCCCCCGCCCCGGCTCCCCCGCACGCATGCATCCACTGCGG  
CCGGAGGAGGCCATGGAGCCCGAGTAG

SEQ ID NO: 67\_5R69\_17\_2\_H

CCGGGATGTGAGCCTGGTGGTTGGCAGCTGGAGCCACGTCCGAGGGGGAAGTGTGCGCAGC  
ATTCTCTGCAGGCATCACAGACCTGAGGCAGTGGCCTCCGGAGGGCACTGGACAGAAACA  
GCCATCCAAGTGGCTGAGTGGAGGGACCTGCTCAAGTGCAGCTGCAGTGGCCGGGGTTT  
CCCTCAGGTAGGATCGGGGCGCCTTGTCGCCGCCAGCCACGTGTGGCGTCCGGTACAGT  
CAGCAGAGTGCAGGGTGCGGGCACCAAGGAAAGGGGGCGCAGGGGAACCTCCCGCGGGCCTC  
GCGTTTGCAAACCTTCTCGCCTGGGCAGGAGGCGGTGCTGGGAAAGAAGGTGGAAGAGCGA  
GCTTTTGGAACTGTGCACGGGACAGATTGGACGCACACCCCTCGGGAGGCGCGAAGGCA  
TGGAATAATTTGAAGCATATTATCACCCCTTGCCAGGTATCCACAAACGGTGTGAAGAGA  
TGAAATACTGCAAGAAACAGTGCCGGCGCCTGGGCCACCGCGTCTCGGCCTGATCAAGC  
CTCTGGAGATGCTCCAGGACCAAGGAAAGAGGAGCGTGCCCTCTGAGAAGTTAACCACAG  
CCATGAACCGCTTCAAGGCTGCCCTGGAGGAGGCTAATGGGGAGATAGAAAAGTTCAGCA  
ATAGATCCAATATCTGCAGGTTTCTAACAGCAAGCCAGGACAAAATACTCTTCAAGGACG  
TGAACAGGAAGCTGAGTGATGTCTGGAAGGAGCTCTCGCTGTACTTCAGGTTGAGCAAC  
GCATGCCGTGTTTACCCATAAGCCAAGGAGCGTCTGGGCACAGGAAGATCAGCAGGATG  
CAGACGAAGACAGGCGAGCTTTCAGATGCTAAGAAGAGATAATGAAAAAATAGAAGCTT  
CACTGAGACGATTAGAAATCAACATGAAAGAAATCAAGGAACTTTGAGGCAGTGTAAGT  
TATCATGTGCCCTGCTGTTTCTGATGGCCCCCAAACCTAGAAGTCATCAGTTTACTGGGAC

## FIGURE 2CCC

CCCAGCCTCCCGCTACCCCTGCATTTGTCCATTTTCTGTGCTGGATGGCTGGAAGCAGCC  
CACAGGTTTGGGGATCCATTCATGGCTAGCCAGGCTTCTGTCCATGGAATAACATGTGG  
AGAGAGCTTCTTGACCAGTAAGATACCTTCTAGCAGCTGTCAAAGTACTTAAAAACCTCT  
ATGAATAGAATCAAAGCTTCAGTTCAGTTGCTGAATTTCCAAGAAGAAATTCAAATCAAA  
TTTAAATGCCCACTCATTCAATTCATTCAACAAAACCTGTGAGTATCTGGTTTATGCCAGA  
GGCCATGCAAAGAGGTAACATAAGATGCAGAGAAGGACACTGCCTTCCAGGAGCTCACGGG  
GTGGAGGAGGAAAGAGGAAAGACAGACAGTGAACACACAACAGCAAGGTTACTGAGCTTG  
AACTATGTCCCTAACTACTAGATCTGAAATGACTACGCCAGATGCCAGATGCTCAAGTGC  
CAAGCTCTGGGTAACAGGAATAGACATCCTTCCAGGATGAGAGAGATGAGTCTGGATGAG  
GGTTAAGGCTGGAGGGACAGGCGGGATTGAAAGAGGAGGGAAGGAAGTGGATGACACAT  
TCTGTTAACTGTCCAGCTGTGTCTCTACTGGTCACTCAGAGGCACGGGAGCCGCTCCCTT  
GGGCTGAGTCCATCAGAAGCCCCAGCCACCACAGCTCTGGTTTATGTAGTAGAGCTTCC  
CACTCACACATCACAATATGCCACCTCCCTTAGGACCCCTTCTCTGCTCATTGACTCT  
TTTGTCTTCTTCTCTCGGGGGTGAGGTGAGATTTACCACCAAAATGCATGCAGGAGAT  
CCCAGCAAGAGCAAATCAAGGAGATCAAGAAGGAGCAGCTTTCAGGATCCCCGTGGATTCT  
GCTAAGGGAAAATGAAGTCAGCACACTTTATAAAGGAGAATACCACAGAGCTCCAGTGGC  
CATAAAAGTATTCAAAAACTCCAGGCTGGCAGCATTTGCAATAGTGAGGCAGACTTTCAA  
TAAGGAGATCAAAACCATGAAGAAATTCGAATCTCCCAACATCCTGCGTATATTTGGGAT  
TTGCATTGATGAAACAGTGACTCCGCCTCAATTCTCCATTGTGATGGAGTACTGTGAACT  
CGGGACCCCTGAGGGAGCTGTTGGATAGGGAAAAAGACCTCACACTTGGCAAGCGCATGGT  
CCTAGTCCTGGGGGAGCCCCGAGGCCATACCGGCTACACCATTGAGAAGCACCTGAACT  
CCACGGAAAAATCAGAAGCTCAAACTTCTGGTAACTCAAGGCTACCAAGTGAAGCTTGC  
AGGATTTGAGTTGAGGAAAAACACAGACTTCCATGAGTTTGGGAACTACGAGAGAAAAGAC  
AGACAGAGTCAAATCTACAGCATATCTCTCACCTCAGGAACTGGAAGATGTATTTTATCA  
ATATGATGTAAAGTCTGAAATATACAGCTTTTGAATCGTCCTCTGGGAAATCGCCACTGG  
AGATATCCCGTTTCAAGGTGAAGAATGTGAAGACTGGCTCAGCCAGTGGCTGTAATTCTG  
AGAAGATCCGCAAGCTGGTGGCTGTGAAGCGGCAGCAGGAGCCACTGGGTGAAGACTGCC  
CTTCAGAGCTGCGGGAGATCATTGATGAGTGCCGGGCCATGATCCCTCTGTGCGGCCCT  
CTGTGGATGAAATCTTAAAGAACTCTCCACCTTTTCTAAGTAGTGATCAAAATCTAAA  
CCAAGGAGTCTCTGGACAAGAAGCTGGGAGAGGCACGAACTGGACATCTCTCTCTCAT  
ATCCTTCGGCATTGGGTTATCTATGGGTGCAAGGAGTGGGCACGCTTCTCTGTTACAAAT  
AGAAAACGATTCCAGTCATACAGACACATCCCACTCCAAATGATATTTCCAAAAACATA  
CCTCTGACAGTAACTTTGATAGATGGTTTGTCAAATGTATCTTTCTGGGTATCCACACCT  
CTTGGCAATGAAATTTGCAGCTCCTCCCTTCCATAAATGAAGTCTCTTTCCCCACCATT  
GAATCTGGGCTGGCACTGTGACTTGATTTGATCAATAGAATGTGGAAGAAGTGACTGTAT  
GCCAGTTCCAAGCCTAGGTTTCAAGAGGCCTTATAAATGTCTGTTGGAACCTTACCCAGC  
CATGGACATGTTGAGTGAGCATGCTGGAGAATGAGAGACCACATGAAGCAGAAACATGCT  
TTCCTAGCTGAAGTCATACTAGCCCAACCAACATGGCAGCTAACACATGAATGAGGCCAA  
TCAAGACCAGAAGAACCACTCAAGCAGATCCCAGCCCAAATTGCCCATTCACACAATCAG  
GAGCTAAATAAATTACTGTTGTCTTTT

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CGCCCCGGCCCCCTCCCCGGCGCCGGCCACGGGAGGCGGTGATGCGGGCGCGGGCGGCCT  
CGGCTGCGCCGAGAGCGGAGACACAGGCTCAAGATGGCAGATTCCGACTGAGGCTGGGGG  
GGCCGAGCTCGCGCGCCGCTTTCCCGTCCCGTTGCCATGAACCGCGGACACCCCGGCC  
CGATGGCCCCCGTGTACGAAGGTATGGCCTCACATGTGCAAGTTTCTCCCTCACACCC  
TTCAATCAAGTGCCCTTCTGTAGTGTGAAGAACTGAAAATAGAGCCGAGTTCCAAGTGG  
ACATGACTGGGTACGGCTCCACAGCAAAGTGTATAGCCAGAGCAAGAACATCCCCCTGT  
CGCAGCCAGCCACCACAACCGTCAGCACCTCCTTGCCGGTCCCAAACCAAGCCTACCTT  
ACGAGCAGACCATCGTCTTCCAGGAAGCACCGGGCACATCGTGGTCACCTCAGCAAGCA

## FIGURE 2DDD

GCACCTTCTGTCACCGGGCAAGTCCTCGGCGGACCACACAACCTAATGCGTTCGAAGCACTG  
TGAGCCTCCTTGATACCTACCAAAAATGTGGACTCAAGCGTAAGAGCGAGGAGATCGAGA  
ACACAAGCAGCGTGCAGATCATCGAGGAGCATCCACCCATGATTGAGAATAATGCAAGCG  
GGGCCACTGTGCGCACTGCCACCACGTCTACTGCCACCTCCAAAAACAGCGGCTCCAACA  
GCGAGGGCGACTATCAGCTGGTGCAGCATGAGGTACTGTGCTCCATGACCAACACCTACG  
AGGTCTTAGAGTTCTTGGGCGGAGGGACGTTTGGGCAAGTGGTCAAGTGCTGGAAACGGG  
GCACCAATGAGATCGTAGCCATCAAGATCCTGAAGAACCACCCATCCTATGCCCCGACAAG  
GTCAGATTGAAGTGAGCATCCTGGCCCGGTTGAGCACGGAGAGTGCCGATGACTATAACT  
TCGTCCGGGGCTACGAATGCTTCCAGCACAAGAACCACACGTGCTTGGTCTTCGAGATGT  
TGGAGCAGAACCTCTATGACTTTCTGAAGCAAAACAAGTTTAGCCCCCTTGCCCCCTCAAAT  
ACATTGCGCCAGTTCTCCAGCAGGTAGCCACAGCCCTGATGAAACTCAAAGCCTAGGTC  
TTATCCACGCTGACCTCAAACCAGAGAACATCATGCTGGTGGATCCATCTAGACAACCAT  
ACAGAGTCAAGGTTCATCGACTTTGGTTTCAGCCAGCCACGTCTCCAAGGCTGTGTGCTCCA  
CCTACTTGCAGTCCAGATATTACAGGGCCCCCTGAGATCATCCTTGGTTTACCATTTTGTG  
AGGCAATTGACATGTGGTCCCCTGGGCTGTGTTATTGCAGAATTGTTCTGGGTTGGCCGT  
TATATCCAGGAGATTTCGGAGTATGATCAGATTTCGGTATATTTTCAAAACACAGGGTTTGC  
CTGCTGAATATTTATTAAGCGCCGGGACAAAGACAACCTAGGTTTTTCAACCGTGACACGG  
ACTCACCATATCCTTTGTGGAGACTGAAGACACCAGATGACCATGAAGCAGAGACAGGGA  
TTAAGTCAAAAGAAGCAAGAAAGTACATTTTCAACTGTTTAGATGATATGGCCCAGGTGA  
ACATGACGACAGATTTGGAAGGGAGCGACATGTTGGTAGAAAAGGCTGACCGGCGGGAGT  
TCATTGACCTGTTGAAGAAGATGCTGACCATTGATGCTGACAAGAGAATCACTCCAATCG  
AAACCTGTAACCATCCCTTTGTACCATGACACACTTACTCGATTTTCCCCACAGCACAC  
ACGTCAAATCATGTTTCCAGAACATGGAGATCTGCAAGCGTCGGGTGAATATGTATGACA  
CGGTGAACCAGAGCAAAACCCCTTTCATCACGCACGTGGCCCCCAGCACGTCCACCAACC  
TGACCATGACCTTTAACAACCAGCTGACCACTGTCCACAACCAGCCCTCAGCGGCATCCA  
TGGCTGCAGTGGCCCAGCGGAGCATGCCCCCTGCAGACAGGAACAGCCCAGATTTGTGCCC  
GGCCTGACCCGTTCCAGCAAGCTCTCATCGTGTGTCCCCCGGCTTCCAAGGCTTGCAAG  
CCTCTCCCTCTAAGCACGCTGGCTACTCGGTGCGAATGGAAAATGCAGTTCCCATCGTCA  
CTCAAGCCCCAGGAGCTCAGCCTCTTCAGATCCAACCAGGTCTGCTTGCCCAGCAGGCTT  
GGCCAAGTGGGACCCAGCAGATCCTGCTTCCCCCAGCATGGCAGCAACTGACTGGAGTGG  
CCACCCACACCTCAGTGCAGCATGCCACCGTGATTCCCGAGACCATGGCAGGCACCCAGC  
AGCTGGCGGACTGGAGAAATACGCATGCTCACGGAAGCCATTATAATCCCATCATGCAGC  
AGCCTGCACTATTGACCGGTCATGTGACCTTCCAGCAGCACAGCCCTTAAATGTGGGTG  
TGGCCACAGTGATGCGGCAGCAGCCAACCAGCACCACTCCTCCCCGAAGAGTAAGCAGC  
ACCAGTCATCTGTGAGAAATGTCTCCACCTGTGAGGTGTCTCCTCTCAGGCCATCAGCT  
CCCCACAGCGATCCAAGCGTGTCAAGGAGAACACACCTCCCCGCTGTGCCATGGTGCACA  
GTAGCCCGGCTGCAGCACCTCGGTACCTGTGGGTGGGGCGACGTGGCCTCCAGCACCA  
CCCGGGAACGGCAGCGGCAGACAATTGTCAATCCCCGACACTCCAGCCCCACGGTCAGCG  
TCATCACCATCAGCAGTGACACGGACGAGGAGGAGGAACAGAAACACGCCCCCACCAGCA  
CTGTCTCCAAGCAAAGAAAAACGTCACTAGCTGTGTACAGTCCACGACTCCCCCTACT  
CCGACTCCTCCAGCAACACCAGCCCCCTACTCCGTGCAGCAGCGTGCTGGGCACAACAATG  
CCAATGCCTTTGACACCAAGGGGAGCCTGGAGAATCACTGCACGGGGAACCCCCGAACCA  
TCATCGTGCCACCCCTGAAAACCCAGGCCAGCGAAGTATTGGTGGAGTGTGATAGCCTGG  
TGCCAGTCAACACCAGTCAACACTCGTCTCTCTACAAGTCCAAGTCTCCTCAGCAACGTGA  
CCTCCACCAGCGGTCACTCTTCAGGGAGCTCATCTGGAGCCATCACCTACCGGCAGCAGC  
GGCCGGGCCCCCACTTCCAGCAGCAGCAGCCACTCAATCTCAGCCAGGCTCAGCAGCACA  
TCACCACGGACCGCACTGGGAGCCACCGAAGGCAGCAGGCCTACATCACTCCCACCATGG  
CCCAGGCTCCGTACTCCTTCCCGCACAAACAGCCCCAGCCACGGCACTGTGCACCCGCATC  
TGGCTGCAGCCGCTGCGCTGCCACCTCCCCACCCAGCCCCACCTCTACACCTACACTG  
CGCCGGCGGCCCTGGGCTCCACCGGCACCGTGGCCACCTGGTGGCCTCGCAAGGCTCTG



## FIGURE 2EEE

CGCGCCACACCGTG CAGC A C T G C C T A C C C A G C C A G C A T C G T C C A C C A G G T C C C C G T G A  
G C A T G G G C C C C C G G G T C C T G C C C T C G C C C A C C A T C C A C C C G A G T C A G T A T C C A G C C C A A T  
T T G C C C A C C A G A C C T A C A T C A G C G C C T C G C C A G C C T C C A C C G T C T A C A C T G G A T A C C C A C  
T G A G C C C C G C C A A G G T C A A C C A G T A C C C T T A C A T A T A A A C A C T G G A G G G G A G G G A G G G A G  
G G A G G G A G G G A G A G A A T G G C C C G A G G G A G G A G G G A G A G A A G G A G G G A G G C G C T C C T G G G A  
C C G T G G G C G C T G G C C T T T T A T A C T G A A G A T G C C G C A C A C A A A C A A T G C A A A C G G G G C A G G  
G G C G G G G G G G G G G G C A G A G G G C A G G G G A C G G G T C G G G A C A C C A G T G A A A C T T G A A C C  
G G G A A G T G G G A G G A C G T A G A G C A G A G A A G A G A A C A T T T T T A A A A G G A A G G G A T T A A A G A G  
G G T G G G A A A T C T A T G G T T T T T A T T T T A A A A A A G

SEQ ID NO: 69\_DYRK3\_H

C G G G A G C G A A A G T G C G C T G A G C T G C A G T G T C T G G T C G A G A G T A C C C G T G G G A G C G T C G C G  
C C G C G G A G G C A G C C G T C C C G G C G T A G G T G G C G T G G C C G A C C G G A C C C C A A C T G G C G C C T  
C T C C C C G A G C G G G G T C C C G A G C T A G G A G A T G G G A G G C A C A G C T C G T G G G C C T G G G C G G A A  
G G A T G C G G G G C C G C C T G G G G C C G G G C T C C C G C C C A G C A G C G G A G T T G G G G G A T G G T G T C  
T A T G A C A C C T T C A T G A T G A T A G A T G A A A C C A A A T G T C C C C C C T G T T C A A A T G T A C T C T G C  
A A T C C T T C T G A A C C A C C T C C A C C C A G A A G A C T A A A T A T G A C C G C T G A G C A G T T T A C A G G A  
G A T C A T A C T C A G C A C T T T T T G G A T G G A G G T G A G A T G A A G G T A G A A C A G C T G T T T C A A G A A  
T T T G G C A A C A G A A A A T C C A A T A C T A T T C A G T C A G A T G G C A T C A G T G A C T C T G A A A A A T G C  
T C T C C T A C T G T T T C T C A G G G T A A A A G T T C A G A T T G C T T G A A T A C A G T A A A A T C C A A C A G T  
T C A T C C A A G G C A C C C A A A G T G G T G C C T C T G A C T C C A G A A C A A G C C C T G A A G C A A T A T A A A  
C A C C A C C T C A C T G C C T A T G A G A A A C T G G A A A T A A T T A A T T A T C C A G A A A T T T A C T T T G T A  
G G T C C A A A T G C C A A G A A A A G A C A T G G A G T T A T T G G T G G T C C C A A T A A T G G A G G G T A T G A T  
G A T G C A G A T G G G G C C T A T A T T C A T G T A C C T C G A G A C C A T C T A G C T T A T C G A T A T G A G G T G  
C T G A A A A T T A T T G G C A A G G G A G T T T T G G G C A G G T G G C C A G G G T C T A T G A T C A C A A A C T T  
C G A C A G T A C G T G G C C C T A A A A A T G G T G C G C A A T G A G A A G C G C T T C A T C G T C A A G C A G C T  
G A G G A G A T C C G G A T T T T G G A G C A T C T T A A G A A A C A G G A T A A A A C T G G T A G T A T G A A C G T T  
A T C C A C A T G C T G G A A A G T T T C A C A T T C C G G A A C C A T G T T T G C A T G G C C T T T G A A T T G C T G  
A G C A T A G A C C T T T A T G A G C T G A T T A A A A A A A T A A G T T T C A G G G T T T T A G C G T C C A G T T G  
G T A C G C A A G T T T G C C C A G T C C A T C T T G C A A T C T T T G G A T G C C C T C C A C A A A A T A A G A T T  
A T T C A C T G C G A T C T G A A G C C A G A A A A C A T T C T C C T G A A A C A C C A C G G G C G C A G T T C A A C C  
A A G G T C A T T G A C T T T G G G T C C A G C T G T T T C G A G T A C C A G A A G C T C T A C A C A T A T A T C C A G  
T C T C G G T T C T A C A G A G C T C C A G A A A T C A T C T T A G G A A G C C G C T A C A G C A C A C C A A T T G A C  
A T A T G G A G T T T T C G C T G C A T C C T T G C A G A A C T T T T A A C A G G A C A G C C T C T C T C C C T G G A  
G A G G A T G A A G G A G A C C A G T T G G C C T G C A T G A T G G A G C T T C T A G G G A T G C C A C C A C C A A A A  
C T T C T G G A G C A A T C C A A A C G T G C C A A G T A C T T T A T T A A T T C C A A G G G C A T A C C C G C T A C  
T G C T C T G T G A C T A C C C A G G C A G A T G G G A G G G T T G T G C T T G T G G G G G T C G C T C A C G T A G G  
G G T A A A A A G C G G G G T C C C C C A G G C A G C A A A G A C T G G G G G A C A G C A C T G A A A G G G T G T G A T  
G A C T A C T T G T T T A T A G A G T T C T T G A A A A G G T G T C T T C A C T G G G A C C C C T C T G C C C G C T T G  
A C C C C A G C T C A A G C A T T A A G A C A C C C T T G G A T T A G C A A G T C T G T C C C C A G A C C T C T C A C C  
A C C A T A G A C A A G G T G T C A G G G A A A C G G G T A G T T A A T C C T G C A A G T G C T T T C A G G G A T T G  
G G T T C T A A G C T G C C T C C A G T T G T T G G A A T A G C C A A T A A G C T T A A A G C T A A C T T A A T G T C A  
G A A A C C A A T G G T A G T A T A C C C C T A T G C A G T G T A T T G C C A A A A C T G A T T A G C T A G T G G A C A  
G A G A T A T G C C C A G A G A T G C A T A T G T G T A T A T T T T A T G A T C T T A C A A A C C T G C A A A T G G A  
A A A A A T G C A A G C C C A T T G G T G G A T G T T T T T G T T A G A G T A G A C T T T T T T A A A C A A G A C A A  
A A C A T T T T T A T A T G A T T A T A A A A G A A T T C T T C A A G G G C T A A T T A C C T A A C C A G C T T G T A T  
T G G C C A T C T G G A A T A T G C A T T A A A T G A C T T T T T A T A G G T C A

## FIGURE 2FFF

SEQ ID NO: 70\_AA589241\_M\_DYRK3\_M

CCACGCGTCCGGAGTTGCTAGGAATGCCACCGCAGAACTTCTGGAGCAATCCAAGCGTG  
CCAAGTACTTTATTAACCTCAAAGGCTTGCCCTCGATACTGCTCCGTATCTACCCAGACGG  
ACGGGAGGGTGGTGCTTCTCGGGGGTCTGCTCACGCAGGGGTAAAAAGCGAGGCCCGCCAG  
GCAGCAAAGACTGGGCAACCGCACTGAAGGGCTGTGGTGACTACTTGTTTCATAGAGTTTC  
TGAAACGATGCCTCCAGTGGGACCCCTCTGCCCGCCTCACCCCGGCTCAAGCATTAAAGAC  
ATCCTTGGATTAGCAAGTCTACACCCAAACCTCTCACCATGGACAAGGTGCCAGGGAAGC  
GGGTAGTTAACCCTACAAATGCTTTCCAGGGACTGGGTTCCAAGCTGCCTCCAGTCGTTG  
GGATAGCCAGTAAGCTTAAAGCTAACCTAATGTCCGAAACCAGTGGTAGTATACCTCTGT  
GCAGTGTATTGCCAAAGCTGATTAGCTAGTGGACCACTCAGAGACTGATACATATCATAT  
GTATTTTAAATTACCTTGCAAACATGCAAATGGAAAACGGAATAATTGAAGCCCATTAC  
TGATGGATATGTTTTTGTAGACTTTTTTTTTTAACAAGGCAGAACATTTTTATATGACTAT  
AAAAGAACGCTTCAAGGGCTAATGTCAAACCAGCTTGTATTGGCCATCTGGAGTATACAT  
TAAATGACTTTTTTCATAGGTC

SEQ ID NO: 71\_5R72\_16\_2\_H

GTCGAGGCGCAGCGCTGCCATGGCTGGGGGGCCGTGGGGCCCCCGGGCGCGGCGGGGACGA  
GCCTCCGGAGAGCTACCCGCAACGACAGGACCACGAGCTACAGGCCCTGGAGGCCATCTA  
CGGCGCGGACTTCCAAGACCTGCGGCCGACGCTTGCGGACCGGTCAAAGAGCCCCCTGA  
AATCAATTTAGTTTTGTACCTCAAGGCCTAACTGGTGAAGAAGTATATGTAAAAGTGGA  
TTTGAGGGTTAAATGCCACCTACCTATCCAGATGTAGTTCTGAAATAGAGTTAAAAAA  
TGCCAAAGGTCTATCAAATGAAAGTGTCAATTTGTTAAAATCTCGCCTAGAAGAACTGGC  
CAAGAAACACTGTGGGGAGGTGATGATCTTTGAACTGGCTTACCACGTGCAGTCATTTCT  
CAGCGAGCATAACAAGCCCCCTCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGC  
TCAGGAGGAGCAGCAGAGGCTGTTGGAGGCCAAGCGGAAAGAAGAGCAGGAGCAACGTGA  
AATCCTGCATGAGATTAGAGAAGGAAAGAAGAGATAAAAGAAGAGAAAAAAGGAAAGA  
AATGGCTAAGCAGGAACGTTTGAAATTGCTAGTTTGTCAAACCAAGATCATACCTCTAA  
GAAGGACCCAGGAGGACACAGAACGGCTGCCATTCTACATGGAGGCTCTCCTGACTTTGT  
AGGAAATGGTAAACATCGGGCAAACCTCTCAGGAAGGTCTAGGCGAGAACGTGAGTATTC  
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TCCTGATCAGCTCATGGTGCAAAAGGGAAATGTATTGGCAGTGATGAACAACCTTGAAA  
ATTAGTCTACAATGCTTTGGAAACAGCCACTGGTGGCTTTGTCTTGTGTATGAGTGGGT  
CCTTCAGTGGCAGAAAAAATGGGTCCATTCTTACCAGTCAAGAAAAAGAGAAGATTGA  
TAAGTGCAAAAAGCAGATTCAAGGAACAGAAACAGAATTCAACTCACTGGTAAAATTGAG  
CCATCCAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGAGCAAGACGACTCCATCGT  
GGTGGACATTTTAGTGGAGCACATTAGTGGGGTCTCTCTTGCTGCACACCTGAGCCACTC  
AGGCCCCATCCCTGTGCATCAGCTTCGCAGGTACACAGCTCAGCTCCTGTGAGGCCTTGA  
TTATCTGCACAGCAATTCTGTGGTGCATAAGGTCTGAGTGCATCTAATGTCTTGGTGGA  
TGCAGAAGGCACCGTCAAGATTACGGACTATAGCATTTCTAAGCGCCTCGCAGACATTTG  
CAAGGAGGATGTGTTTGAGCAAACCCGAGTTTCGTTTTAGTGACAATGCTCTGCCTTATAA  
AACGGGGAAGAAAGGAGATGTTTGCGCTCTTGGCCTTCTGCTGCTGTCCCTCAGCCAAGG  
ACAGGAATGTGGAGAGTACCCTGTGACCATCCCTAGTGACTTACCAGCTGACTTTCAAGA  
TTTTCTAAAGAAATGTGTGTGCTTGGATGACAAGGAAAGATGGAGTCCCCAGCAGTTGTT  
GAAACACAGCTTTATAAATCCCCAGCCAAAAATGCCTCTAGTGGAACAAAGTCTGAAGA  
TTCTGGAGGACAAGATTATGTTGAGACTGTTATTCTTAGCAACCGGCTACCCAGTGCTGC  
CTTCTTTAGTGAGACACAGAGACAGTTTTTCCCGATACTTCATTGAGTTTGAAGAATTACA  
ACTTCTTGGTAAAGGAGCTTTTGGAGCTGTCTCAAGGTGCAGAACAAAGTTGGACGGCTG  
CTGCTACGCAGTGAAGCGCATCCCCATCAACCCGGCCAGCCGGCAGTTCCGCAGGATCAA  
GGGCGAAGTGACACTGCTGTACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGC  
CTGGATCGAGCGGCACGAGCGGCCGGCGGGACCGGGACGCCGCCCCCGGACTCCGGGCC

## FIGURE 2GGG

CCTGGCCAAGGATGACCGAGCTGCACGCGGGCAGCCGGCGAGCGACACAGACGGCCTGGA  
CAGCGTAGAGGCCGCGCCGCCACCCATCCTCAGCAGCTCGGTGGAGTGGAGCACTTC  
GGGCGAGCGCTCGGCCAGTGCCCGTTTTCCCGCCACCGGCCCGGGCTCCAGCGATGACGA  
GGACGACGACGAGGACGAGCACGGTGGCGTCTTCTCCCAGTCCTTCTGCTGCTTCAGA  
TTCTGAAAGTGATATTATCTTTGACAATGAAGATGAGAACAGTAAAAAGTCAGAATCAGGA  
TGAAGATTGCAATGAAAAGAATGGCTGCCATGAAAGTGAGCCATCAGTGACGACTGAGGC  
TGTGCACTACCTATACATCCAGATGGAGTACTGTGAGAAGAGCACTTTACGAGACACCAT  
TGACCAGGGACTGTATCGAGACACCGTCAGACTCTGGAGGCTTTTTTCGAGAGATTCTGGA  
TGGATTAGCTTATATCCATGAGAAAGGAATGATTCACCGGGATTTGAAGCCTGTCAACAT  
TTTTTTGGATTCTGATGACCATGTGAAAATAGGTGATTTTGGTTTGGCGACAGACCATCT  
AGCCTTTTCTGCTGACAGCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAGACCC  
TTCAGGTCACTTAAGTGGGATGGTTGGCACTGCTCTCTATGTAAGCCCAGAGGTCCAAGG  
AAGCACCAAATCTGCATACAACCAGAAAGTGGATCTCTTCAGCCTGGGAATTATCTTCTT  
TGAGATGTCTTATCACCCCATGGTCACGGCTTCAGAAAGGATCTTTGTTCTCAACCAACT  
CAGAGATCCCACCTTCGCCTAAGTTTCCAGAAGACTTTGACGATGGAGAGCATGCAAAGCA  
GAAATCAGTCATCTCCTGGCTGTTGAACCACGATCCAGCAAACCGGCCACAGCCACAGA  
GCTGCTCAAGAGTGAGCTGCTGCCCCACCCAGATGGAGGAGTCAGAGCTGCATGAAGT  
GCTGCACCACACGCTGACCAACGTGGATGGGAAGGCCTACCGCACCATGATGGCCCAGAT  
CTTCTCGCAGCGCATCTCCCTGCCATCGATTACACCTATGACAGCGACATACTGAAGGG  
CAACTTCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTGTGAAACCATCATCCGCAT  
CTTTAAAGACATGGAGCTGTTCAAGTTGTGTAAGTCTCACTACTGCTTCCCCGAAACAGACA  
AATATATGAGCACAACGAAGCTGCCCTATTATGAGGACACAGCGGGATGCTGGTGATGCT  
TCCTTTTGACCTGCGGATCCCTTTTGCAAGATATGTGGCAAGAAATAATATATTGAATTT  
AAAACGATACTGCATAGAACGTGTGTTCAAGCCGCGCAAGTTAGATCGATTTTCATCCCAA  
AGAACTTCTGGAGTGTGCATTTGATATTGTCACTTCTACCACCAACAGCTTTCTGCCAC  
TGCTGAAATTATCTACACTATCTATGAAATCATCCAAGAGTTTCCAGCACTTCAGGAAAG  
AAATTACAGTATTTATTTGAACCATAACCATGTTATTGAAAGCAATACTCTTACACTGTGG  
GATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTATGATGCTGTGACAGAGAA  
GCTGACGAGGAGAGAAGTGAAGCTAAATTTTGTAACTCTGTCTTTGTCTTCTAATAGTCT  
GTGTGACTCTACAAGTTTATTGAACAGAAGGGAGATTTGCAAGATCTTATGCCAACAAAT  
AAATTCATTAATAAAACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGGCTTAAAGA  
CCTAGAGGAGGTTGTTGGACTGTTGAAGAACTCGGCATCAAGTTACAGGTCTTGATCAA  
TTTGGGCTTGGTTTACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTTGTGGCTTT  
CATCAAACGAAGGCAAAGGGCTGTACCTGAAATCCTCGCAGCTGGAGGCAGATATGACCT  
GCTGATTCCCCAGTTTGAAGGGCCACAAGCTCTGGGGCCAGTTCCTACTGCCATTGGGGT  
CAGCATAGCTATAGACAAGATATCTGCTGCTGTCTCAACATGGAGGAATCTGTTACAAT  
AAGCTCTTGTGACCTCCTGGTTGTAAGTGTGGTCAGATGTCTATGTCCAGGGCCATCAA  
CCTAACCCAGAACTCTGGACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCACA  
GTCCCAAGAGGAATTACAAGAGTACTGCAGACATCATGAAATCACCTATGTGGCCCTTGT  
CTCGGATAAAGAAGGAAGCCATGTCAAGGTTAAGTCTTTGAGAAGGAAGGCAGACAGA  
GAAGCGTGTGCTGGAGACTGAACTTGTGGACCATGTACTGCAGAACTGAGGACTAAAGT  
CACTGATGAAAGGAATGGCAGAGAAGCTTCCGATAATCTTGCAAGTGCAAAATCTGAAGGG  
GTCATTTTCTAATGCTTCAGGTTTGTGTTGAAATCCATGGAGCAACAGTGGTTCCCATTTGT  
GAGTGTGCTAGCCCCGAGAAGCTGTGAGCCAGCAC'TAGGAGGCGCTATGAAACTCAGGT  
ACAAACTCGACTTCAGACCTCCCTTGCCAACTTACATCAGAAAAGCAGTGAAATTGAAAT  
TCTGGCTGTGGATCTACCCAAAGAAACAATATTACAGTTTTTATCATTAGAGTGGGATGC  
TGATGAACAGGCATTTAACACAACGTGTAAGCAGCTGCTGTACGCCCTGCCAAAGCAAAG  
ATACCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAGGTGTCTGT  
GCTATTTCTGTACAGCTATAGAGATGACTACTACAGAATCTTATTTTAACCCTAAAGAAC  
TGTGCTTAACCTCATTCAAACAGACAGAGGCTTATACTGGAATAATGGAATGTTGTACAT

## FIGURE 2HHH

TCATCATAATTTAAATTAATTTCTAAGAAGAGGCTGGGTGCAGTGGCTCACACCTTTAA  
TCCAGCACTTTGGGAAGCCAAGGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAG  
CCT

SEQ ID NO: 73\_R43524\_H, HRI\_H

ATGCTGGGGGGCAACTCCGGGTCCGCAAGCGCGAAGAGGAGGGCGACGGGGCTGGGGCT  
GTGGCTGCGCCCGCGGCCATCGACTTTCCCGCCGAGGGCCCGGACCCCGAATATGACGAA  
TCTGATGTTCCAGCAGAAATCCAGGTGTTAAAGAACCCCTACAACAGCCAACCTTCCCT  
TTTGAGTTGCAAACCAACTCTTGCTGGTTTCTTTGCTGGAGCACTTGAGCCACGTGCAT  
GAACCAAACCCACTTCGTTCAAGACAGGTGTTTAAAGCTACTTTGCCAGACGTTTATCAAA  
ATGGGGCTGTTGTCTTCTTTCACTTGTAGTGACGAGTTTAGCTCATTGAGACTACATCAC  
AACAGAGCTATTACACACTTAATGAGGTCTGCTAAAGAGAGAGTTTCGTCAGGATCCTTGT  
GAGGATATTTCTCGTATCCAGAAAATCAGATCAAGGGAAGTAGCCTTGGAAGCACAAACT  
TCACGTTACTTAAATGAATTTGAAGAACTTGTCTATCTTAGGAAAAGGTGGATACGGAAGA  
GTATACAAGGTCAGGAATAAATTAGATGGTCAGTATTATGCAATAAAAAAATCCTGATT  
AAGGGTGCAACTAAACAGTTTGCATGAAGGTCTACGGGAAGTGAAGGTGCTGGCAGGT  
CTTCAGCACCCCAATATTGTTGGCTATCACACCGCGTGGATAGAACATGTTTATGTGATT  
CAGCCACGAGCAGACAGAGCTGCCATTGAGTTGCCATCTCTGGAAGTGCTCTCCGACCAG  
GAAGAGGACAGAGAGCAATGTGGTGTAAAAATGATGAAAGTAGCAGCTCATCCATTATC  
TTTGCTGAGCCACCCAGAAAAAGAAAAACGCTTTGGAGAATCTGACACTGAAAATCAG  
AATAACAAGTCGGTGAAGTACACCACCAATTTAGTCATAAGAGAATCTGGTGAACCTTGAG  
TCGACCCTGGAGCTCCAGGAAAATGGCTTGGCTGGTTTGTCTGCCAGTTCAATTGTGGAA  
CAGCAGCTGCCACTCAGGCGTAATTCACCTAGAGGAGAGTTTACATCCACCGAAGAA  
TCTTCCGAAGAAAATGTCAACTTTTGGGTGAGACAGAGGCACAGTACCACCTGATGCTG  
CACATCCAGATGCAGCTGTGTGAGCTCTCGCTGTGGGATTGGATAGTCGAGAGAAACAAG  
CGGGGCCGGGAGTATGTGGACGAGTCTGCCTGTCTTATGTTATGGCCAATGTTGCAACA  
AAAATTTTTCAAGAATTGGTAGAAGGTGTGTTTTACATACATAACATGGGAATTGTGCAC  
CGAGATCTGAAGCCAAGAAATATTTTTCTTCATGGCCCTGATCAGCAAGTAAAAATAGGA  
GACTTTGGTCTGGCCTGCACAGACATCTACAGAAGAACACAGACTGGACCAACAGAAAC  
GGGAAGAGAACACCAACACATACGTCCAGAGTGGGTACTTGTCTGTACGCTTCACCCGAA  
CAGTTGGAAGGATCTGAGTATGATGCCAAGTCAGATATGTACAGCTTGGGTGTGGTCCTG  
CTAGAGCTCTTTCAGCCGTTTGGAAACAGAAATGGAGCGAGCAGAAGTTCTAACAGGTTTA  
AGAACTGGTCAGTTGCCGGAATCCCTCCGTAAAAGGTGTCCAGTGCAAGCCAAGTATATC  
CAGCACTTAACGAGAAGGAACCTCATCGCAGAGACCATCTGCCATTAGCTGCTGCAGAGT  
GAACTTTTCAAATTTCTGGAATGTTAACCTCACCTACAGATGAAGATAATAGAGCAA  
GAAAAAGAAATTGCAGAACTAAAGAAGCAGCTAAACCTCCTTTCTCAAGACAAAGGGGTG  
AGGGATGACGGAAGGATGGGGCGTGGGATGA

SEQ ID NO: 74\_17000057519457\_H

CACAAGAGCCCTTCTGCAGGGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGT  
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GGATTGCCGAAGAAGTCCAGGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTCAG  
AGACAGCTGATCGGTTGGAGCTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTA  
CGCCGGCCGATGGCGAGGAGCCCGCCCGGAGGCTGAGGCTCTGGCCGAGCCCGGGAGC  
GGAGCAGCCGCTTCTTGAGCGGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCTGT  
TCCGTGGCCGCTTCCAGGGCCGCGCGCGGTGATCAAGCACCGCTTCCCAAGGGCTACC  
GGCACCCGGCGCTGGAGGCGCGGCTTGGCAGACGGCGGACGCTGCAGGAGGCCCGGGCGC  
TCCTCCGCTGTGCGCCGCTGGAATATCTGCCCCAGTTGTCTTTTTTTGTGGACTATGCTT  
CCAACCTGCTTATATATGGAAGAAATTGAAGGCTCAGTGAAGTGTTCGAGATTATATTCAGT  
CCACTATGGAGACTGAAAAAATCCCCAGGGTCTCTCCAACCTAGCCAAGACAATTGGGC

FIGURE 2III

AGGTTTTGGCTCGAATGCACGATGAAGACCTCATTTCATGGTGATCTCACCACCTCCAACA  
TGCTCCTGAAACCCCCCTGGAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTT  
TCATTTTCAGCACTTCCAGAGGATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCC  
TCAGTACCCATCCCAACACTGAAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCT  
CCTCCAAAAAGGCCAGGCCAGTGCTAAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAA  
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ATGTGTCTAAGTCATGTTCTAGGCAGAAATTGGGTATTTAAAGTAAATTGAGGACAGGCCTT  
CTCCCAGATTGTGACATGTATATCTCAGATACATGGGTGTGGCATTGAACCACATAATGA  
GAACATTATTCTCTTTTAGTCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTC  
GCTGAGCTTACTGGCCCTCTAACCCAGTGTTTTTTTTTTGTTGTTGTTGTGTACATGTTAT  
ATTTATTTTTGAAACCAGTTTAATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATA  
CAGCATGGAAAATATCAGTGTATTGTTTTATGAAACTTTCACGTGTATATATAGACCAAG  
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TCATTCACCACAGTCAGCATGCCCCAAGTGCCAGCATGGGGCGGATGGCCAGGAATGAG  
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AGTTAGGCATTATCCCCATTTTATAGATGGAGAACTGGCCCCAAAAGGTGGGAACCTGT  
CCAAGACGTCACAGGTAGCAAGAGGTACTTTTACCTGGCTCCAAATCTGTGTTCTTTCCA  
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TAACATTATTTTCAAGGAACTCCAAGGGCCACAGGAGCTGACAGGTTTTTCAATTAATAT  
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SEQ ID NO: 75\_AA013524\_M

CTGGTGCAGCAGGGCGCGGAGGCGCGCTTTTCCGTGGCCGCTTCCAGGGCGCGCGGCC  
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GCCCCAGTCGTCTTCTTTGTGGACTATGCGTCTAACTGCTTATATATGGAAGAAATCGAA  
GACTCGGTGACTGTTTGGGATTATATCCAATCCACTATGGAGACTGAAAAGGACCCCCAG  
TGCTCTTGGACCTGGCCAGGAGGATGGGGCAGGTTCTGGCCGGAATGCACGACCAAGAC  
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CACATCGTGTCTCATCGACTTTGGGCTGAGCTTTGTCTCAGGACTGCCGGAAGATAAAGGC

## FIGURE 2JJJ

GTCGACCTCTATGTCCTGGAGAAGGCCTTCCTCAGCACGCACCCCCACACCGAGACCGCG  
TTTGAAGCCTTTCTGAAGAGTTACGGGGCCTCGTCCAAGAAGTCCAGTCCAGTGCTGAAG  
AAGTTAGATGAGGTGCGCCTGAGAGGGCGAAAGCGGTCCATGGTCGGGTAGTGGAGCTGT  
GGTGAACCTGGCTCACGGTGAAGGATGATGTAGACGAGGCTGGACCCCTCAGCAAAGCATG  
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GGGCTTCATGTACATGAGGTTTATTCTGGGCAGAACTGGGTAGGTAGCCCAGGCTAGCCT  
TGAATTTATGGCAACATCCTACCTCAGCTTGCTTGGAAGAGGTTATAAGCCACCATACT  
GACTTTGCACTGATTCTGTCAGAAAC

SEQ ID NO: 76\_17000139801197\_H, IRAKM\_H

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GAACATAATGAAAAAGGAGTACTGCTTAAATCTTCCATCAGCTTTCAAATATCATAGAA  
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AGAGTGGAGATTCAAACCTAACATATGCTGTCAAATTATTTAAACAGGAGAAAAAATG  
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CACCCAAACATACTAGAGTTGGCTGCATATTTTACAGAGACTGAGAAGTTCTGTCTGATT  
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CCACTCCCTTGGCACATTCGAATCGGTATATTAATAGGAATATCCAAAGCCATTCACTAC  
CTGCACAACGTTCAACCATGCTCGGTATCTGTGGCAGTATATCAAGTGCAAACATCCTT  
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CTAGAACATCAGAGTTGTACCATAAATATGACCAGCAGCAGCAGTAAACATCTGTGGTAC  
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GGAATTGTAATAATGGAAGTTCTAACAGGATGTAGAGTAGTGTAGATGATCCAAACAT  
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SEQ ID NO: 77\_AA840598\_M IRAKM\_M

ATGTGGAAGAGATTTTATCAGAAGTGAAGTTCTACTCCTGTTCCGTCACCCCCACATA  
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CACGTTTGAATCAGCGTATTGATAGGAATAGCCAAAGCCATCCAATACTTGACAAACACT  
CAGCCGTGCGCCGTATCTGTGGCAACGTTTCCAGTGCAAACATACTCTTGGATGACCAG  
CTCCAACCCAACTAACGGATTTTGTCTGCAGCGCACTTCCGACCCAATCTAGAGCAGCAG  
AGTTCTACCATAAATATGACCGGCGGTGGCAGGAAACATCTGTGGTACATGCCAGAAGAA

## FIGURE 2KKK

TACATCAGACAGGGAAGACTTTCCGTTAAACTGATGTCTACAGCTTCGGAATCGTGATC  
ATGGAGGTTCTAACGGGCTGCAAAGTGGTGTGGATGACCCGAAACACGTTTCAGCTGCGG  
GACCTCCTCATGGAAGTGTGGAGAAAAGAGGCCTAGACTCCTGCCTGTCTTCTTAGAC  
AGGAAGATAACCACCTGTCTCGGAACCTTCTCTGCAAAGCTCTTCTCTCTGGCGGGCCGG  
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AGCACCCAGCCTAGCTTGTATTTTGCAGAAGACCCTCCCACGTCCTTGAAGTCCTTCAGG  
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CAGAATAACCATTCAGTACCTCCCAAGGAAGTTTGGGGACAGATAGAGTGACTCAGAAA  
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AACAGGGGAAGTGAAGCGGATTGCAACGTGCCAGTCTTCTCATGAGGAATGCTGGTCC  
CCAGAGCTTGTGGCGCCATCCCAGGACTTAAGTCCTACTGTGATCAGTTTGGGCTCGTCT  
TGGGAAGTACCAGGCCATTCTTATGGGAGCAAGCCAATGGAGAAGAGGTGTTCTCTGGG  
CTCTTTTGCAGTGAGCATGAACAGTCCAAAAAGCAGTGAATCCACCAGAAGATCAAGCAA  
AAAATAAAAGCAAACGTCACTGAAGGCACTGAGCAAATAGCATCCCCGTGAAAAGACACG  
AGCTCTGAGCTCCGTGAGTACAGCCAAGGGACCAACTGATGGAGAATTTGAATGGTGCAG  
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TCAAGTGACCGCTCTCAGTCAAACCTGAGAAGCTAAACTGGAGCCAATCAGAATTATCC  
AAGATTCCGGGTTCTGACAACCAAAACCTAGCAAAGAGTAGCAGGACAAGTCTCTCTCTT  
AAGTCTCTCACTCTCTCTCATCATCCGAGTGAGATCTTGGTATAGGTGAACAGAGAACCA  
CCCACCTTCCAGAACCAGAACCACCTTCTCCCCAAGCCAGCAGTCAGTCACTCACCATCA  
GCAGCCAGTAGTCACCAGCAGCCAATCATGATACAGTGTCACTCTCCCTCTGCGCATGCC  
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CAGAGGCAGCCTTTTGTATACATTCCCTGACCCCAACCCCAATTATATCTCTCATATGATA  
TCTGTTGCGTAGTGTGACTTTGTGGCATGACTTGGTTGTCAGATCATTTGCACAAGAACA  
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TGCTAGGGATACTGACAGTCTATTGTCTTCCCATGGTTCATAGGGAAGTTGCTCAAATGCA  
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TTTTACAGCCAGTTGCTACTCTTGTATTATCGCTGGTTAACCGGTCTGTCCGGAAGTGAGC  
CAAGTCATCCTTGCTAGGGCTTTTTCTGTGTAGAGAGGGAATTCCAGTCCAAAGTCTGCT  
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SEQ ID NO: 78\_AA088547\_H

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GGCCACATCCGACTGCCTGCCTCAGGCCCCCGGGACACAGCCACCCTCTTCTCTACCTTG  
GACACCCAGCTGCTAATGACGCTGTATGTGGGGAAGGATGAACTGGCTTCTATGTCTCT  
AAAGCACTGGTCCACACAGGAGTGGCCCCGGTGCCTCGTGGACTGACCCTGGCCCCCGCA  
GATGGCCCCACCACAGATGAGGTGACACTCCAAGTCTCAGGAGAGCGAGAGGGCTCACCC

## FIGURE 2LLL

AGCACTGCTGTTAGATACCCCTCAGGCAGTGTGGCCCTCCCAAGCCAGTGGCTGCTCAT  
GGACACCACGAGCTACCCCCAGTCCTGCACACCACCATGCTGAGGGTCCATCCACCCCTG  
GGGAGTGGAAGTGCAGAGACAAGACCTCCAGAGAATACCCAGGCCCCAGCCTTCTTCTTG  
GAGCTATTGAGCCTGAGCCGAGAGAACTTTGGGACTCCGAGCTGCATCCAGAAGAAAA  
ACTCCAGACTCTTACTTGGGGCTGGGACCCCAAGACCTGCTGGCAGCTAGCCTCACTGCT  
GTCCTCCTGGGAGGGTGGATTCTCTTTGTGATGAGGCAGGTGGTGGAGAAGCAGCAGGAG  
ACCCCCCTGGCACCCTGCAGACTTTGCTCACATCTCCAGGATGCCAGTCCCTGCACTCG  
GGGGCCAGCCGGAGGAGCCAGAAGAGGCTTCAGAGTCCCTCAAAGCAAGCCCAGCCACTC  
GACGACCCTGAAGCTGAGCAACTACCGTAGTGGGGAAGATTTCTTCAATCCCAAGGAC  
GTGCTGGGCCCGGGGAGGCGGGACTTTCGTTTTCCGGGGACAGTTTGAGGGACGGGCA  
GTGGCTGTCAAGCGGCTCCTCCGCGAGTGCCTTGGCTGCTTCGGCGGGAAAGTTCAACTG  
CTGCAGGAGTCTGACAGGCACCCCAACGTGCTCCGCTACTTCTGCACCGAGCGGGACCC  
CAGTTCCACTACATTGCCCTGGAGCTCTGCCGGGCTCCTTGCAGGAGTACGTAGAAAAAC  
CCGGACCTGGATCGCGGGGTCTGGAGCCCGAGGTCGTGCTGCAGCAGCTGATGTCTGGC  
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ATCACCGGGCTGACAGCCAGGGCCTGGGCAGAGTGGTGTCTCTCAGACTTCGGCCTCTGC  
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GGAGACAGTCTTTATCGCCAGGCAAACATCCTCACAGGGGCTCCCTGTCTGGCTCACCTG  
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SEQ ID NO: 79\_HGP\_6644466

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GGAAGGGATCAGTAATTTCAAGACACCAAGCAAATTATCAGAAAAAAGAAATCTGTATT  
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TGGTGTATTACTGACAAGGCAGACATATTTGCCTTTGGCCTTACTTTGTGGGAAATGAT  
GACTTTATCGATTCCACACATTAATCTTTCAAATGATGATGATGATGAAGATAAACTTT  
TGATGAAAGTGATTTTGATGATGAAGCATACTATGCAGCGTTGGGAACTAGGCCACCTAT  
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## FIGURE 2MMM

TAATGAAGACCCCTAAAGATCGTCCTTCTGCTGCACACATTGTTGAAGCTCTGGAAACAGA  
TGCTAGTGATCATCTCAGCTGAAGTGTGGCTTGCCTAAATAACTGTTTATTCCAAAATA  
TTTACATAGTTACTATCAGTAGTTATTAGACTCTAAAATTGGCATATTTGAGGACCATAG  
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CACTTGGAAATTGTACTGGGTTTTCTGTAAAGTTTTAGAACTAGCTACATAAGTACTTTG  
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TGAATGACCATTACTTTTTATTAATGATCTTTCTTAAATATTCTATATTTTAAATGGATCTA  
CTGACATTAGCACTTTGTACAGTACAAAATAAAGTCTACATTTGTTTAAAACACTGAACC  
TTTTGCTGATGTGTTTATCAAATGATAACTGGAAGCTGAGGAGAATATGCCTCAAAAAGA  
GTAGCTCCTTGGATACTTCAGACTCTGGTTACAGATTGTCTTGATCTCTTGGATCTCCTC  
AGATCTTTGGTTTTTGTCTTAATTTATTAAATGTATTTTCCATACTGAGTTTAAAATTTA  
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SEQ ID NO: 80\_AA449542\_M

ATCTCCAAGAGGGTGTCTCATTCTCCTTGGGCCGTGAAAAAGATAAGTCTTTTATGCGA  
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CCTTAATCACCCAAACATTATAGGATATCGTGCTTTTACTGAAGCCAGTGATGGTAGTCT  
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CAAAGACAGTGGAAGTCTTTTCCAGCAGCTGTAATTCTCAGAGTTGCTTTGCACATGGC  
CAGAGGGCTAAAGTACCTGCACCAAGAAAAGAAGCTGCTTCATGGAGACATAAAGTCTTC  
AAATGTTGTAATTAAAGGTGATTTTGAAACAATTAAAATCTGTGATGTAGGAGTCTCTCT  
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TTATGCAGCTCTGGGGACAAGGCCATCCATCAACATGGAAGAGCTGGATGACTCCTACCA  
GAAGGCCATTGAACTCTTCTGTGTGTGCACATAATGAGGATCCTAAAGATCGCCCGTCTGC  
TGCACACATCGTTGAAGCTTTGGAAGTAGATGGCCAATGTTGTGGTCTAAGCTCAAAGCA  
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CCATTGCTTTGTTACAGATCTTTTATAGATATTCTTGCTTCTTTAGTGGGTACTAAAAAT  
TTCCTACGTACATGTGGTACAGATATCTGTCTGCTCATAGTGTGAGTCTTTCAGCTGGC  
CTGTGAGCCCATGCGCCCTGGGACTTGAGAAGAGTTTCATAAACGTAGCTCCTAGGGTGTG  
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SEQ ID NO: 81\_5R57\_10\_2\_M TESK2\_M

GCTGCTGGACAGTGACTTGTATTTACCGTGGACTGTGAGAGTGAACTGGCCTATGGCAT  
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SEQ ID NO: 82\_AA232253\_H

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AGTCACAGAAACATCATCCAGTTTTATGGAGTAATTCTTGAACCTCCCAACTATGGCATT  
GTCACAGAATATGCTTCTCTGGGATCACTCTATGATTACATTAACAGTAACAGAAGTGAG  
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## FIGURE 2NNN

ATAGCTGCTGATGGAGTATTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAACCAT  
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CTCCCTGTGTGAGAACTTGTGACACATATTCCTATGGTGTGGTTCTCTGGGAGATGCTA  
ACAAGGGAGGTCCCTTTAAAGGTTTGAAGGATTACAAGTAGCTTGGCTTGTAGTGGAA  
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GCGGAGTGGAGGTGCGAAATTGAGGCAACTCTTGAGAGGCTAAAGAAACTAGAGCGTGAT  
CTCAGCTTTAAGGAGCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAA  
AAGCTGACAGAGCAGTCCAACACCCCGCTGCTGCCTTCTTTGAGATTGGTGCATGGACG  
GAAGACGATGTGTATTGGTGGGTTGAGCAGCTCGTCAGAAAAGGTGACTCTTCAGCAGAG  
ATGAGTGTATATGCAAGCTTGTTTAAAGAAAACAACATTACAGGGAAGCGGCTGCTGCTG  
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GTTTTTGGTTTTCACTTGAACACAGGAACTGGCCACAGGATTGTAAGTGGAAAATGTAT  
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CCTGGAAGCAGGTCCGACTCAAGTGCTGATTGCCAGTGGTTAGATACTCTGAGGATGCGG  
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CCCATTAAAGTATCAACAGATTACACCTGTGAACCAGTCCAGAAGCTCGTCTCTACTCAG  
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TATGGACGTGGTAGTATATCACTCAATTCTTCTCTAGAGGAAGATACAGTGGAAAGAGT  
CAGCATTCCTCATCAAGAGGAAGATACCTGGAAAGTTCTACAGGGTTTCTCAGTCA  
GCACTCAATCCTCACCAGTCGCCTGACTTCAAGAGAAGCCCCAGGGACCTCCACCAACCC  
AACACCATAACAGGGATGCCCTTGCACCCTGAGACTGACTCAAGAGCCAGTGAAGAGGAC  
AGCAAAGTCAGCGAAGGGGGCTGGACAAAAGTGGGAATACCGGAAAAAGCCCCACAGGCCA  
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TGA

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GCTACAATAGCTGGCCACCTAGAGGCTGCTGATGTGCTGTTGCAACATGGAGCTAATGTC  
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CAGGTAACCTCGCCTTCTTTTGAATTTGGTGTGATGTAAATGTAAGTGGTGAAGTTGGA  
GATAGACCCCTCCACCTAGCATCTGCAAAAGGATTCTTGAATATTGCAAACTCTTGATG  
GAAGAAGGCAGCAAAGCAGATGTGAATGCTCAAGATAATGAAGACCATGTCCCACTCCAT  
TTCTGTTCTCGATTTGGACACCATGATATAGTTAAGTATCTGCTGCAAGTGATTTGGAA  
GTTCAACCTCATGTTGTTAATATCTATGGAGATACCCCTTACACCTGGCATGCTACAAT

## FIGURE 2000

GGCAAATTTGAAGTTGCCAAGGAAATCATCCAAATATCAGGAACAGAAAGTCTGACTAAG  
GAAACATCTTCAGTGAAACAGCTTTTCATAGTGCTTGACCTATGGCAAGAGCATTGAC  
CTAGTCAAATTTCTTCTTGATCAGAATGTCATAAACATCAACCACCAAGGAAGGGATGGG  
CACACTGGATTACACTCTGCTTGCTACCACGGTCACATTGCGCTGGTTCAGTTCTTACTG  
GATAATGGAGCTGATATGAATCTAGTGGCTTGATGCCAGCAGGTCTAGTGGTGAAAAA  
GATGAGCAGACATGTTTGATGTGGGCTTATGAAAAAGGGCATGATGCCATTGTCACTC  
CTGAAGCATTATAAGAGACCACAAGATGAATTGCCCTGTAATGAATATTCTCAGCCTGGA  
GGAGATGGCTCCTATGTGTCTGTTCCATCACCTTGGGGAAGATTAAAAGCATGACAAAA  
GAGAAGGCAGATATTCTCCTCCTAAGAGCTGGATTGCCTTCACATTTCATCTTCAGCTC  
TCAGAAATTGAGTTCATGAGATTATTGGCTCAGGTTCTTTTGGGAAAGTATATAAAGGA  
CGATGCAGAAATAAAATAGTGGCTATAAAACGTTATCGAGCCAATACCTACTGCTCCAAG  
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GTAATTCAGTTTGTGGGTGCTTGCTTGAATGATCCCAGCCAGTTTGCCATTGTCACTCAA  
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CAGTCTAAATTAATTATTGCAGTAGATGTTGCCAAAGGCATGGAGTACCTTCACAACCTG  
ACACAGCCAATTATACATCGTGACTTGAACAGTCACAATATTCTTCTCTATGAGGATGGG  
CATGCTGTGGTGGCAGATTTTGGAGAATCAAGATTTCTACAGTCTCTGGATGAAGACAAC  
ATGACAAAAACAACCTGGGAACCTCCGTTGGATGGCTCCTGAGGTGTTACGCAGTGCCT  
CGGTACACCATCAAAGCAGATGTCTTCAGCTATGCTCTGTGTCTGTGGGAAATTCTCACT  
GGCGAAATTCCATTGCTCATCTCAAGCCAGCGCTGCGGCAGCAGACATGGCTTACCAC  
CACATCAGACCTCCCATTTGGCTATTCCATTCCCAAGCCCATATCATCTCTGCTGATACGA  
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GAGTGTCTCTGCAACATTGAGCTGATGTCTCCTGCATCAAGTAACAGCAGTGGGTCTCTC  
TCACCTTCTTCTTCTTCTGATTGCCTGGTGAACCGGGGAGGACCTGGCCGGAGTCATGTG  
GCAGCATTAAGAAGTCGTTTGAATTTGGAATATGCTCTAAATGCAAGGTCCTATGCTGCT  
TTGTCCCAAAGTGCTGGACAATATTCCCTCTCAAGGTCTGTCTTTGGAGGAGATGAAAAGA  
AGTCTTCAATACACACCCATTGACAAATATGGCTATGTATCCGATCCCATGAGCTCAATG  
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GAAACTGGGCTCGGAGATAATAGACTCCTCAACCAGGAGAATGGAGAGCGAAAGATCACC  
GCTTTATCGCCAGCTAATTGACCTGGCTATCTGAGCAGCAGTCACTGGAACGTGTGGGGC  
TCCTGGCCAGGATACTAAAGCTCAGAGCATGTTGGTGGAACAGAGTGAAAAGCTGAGACA  
CTTGAGCACATTTCTCACCAGGTGTTACAGACTCGCCTGGTGGATGCAGCCAAGGCCCT  
GAACCTGGTGCAGCTGCCACTGCCTTGACATCTTTATTAACCAGGCATTTGACATGCAGCG  
GGACCTGCAGATCACTCCCAAACGTCTGGAATATACTCGAAAAAAGGAGAATGAGTTGTA  
TGAATCATTGATGAATATTGCCAACCGAAAGCAGGAGGAAATGAAGGATATGATTGTTGA  
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CGTCATTGTCCCTGAGAATGGAGAACCAGTAGGCACCAGAGAGATCAAATGCTGCATCCG  
ACAGATCCAGGAACTCATCATCTCCGACTTAATCAGGCAGTGGCTAATAAGCTGATCAG  
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TGCTGCCTATCATGTTGAAGTCACGTTTCACTCAGGGTCGTGAGTTACAAGGATGCTATG  
GGAGCAAATCAAACAGATCATCCAGCGCATCACATGGGTGAGCCCACCTGCCATCACTCT  
GGAATGGAAGAGGAAGGTGGCCCAGGAAGCCATTGAGAGCCTCAGCGCCTCCAAATTGGC  
TAAGAGCATTTCAGCCAATTCGGGACTCGGCTCAATAGTTCCACGAGGCTTTTGCAGC  
CTCCTTGCGGCAGCTGGAAGCTGGCCACTCAGGCCGGTTAGAGAAAACGGAAGATCTATG  
GCTGAGGGTTGCGAAAGATCATGCTCCCCGCTGGCCCGCTTTCTCTGGAAGCCGTTCT

## FIGURE 2PPP

TTTACAGGATGTCTTGCTTCATCGTAAACCTAAACTGGGACAGGAACTGGGCCGGGGCCA  
GTATGGTGTGGTATACCTGTGTGACAACCTGGGGAGGACACTTCCCTTGTGCCCTCAAATC  
AGTTGTCCCTCCAGATGAGAAGCACTGGAATGATCTGGCTTTGGAATTCACATATATGAG  
GTCTCTGCCGAAGCATGAGCGATTGGTGGATCTCCATGGTTTCAGTCATTGACTACAACCTA  
TGGTGGTGGCTCCAGCATTGCTGTGCTCCTCATTATGGAGCGGCTACACCGGGATCTCTA  
CACAGGGCTGAAGGCTGGGCTGACCCTGGAGACACGTTTGCAGATAGCACTAGATGTGGT  
GGAGGGAATCCGCTTCCTGCACAGCCAGGGACTTGTCCATCGTGATATCAAACCTGAAAAA  
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GGCCATGATGTCAGGCAGCATTGTGGGGACACCAATCCATATGGCCCCCTGAACCTTTTCAC  
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CTCAGGCTCTGTCAAGCTCCCTGAGGCATTTGAGAGGTGTGCTAGCAAAGACCATCTCTG  
GAACAATGTGCGGAGGGGGGCTCGCCAGAACGTCTTCTGTGTTTGTATGAGGAGTGCTG  
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CCAGCCCATGCTCCAGGGCATCATGAATCGGCTCTGCAAGTCCAATTCTGAGCAGCCAAA  
CAGAGGACTAGATGATTCTACTTGAAAGCAAAGACCTTTCTCTTTCACTCTCTAGTTATT  
TCCTTCCCCCTCACCATTTGGCCATGGGGAGAATTTGACATTTATTCACTATAGGACACA  
CTCCCAAGGGAACCTGGTGCTTGGTGGAACTTGGAACTTCCCAGGCAGGGATGACTCC  
TGGACAGTGAAGAGTTGAATGACTGAGCATATTGAGCAGCTCACTGAAGCGCCAAGCTAT  
CCCTTTAGCAAAAAAGTGTCTCAGATGTGTAAAAGCTGAGGAATGTGGTGTCTGGCTTC  
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CTCCCGGCTTGGAAAACTGAAGGAGTTAATGATTCAATTGCTGGGGTTCCAGTCCGAAA  
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GCACAACACCTGGGCCAGTCTTTACTGAGACTCCCGGTCTCACCCTTCAAGGAATCAGG  
GAGATGGAAGACACGGCACTCCTTGGTATCCTTGGACCCACCGAATCCAATGACAGGGC  
CACCGGCTCTCGTCTTCAACAACCTGTTCTGAAGTGCAGATTGGGAACTACAACCTCCTTGG  
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GGGGTAGGGGCTGGCAGCCCTTCCACAAGTAGACTTCAGAGAATCACTGCAAGAGCCTGA  
AGTGTGCCATTTCAGCGTGGCAATAAAAAGCACGTTTTTAAGCAACCTGGACTGGCTAAGAC  
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CGTCACCTTGCTTGCTAAGATTTTATCTTGTACTGTGGAAGCGGATGGCATTTCATCTT  
GTCAGTGAAGGAGTACAGCCCTTGAAGTGGCTTTGGAAACATTGTCTTCTGCAGAGGTC  
TGTGCTGGGATCTATGACATATTGCTGGCTCTTATCTTCTTCATGACAGAGGACACCTA  
ACACACAATAATGTCTGTTTATCATCTGTGTTTGTGAGTGAAGATGGACACTGGAAGCTA  
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## FIGURE 2QQQ

CAGTCAATAAGAGACCCAGCATCTATCCCTCCTGAAGAGATGTCTCCAGAATTCACAACT  
CTCCAGAGTGTGATGGACATGCCCCGGGATGCCTTTTCATTTGGAACATTGGTGGAAAGT  
TTGCTCACAATCTTAAATGAACAGGTTTCAGCGGATGTTCTCTCCAGCTTTCAACAGACC  
TTGCACTCAACTTTGCTGAATCCCATTCCAAAATGTGCGCCAGCGCTCTGCACCTTACTA  
TCTCATGACTTCTTCAGAAATGATTTTCTGGAAGTTGTGAATTTCTTGAAAAGTTTAAACA  
TTGAAGAGTGAAGAGGAGAAAACGGAATTCCTTAAATTTCTGCTGGACAGAGTCAGCTGC  
TTGTCAGAGGAATTGATAGCTTCAAGGTTGGTGCCTCTTCTGCTTAATCAGTTGGTGT  
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GCGCAGGGAGAAACTCCTTGCTTGCTCTCACCAGCCCTGTTCCAGTCACGGGTGATCCCC  
GTGCTTCTCCAGTTGTTTGAAGTTCATGAAGAGCATGTGCGGATGGTGTGCTGTCTCAC  
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GCAGTGCTGGTCTCTCTGCTTGGACCAGAGGTGGTTGTGGGAGGAGAACGAACCAAGATC  
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TTTTCTCAGCCTATTAAATTTCCCATAAATGGACTCTCAGATGTAAAAATACTTCGGAG  
GACAGTGA AAACTTCCCATCAAGTTCTAAAAAGTCTGAGGAGTGGCCTGACTGGAGTGAA  
CCTGAGGAGCCTGAAAATCAAACGTCAACATACAGATTTGGCCTAGAGAACCTTGTGAT  
GATGTCAAGTCCCAGTGCACCTTGGATGTGGAAGAGTCATCTTGGGATGACTGCGAG  
CCCAGCAGCTTAGATACTAAAGTAAACCCAGGAGGTGGAATCACTGCTACAAAACCTGTT  
ACCTCAGGGGAGCAGAAGCCTATTCTGCTTTGCTTTCACTCACTGAAGAGTCTATGCCT  
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ATCGAGCCGCCAAAAGTGTATCACAAGAAAGGCCCTTAAGGTTCCATCAGAACTTGGT  
TTAGGAGAGGAATTCACCATTCAAGTAAAAAAGAAGCCAGTAAAAGATCCTGAGATGGAT  
TGTTTTGCTGATATGATCCAGAAATTAAGCCTTCTGCTGCTTTTCTTATATTACCTGAA  
CTGAGGACAGAAATGGTCCCCAAAAGGATGATGTCTCCCAGTGATGCAGTTTTCTCA  
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CCATGCTTAATAAATTGAAGAGTACTGTTACAAAAGTCACAGCTGATGTCACTAGTGC  
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AAAGAGATAATCTTCAGAAATCACAGTTTTTCAAAGGACTGCCAAAGGTTCTACCAAAC

## FIGURE 2RRR

TGCCCCAAGCGTGTCAATTGTGCAGAGAATTTTGCCTTGTTTGACTTCAGAATTTGTAAACC  
CTGACATGGTACCTTTTGTGTTTGTCCCAATGTTCTACTTATTGCTGAGGAATGCACCAAAG  
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TCCAGATTTTGTAAATTTTCTACAAAAAATGGATTTGCTACTAACCAAAACCCCTCCTG  
ATGAGATAAAGAACAGTGTCTACCCATGGTTTACAGAGCACTAGAAGCTCCTTCCATTTC  
AGATCCAGGAGCTCTGTCTAAACATCATTCCAACCTTTGCAAATCTTATAGACTACCCAT  
CCATGAAAAACGCTTTGATACCAAGAATTAAAAATGCTTGCTACAAACATCTTCCCTTGC  
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GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCCCCGGCTCGGGCGGCCGGAG  
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CCGGGCCCTGGGCCCTGCACCGCGGCCGCAAGAAGGCCACAGGCAGCCCCGTGTCCATCT  
TCGTCTATGATGTGAAGCCTGGCGCGGAAGAGCAGACCCAGGTGGCCAAAGCTGCCTTCA  
AGCGCTTCAAACTCTACGGCACCCCAACATCCTGGCTTACATCGATGGACTGGAGACAG  
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TGGAGCTGATGAAGCACTTTGCACGGCTACAGGCCAAGGATGAACAGGGCCCCATCCGCT  
GCAACACCACAGTCTGCCTGGGCAAAATCGGCTCCTACCTCAGTGCTAGCACCAGACACA  
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ACTGGGGTGGCCAGAGTCCAGCGACAAGGGCGACCCCTTCGCTACCCTGTCTGCACGTC  
CCAGCACCCAGCCGAGGCCAGACTCTTGGGGTGAGGACAACCTGGGAGGGCCTCGAGACTG

## FIGURE 2SSS

ACAGTCGACAGGTCAAGGCTGAGCTGGCCCCGGAAGAAGCGCGAGGAGCGGCGGCGGGAGA  
TGGAGGCCAAACGCGCCGAGAGGAAGGTGGCCAAGGGCCCCATGAAGCTGGGAGCCCCGA  
AGCTGGACTGAACCGTGGCGGTGGCCCTTCCCGGCTGCGGAGAGCCCCGCCACAGATGT  
ATTTATTGTACAAACCATGTGAGCCCCGCCGCCAGCCAGGCCATCTCACGTGTACATA  
ATCAGAGCCACAATAAATTCTATTTAC

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CAAGGAGGAATTTCTGTGGAAAACAGCTGGCAGATTGTTAGAAGATACAGTGACTTTGAT  
TTGCTTAACAACAGCTTACAGATTGCAGGCCTAAGTCTACCTCTTCCTCCAAAAAATTG  
ATTGGTAACATGGATCGTGAATTCATAGCTGAAAGGCAGAAAGGTCTTCAGAACTATCTC  
AACGTGATCACAACAAATCATATCTTGTCTAATTGTGAGCTGGTTAAGAAGTTTTTAGAT  
CCAAACAACATATCCGCAAACATACTGAGATTGCCTTGCAACAGGTTTCATGTTCTTC  
CGATCAGAGCCAAAGTGGGAGGTGGTGGAACTTTGAAAGACATAGGTTGGAGAATAAGG  
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GCTGACCTTGGCCCAGACAAGTATTTGTCAGATAAAGATTTTCAGTGTCTAATCAAACCTT  
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CCACCACCACCAGCAGCTCCCTTGCCCTCTGCGAGCACCGAGGCACCTGCCCAGCTCTCG  
TCTCAGGCTGTGAATGGCATGAGCCGAGGGGCCCTTGCTCAGCTCCATCCAGAATTTCAA  
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TCCTGTTTACACTTGGAGGGAAGTTCTTTTTTATTCTACTCACCCCTACCCCCAAC  
TACCCTCTTCTGGGAAAGTAATTGCTGAGCCAGTACAGCCACAAACAGTACTATTTTGC  
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ATGAGCGCCAGCACGGGCGGTGGTGGGGACAGCGGCGGCAGCGGCGGCAGTAGCAGCAGC  
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CCTCAGATGCTGCAGGGCCTTCTGGGCTCCGACGACGAGGAACAGGAAGACCCCAAAGAC  
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GTGGTGCGCAAACTGGGCTGGGGCCACTTCTCCACCGTCTGGCTCTGCTGGGACATCCAG  
CGCAAGCGCTTTGTGGCCCTCAAAGTGGTGAAGAGTGCGGGGCATTACACGGAGACAGCT  
GTGGATGAGATCAAGCTCCTGAAATGTGTCCGGGACAGCGACCCCAAGTGACCCCAAGA  
GAGACCATTGTCCAGCTCATTGATGACTTCAGGATCTCAGGAGTCAATGGAGTCCATGTG

## FIGURE 2TTT

TGCATGGTGCTGGAGGTGCTGGGCCACCAGCTCCTCAAATGGATCATCAAGTCCAACTAC  
CAGGGCCTGCCCCTGCCCTGCGTGAAGAGCATCGTGAGGCAGGTGCTGCACGGCCTGGAC  
TACCTCCACACCAAGTGCAAGATCATCCACACGGACATCAAGCCCCGAGAACATCTTGCTG  
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AAGCTGTCCAAAAACAAGAGGAAGAAGATGAGGCGCAAACGGAAACAGCAGAAGCGGCTG  
CTGGAGGAGCGGCTGCGGGACCTGCAGAGGCTGGAGGCCATGGAGGCTGCCACCCAGGCT  
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CTGGAGCCCCAAAATGCAGATAAGATCAAGATCAAGATCGCAGACCTGGGCAACGCCTGC  
TGGGTGCACAAGCACTTCACGGAAGACATCCAGACTCGGCAGTACCGGGCCGTCGAGGTG  
CTGATCGGCGCCGAATACGGCCCCCGGCAGACATCTGGAGCACAGCCTGCATGGCCTTC  
GAGCTGGCCACTGGTGACTACCTGTTTCGAGCCGCATTCTGGAGAAGACTACAGTCGTGAT  
GAGGACCACATCGCTCACATAGTGGAGCTTCTGGGGGACATCCCCCAGCCTTCGCCCTC  
TCAGGCCGCTATTCCCGGGAGTTCTTCAACCGGAGAGGAGAGCTGCGGCACATCCACAAT  
CTCAAGCACTGGGGCCTGTACGAGGTACTCATGGAAAAGTACGAGTGGCCCCTAGAGCAG  
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AGTGCCGCTGACTGCCTCCAGCACCCCTGGCTCAACCCCTAG

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AGCATGGAGGACTTTCTGCTCTCCAATGGGTACCAGCTGGGCAAGACCATTGGGGAAGGG  
ACCTACTCAAAAGTCAAAGAAGCATTTCACAAAAACACCAAAGAAAAGTGGCAATTAA  
GTTATAGACAAGATGGGAGGGCCATCAGAGTTTATCCAGAGATTCTCCCTCGGGAGCTC  
CAAATCGTCCGTACCCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCT  
GCCGACGGGAAAATCTGCCTGGTGTATGGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGC  
GTGCTGAATGGGGGGCCACTGCCTGAAAGCCGGGCCAAGGCCCTCTTCCGTGAGATGGTT  
GAGGCCATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAAC  
GCCTTGTTGCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCCC  
AAGTCACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCGAG  
GTGCTGCAGGGCATTCCCCACGATAGCAAAAAGGTGATGTCTGGAGCATGGGTGTGGTC  
CTGTATGTATGCTCTGTGCCAGCTACCTTTTGACGACACAGACATCCCCAAGATGCTG  
TGGCAGCAGCAGAAGGGGTGTCCTTCCCCACTCATCTGAGCATCTCGGCCGATTGCCAG  
GACCTGCTCAAGAGGCTCCTGGAACCCGATATGATCCTCCGGCCTTCAATTGAAGAAGTT  
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GTAGGGGGAGAAAGCAAA

SEQ ID NO: 92\_AA060026\_M SGK022\_M

CAGACGGAGAATGTTCTAGCCCTGGAGGCAGCTGTGAATGAAGTCCTTGGGGGGAAAAGA  
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TGGGCAAGACCATTGGGGAAGGGACCTACTCAAAAGTCAAAGAAGCATTTCACAAAAAC  
ATCAAAGAAAAGTGGCAATTAAATTTATAGACAAGATGGGAGGGCCAGAAGAGTTTATCC  
AGAGATTCTGCTCGTGAGCTCCAGATTGTCCGTACCCTGGACCACAAAAACATCATCC  
AGGTGTATGAGATGCTGGAGTCAGCAGATGGAAAAATCTACCTGGTGTATGGAAGTGGCTG  
AGGGAGGGGATGTCTTTGACTGTGTGCTGAACGGAGGGCCACTTCCCGAGAGCCGGGCCA  
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## FIGURE 2UUU

ACCGGGACCTTAAGTGTGAGAACGCCTTGTTGCAGGGCTTCAACCTGAAGCTGACCGACT  
TTGGCTTTTGCCAAGGTGCTACCCAAGTCACGCAGGGAGCTGAGCCAGACCTTCTGTGGCA  
GCACAGCCTATGCCGCCCTGAGGTGCTACAGGGCATACCCCATGATAGCAAGAAAGGTG  
ATGTCTGGAGCATGGGTGTGGTCCTGTATGTAATGCTCTGTGCAAGTCTACCTTTTGATG  
ACACAGATATCCCCAAGATGCTGTGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCATT  
TGGGCATCTCAACCGAATGCCAGGACCTGCTCAAGCGGCTCCTGGAACCAGACATGATAC  
TCCGGCCTTCAATCGAAGAAAGTTAGTTGGCACCCATGGCTAGCAAGCACTTGATAAAAGC  
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SEQ ID NO: 93\_AA399669\_H

CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGCACTTCATTCTCAA  
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TCTCTTTCTTTCCCCCTCCAAGTTCCTAGTGGAGGGCTGAGTCCAGCATCCCAGACTCGT  
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CTCAAGGTGTTGGCCTTTGGATAGGAGGCTTCCAAGTAGTAAAGCTCCCTGCTCTCAGCA  
AGCCCAACACCATGGGGAAGGGAGATGTCTTAGAGGCAGCACCAACCACACAGCCTACC  
ATTCCTCATGGATGAATATGGTTATGAGGTGGGCAAGGCCATTGGCCATGGCTCCTATG  
GGTCGGTATATGAGGCTTTCTACACAAAGCAGAAGGTTATGGTGGCAGTCAAGATCATCT  
CAAAGAAGAAGGCCTCTGATGACTATCTTAACAAGTTCCTGCCCCGTGAAATACAGGTAA  
TGAAAGTCTTGCGGCACAAGTACCTCATCAACTTCTATCGGGCCATTGAGAGCACATCTC  
GAGTATACATCATTTCTGGAACCTGGCTCAGGGTGGTGTATGTCCTTGAATGGATCCAGCGCT  
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CCTACCTGCACAGCAAGAGCATCGTGACCCGGGACTTAAAGTTGGAGAACCTGTTGCTGG  
ACAAGTGGGAGAATGTGAAGATATCAGACTTTGGCTTTGCCAAGATGGTGCCTTCTAACC  
AGCCTGTGGGTTGTAGCCCTKCTTACCGCCAAGTGAAGTGCCTTTTCCACCTCAGCCAGA  
CTTACTGTGGCAGCTTTGCTTACGCTTGCCAGAGATCTTACGAGGCTTGCCCTACAACC  
CTTTCTGTCTGACACCTGGAGCATGGGCGTCATCCTTTACACTCTAGTGGTCGCCCATC  
TGCCCTTTGATGACACCAATCTCAAAAAGCTGCTAAGAGAGACTCAGAAGGAGGTCACTT  
TCCCAGCTAACCATAACCATCTCCAGGAGTGCAAGGTCCAAGTGCCTATTGCCTGTGTGG  
CACAATGGAGAAAAACTCAGGCAAGACCTCTCTCTCCCTGCTCTAGAACCTGATCCTCC  
AGATGCTACGCCAAGCCACTAAGCGTGCCACCATTCTGGACATCATCAAGGATTCCTGGG  
TGCTCAAGTTCAGCCTGAGCAACCCACCCATGAGATCAGGCTGCTTGAGGCCATGTGCC  
AGCTCCACAACACCACTAAACAGCACCAATCCTTGCAAATTACGACCTGAAAATGGCTGA  
GGGAGGGGGCTAAGAGAGGAGCAAAGCAGGAGGTCTTGGGCTAAAAATCTTTTTTACCAA  
AAATAAATCTAAGTCTGATTTAGTTTCATCAAAAAA

SEQ ID NO: 94\_AA758539\_H

GACCATTCAGACGCCTCCGGTAGTGTAATGAGGACAATGCCTGCTGGCCACATGACGG  
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AAGGAAGAAGGGTTACATCGTAGGCATCAATCTTGGCAAGGGTTCCTACGCAAAAGTCAA  
ATCTGCCTACTCTGAGCGCCTCAAGTTCAATGTGGCTGTCAAGATCATCGACCGCAGGAA  
AACACCTACTGACTTTGTGGAGAGATTCTTCTCGGGAGATGGACATCCTGGCAACTGT  
CAACCACGGCTCCATCATCAAGACTTACGAGATCTTTGAGACCTCTGACGGACGGATCTA  
CATCATCATGGAGCTTGGCGTCCAGGGCGACCTCCTCGAGTTCATCAAGTGCCAGGGAGC  
CCTGCATGAGGACGTGGCACGCAAGATGTTCCGACAGCTCTCCTCCGCCGTCAAGTACTG  
CCACGACCTGGACATCGTCCACCGGGACCTCAAGTGCGGAGAACCTTCTCCTCGACAAGGA  
CTTCAACATCAAGCTGTCTGACTTTGGCTTCTCCAAGCGCTGCCTGCGGGACAGCAATGG  
GCGCATCATCCTCAGCAAGACCTTCTGCGGGTCCGCGAGCATATGCAGCCCCCGAGGTGCT  
GCAGAGCATCCCCACCAGCCCAAGGTGTATGACATCTGGAGCCTGGGCGTGATCCTGTA

## FIGURE 2VVV

CATCATGGTCTGCGGCTCCATGCCCTATGACGACTCCGACATCAGGAAGATGCTGCGTAT  
CCAGAAGGAGCACCGTGTGGACTTCCCCGCGCTCCAAGAACCTGACCTGCGAGTGCAAGGA  
CCTCATCTACCGCATGCTGCAGCCCCGACGTACGCCAGCGGCTCCACATCGATGAGATCCT  
CAGCCACTCGTGGCTGCAGCCCCCAAGCCCCAAGCCACGTCTTCTGCCTCCTTCAAGAG  
GGAGGGGGAGGGCAAGTACCGCGCTGAGTGCAAAC'TGGACACCAAGACAGGCTTGAGGCC  
CGACCACCGGCCCCGACCACAAGCTTGGAGCCAAAACCCAGCACCGGCTGCTGGTGGTGCC  
CGAGAACGAGAACAGGATGGAGGACAGGCTGGCCGAGACCTCCAGGGCCAAAGACCATCA  
CATCTCCGGAGCTGAGGTGGGGAAAGCAAGCACCTAGCATGACAATGGCCCCGTTGTGTG  
TGGTGGGGGTGCGGGTTGGGGGGCATGGTGCAGTCGGCCTTCACGTAAACTAAGTAGGCA  
GGTAGGATCTGAAGAAGGCACAGGTGCAAGTAAAATTCGTCAATTAAACCACTATTTTGA  
TT

SEQ ID NO: 95\_AA883975\_H

ATGTCCGGAGACAACTTCTGAGCGAACTCGGTTATAAGCTGGGCCGCACAATTGGAGAG  
GGCAGCTACTCCAAGGTGAAGGTGGCCACATCCAAGAAGTACAAGGGTACCGTGGCCATC  
AAGGTGGTGGACCGGCGGAGCGCCCCCGGACTTCGTCAACAAGTTCCTGCCGCGAGAG  
CTGTCCATCCTGCGGGGCGTGCAGACCCCGCACATCGTGCACGTCTTCGAGTTCATCGAG  
GTGTGCAACGGGAACTGTACATCGTGATGGAAGCGGCCGCCACCGACCTGCTGCAAGCC  
GTGCAGCGCAACGGGCGCATCCCCGAGTTTCAAGCGCGCGACCTCTTTCGCGCAGATCGCC  
GGCGCCGTGCGCTACCTGCACGATCATCACCTGGTGCACCGCGACCTCAAGTGCGAAAAC  
GTGCTGCTGAGCCCGGACGAGCGCCGCGTCAAGCTCACCGACTTCGGCTTCGGCCGCCAG  
GCCCATGGCTACCCAGACCTGAGCACCACCTACTGCGGCTCAGCCGCTACGCGTCAACC  
GAGGTGCTCCTGGGCATCCCCTACGACCCCAAGAAGTACGATGTGTGGAGCATGGGCGTC  
GTGCTCTACGTATGGTCAACGGGTGCATGCCCTTCGACGACTCGGACATCGCCGGCCTG  
CCCCGGCGCCAGAAACGCGGCGTGCTCTATCCCGAAGGCCTCGAGCTGTCCGAGCGCTGC  
AAGGCCCTGATCGCCGAGCTGCTGCAGTTTCAAGCCCGTCCGCCAGGCCCTCCGCGGGCCAG  
GTAGCGCGCAACTGCTGGCTGCGCGCCGGGACTCCGGCTAG

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CTGGTAGAGAACAGGGGCTGGTGCCAAGGCCCATGGAGATGAGAAAACGGAAGACAGGGA  
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GGACAAATCAGGCCTTATAATTTGTGATTTCTGTGGCTTTGTCTAAAAGTCCATAAAGCAC  
CTTGATATCCAGTCTCACAGACTGCTCACAACAGTCCACAAGGCTGGTGGGGAGTGCTTC  
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CAGCTAGACACACTTAAGACCATTAAGAAAGCCAAGAAATAAGACCCAGACAAGGTGGGC  
AGAAGTTGGAAGGCAGGAGACAGGTGTGAGGAGGTGGGCCTTTCTGATCTGCCAGCCCAT  
CTCTCCTCCCCTTACTTCCTCAGAGTTTATCCAGAGATTCCCTCCCTCGGGAGCTCCAAAT  
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CGGGAAAATCTGCCTGGTGTGAGGCTCGCTGAGGGAGGGGATGTCTTTGACTGCGTGCT  
GAATGGGGGGCCACTGCCTGAAAGCCGGGCCAAGGCCCTCTTCCGTGAGATGGTTGAGGC  
CATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAACGCCTT  
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ACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCCGAGGTGCT  
GCAGGGCATTCCCNCAAGATGCTGTGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCA  
TCTGAGCATCTCGGCCGATTGCCAGGACCTGCTCAAGAGGCTCCTGGAACCCGATATGAT  
CCTCCGGCCTTCAATTGAAGAAGTTAGTTGGCATCCATGGCTAGCAAGCACTTGATAAAA  
GCAATGGCAAGTGCTCTCCAATAAAGTAGGGGGAGAAAGCAAACCC

## FIGURE 2WWW

SEQ ID NO: 97\_H29974\_H

TTACAGCCTGTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTATGAGGCAGTGGC  
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GGAGCTGGCGCTGGCTGAATTCTGGGCCCTCACCAGCCTCAAGCGGCGCCACCAGAACGT  
CGTGACGTTTGAGGAGTGCCTCCTGCAGCGCAATGGGTTAGCCCAGCGCATGAGTCACGG  
CAACAAGAGCTCGCAGCTTTACCTGCGCCTGGTGGAGACCTCGCTGAAAGGAGAAAGGAT  
CCTGGGTTATGCTGAGGAGCCCTGCTATCTCTGGTTTGTTCATGGAGTTCTGTGAAGGTGG  
AGACCTGAATCAGTATGTCCTGTCCCGGAGGCCAGACCCAGCCACCAACAAAAGTTTCAT  
GCTACAGCTGACGAGCGCCATTGCCTTCCTGCACAAAAACCATATTGTGCACAGGGACCT  
GAAGCCAGACAACATCCTCATCACAGAGCGGTCTGGCACCCCCATCCTCAAAGTGGCCGA  
CTTTGGACTAAGCAAGGTCTGTGCTGGGCTGGCACCCCCGAGGCAAAGAGGGCAATCAAGA  
CAACAAAAATGTGAATGTGAATAAGTACTGGCTGTCTCAGCCTGCGGTTTCGGACTTCTA  
CATGGCTCCTGAAGTCTGGGAGGGACACTACACAGCCAAGGCGGACATCTTTGCCCTGGG  
CATTATCATCTGGGCAATGATAGAAAGAATCACTTTTATTGACTCTGAGACCAAGAAGGA  
GCTCCTGGGGACCTACATTAAACAGGGGACTGAGATCGTCCCTGTTGGTGGGCGCTGCT  
AGAAAACCCAAAGATGGAGTTGCACATCCCCAAAAACGCAGGACTTCCATGTCTGAGGG  
GATCAAGCAGCTCTTGAAAGATATGTTAGCTGCTAACCACAGGACCGGCTGATGCCTT  
TGAAGTTGAAACCAGAATGGACCAGGTACATGTGCTGCTTAAATTCAGGGCTAAGCAT  
TTTGGGTGATTTTAAACTAGGTGATTCCTCGGGACCCACAGTCTCACCACGTCTCCTCC  
AGAGGACGGCAGAGGTACAGGTGGTGGCTGGCCGGTTGGCGATCTCCCGACAGCTGGA  
TCCGGCAATGTGAAGCTTTTGTGGTGGTTCCTTTTGGCTTTTGGCTTTTGGCTTTATTN  
TNNCTTTTCTTTTCTTTTTTTTNTTNNCCANTNCCTTTTAAATTTAAACCATTGAG  
ACTTCAGAAGAGCAGGACACAATGCTGTGGACAGGCACCAATTTCTTTAAAGAAATTCAA  
TGTGGGCAAGGCATATGTGTAAATTTCACTTTTACTTTTATAAGGGGTAGGGAGCTAT  
TTTTGGTTTTGTCTTCACTTTCCCTCTGTCTTCTTCTTATACTTTTCTCAGTTCTAC  
TTATGACACCTCACTTCCCTAGAGAAGGCCTGCCTCCCCATAGGGAATCTGGGGGTANCT  
TCTGGAACGGGGCGTGAGGANACAAGGAGCCTCTGGGCCACNCCTCCCTACCAGATGCAG  
GAACCTCTGACTCCTTGGTGGGCTGGCCCTGGCTAGCCCTTGGGCCTCGGAGATGATCA  
GAGGTGAAGAACCGCC

SEQ ID NO: 98\_AA498104\_M H29974\_M

CCGTTGCTGCTCCCCCGCCCCCGCAGCCATGGAAACGGGGAAAGAGAACGGAGCCCCG  
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CGCAGTGGGGCCAGGGTGGCAGTCAAGAAGATCCGCTGCGACGCTCCCGAGAACGTGGAG  
TTGGCACTAGCAGAATTCTGGGCCCTCACCAGTCTCAAGCGGCGGCACCAGAATATCGTG  
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CAGCTTACAAGCGCCATTGCCTTCCTGCATAAAAAACCATCGTGACAGGGACCTAAAG  
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GCTCCCGAAGTCTGGGAGGGACACTATACAGCCAAGGCGGACATCTTTGCTCTGGGCATT  
ATCATCTGGGCAATGATAGAAAGAATTACCTTTATTGACTCTGAAACCAAGAAGGAGCTC  
CTGGGGACCTACATTAAAGCAAGGGACTGAGATCGTCCCTGTTGGTGGAGCGCTGCTAGAA  
AACCCAAAGATGGAGTTGCATATCCCCCAGAAACGTAGGACTTCCATGTCTGAGGGGCTC

## FIGURE 2XXX

AAGCAGCTCTTGAAAGACATGTTAGCTGCTAACCCACAGGACCGACCTGATGCTTTTGAA  
CTTGAAACCCGAATGGACCAGGTACATGTGCTGCTTAAACTCCAGGGCTGAACGTCTTG  
GGTGTTTTTTAAACTAGGTTCGATCCTTCGGGACCCACAGTCTCATCGTGTCTCGGACAGGA  
TGGCAGAGGGTACAGGTGGTGGTGTATCTCCTGACAGCTGGACCTCCCACAATGTGAAGCT  
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CGRCCGCGCTACGGAAAGCCGGAGGGGGGCGGGGCCGTCGGCGTAAGGGGGTGTGTCCGC  
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GAAACCTCGACCTTGAAGATGGTGAAGTAGCCAGCCAAAGTACGATCTAATACGGGAGGTA  
GGCCGAGGTAGTTACGGTGTGTGTATGAAGCAGTCATCAGAAAGACCTCTGCACGGGTG  
GCAGTGAAGAAAATTCGATGTCACGCACCTGAAAATGTTGAACTAGCCCTTCGTGAGTTC  
TGGGCACTAAGCAGTATCAAGAGCCAACATCCAAATGTGATTCACTTGGAGGAATGCATC  
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CAGCTTGTAGAACTTCATTAAAAGGAGAAATTGCCTTTGATCCCAGAAGCGCCTATTAT  
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GAGTCCAGTTTTCTGGAAATATGTCTTTAAGTATTTTAGACATTCCTCGTCAGTATTAGG  
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AAACATATATGTATATATTTATGTATATGTAAGTATGTGAATGTGCGCATTTTGCATTCC  
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TGCTGGTGAAGTCAGTGACGAAAAATAAACCTTCCCTTATCTTCCTACTCTGCCCTCCC  
CCTAATGAAATCATATTAAGTNGTTTTTCCCTNNTTTTTTTTGTAATATACAGCTTTTTTTTT  
TAAGGCATCATTTTTCGAGGGTCTAAAATTATCTGGTAAACAAATGAAATTAAGTGATCC  
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CATGCAGTCATATGGCAGCAGGTTGGTGATT

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GCGGGGCTCCGTATCCCCACGTGGGCCCTGCAGGAACTGGCGGGGCGCGTGACCCGGCG  
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GCAACCCGCGCGGAACCGCCCGCAGCGAGGAAGCGCCCGCGCGGGCGCAGGCGGCCG  
AATGGCGGGGCGGGCTGGGGTCCCCCGCGCCTGGACGGCTTCATCCTCACCAGCGCCT  
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## FIGURE 2YYY

GGTAGCCATAAAGTGTGTAGCCAAGAAAAGTCTGAACAAGGCATCGGTGGAGAACCTCCT  
CACGGAGATTGAGATCCTCAAGGGCATTCGACATCCCCACATTGTGCAGCTGAAAGACTT  
TCAGTGGGACAGTGACAATATCTACCTCATCATGGAGTTTTGCGCAGGGGGCGACCTGTC  
TCGCTTCATCCATACCCGAGGATTCTGCCTGAGAAGGTGGCGCGTGTCTTCATGCAGCA  
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ACAGAACATTCTACTGAGCTCCTTGGAGAAGCCCCACCTAAAACTGGCAGACTTTGGTTT  
CGCACAACACATGTCCCCGTGGGATGAGAAGCACGTGCTCCGTGGCTCCCCCTCTACAT  
GGCCCCCGAGATGGTGTGCCAGCGGCAGTATGACGCCCGCGTGGACCTCTGGTCCATGGG  
GGTCATCCTGTATGAAGCCCTCTTCGGGCAGCCCCCTTTGCCTCCAGGTCGTTCTCGGA  
GCTGGAAGAGAAGATCCGTAGCAACCGGGTCATCGAGCTCCCCTTGGCGCCCCCTGCTCTC  
CCGAGACTGCCGGGACCTACTGCAGCGGCTCCTGGAGCGGGACCCAGCCGTCGCATCTC  
CTTCCAGGACTTCTTTGCGCACCCCTGGGTGGACCTGGAGCACATGCCAGTGGGGAGAG  
TCTGGGGCGAGCAACCGCCCTGGTGGTGCAGGCTGTGAAGAAAGACCAGGAGGGGGATT  
AGCAGCCGCCTTATCACTCTACTGCAAGGCTCTGGACTTCTTTGTACCTGCCCTGCACTA  
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SEQ ID NO: 101\_AA311714\_H

TGGACCTGTCCTGAGGCAGAGGCCGAGATGCGCGCAACCGCGGGAGCAGCCAAGTGGACT  
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GAAGTCGGCCAGAGATGGAACCTTTATTCTGTATGAGGAGATCGGAAGAGGAAGCAAG  
ACTGTTGTCTATAAAGGGCGACGGAAGGGAACAATCAATTTGTAGCCATTCTTTGTACT  
GATAAGTGCAGAAGGCCTGAAATAACCAACTGGGTCCGTCTCACCCGTGAAATAAAACAC  
AAGAATATTGTAACCTTTTCATGAATGGTATGAAACAAGCAACCACCTCTGGCTAGTGXAT  
GAAAACCTCCCAGAAGATGTTGTGAGAGAATTTGGAATTGACCTGATTAGTGGATTACAT  
CATCTTCATAAACTTGGCATTCTCTTTTGTGACATTTCTCCTAGGAAGATACTCTTGGAA

## FIGURE 2ZZZ

GGGCCTGGCACACTGAAGTTTAGCAACTTTTGCTTGGCAAAAGTGGAAGGTGAAAATTTG  
GAAGAGTTCTTTGCTTTGGTGGCAGCAGAGGAAGGAGGTGATAATGGGGAAAATGTC  
CTGAAGAAAAGCATGAAAAGTAGAGTCAAAGGATCTCCTGTATATACAGCACCAGAAGTT  
GTGAGGGGTGCTGACTTTTCCATCTCCAGTGACCTCTGGTCTTTGGGCTGTCTGCTTTAT  
GAAATGTTTTTCAGGAAAACCTCCATTCTTCTCAGAAAAGTGTTTCAGAATTAAGTGAAG  
ATCTTATGTGAAGATCCTTTGCCACCTATTCCGAAAGATTCTTCTCGTCCTAAAGCTTCT  
TCAGATTTTATTAAATTTGCTTGATGGGTACTTCAAAGAGATCCTCAGAAAAGATTGACT  
TGGACAAGGCTACTGCAGCATTCATTTTGGAAGAAAGCTTTTGCTGGAGCAGATCAGGAA  
TCAAGCGTCGAAGATCTCAGTCTCAGCAGAAACACTATGGAGTGTTCTGGGCCACAAGAT  
TCCAAGGAGCTTTTGCAAGACTCTCAGAGTAGACAAGCAAAAGGGCACAAGAGTGGTCAA  
CCACTAGGTCACCTTTTCAGACTAGAAAATCCAACAGATTTCGGCCTAAGAGTACTCTT  
GAGGGTCAATTGAATGAATCCATGTTTCTTCTCAGTTCTCGTCTACTCCCAGAACTAGC  
ACTGCAGTGGAAGTAAGTCTTGGTGAGGATATGACTCACTGTTCAACACAGAAGACTTCT  
CCTCTGACCAAGATTACAAGTGACACCTGAGTCAGCAGGACCTGGAATCCCAGATGAGA  
GAGCTTATCTACACGGACTCAGATCTTGTTGTCAACCCCATATCGACAATCCAAAGATA  
ATGAAACAGCCACCAGTTAAATTTGATGCAAAAATATTGCATCTACCAACATATTCAGTG  
GATAAGTTATTATTTCTGAAAGATCAAGATTGGAATGACTTTTTTGCAACAAGTGTGCTCG  
CAGATCGACTCCACTGAGAAGAGCATGGGGGCTCCCGAGCCAAGCTGAATCTCCTTTGC  
TATTTGTGCGTGGTGGCTGGTCACCAGGAGGTGGCCACCAGGCTCCTCCATTCCCCCTG  
TTCCAATTGCTAATCCAGCATTTGCGGATAGCTCCAACTGGGATATACGGGGCCAAGGTT  
GCTCACGTGATTGGTTTACTGGCTTCGCACACAACTGAGCTCCAGGAAAATACACCTGTT  
GTTGAGACTACAAGCTCCATTGGAATCGGGATTTTGAAGTGTCTTGTTCAACACTCCACT  
CCAGTGCCTAGACAGTGCCTTGTGTATGTATAGATACTGACAAATATTTCAAATAAATA  
AAACTGTATCAGCATT

SEQ ID NO: 102\_SGK384\_H

TCTTTGGCCACGTGCTGAGGGCGCGGCAGATCCTGACGGAGCCAGAAGTGCGCGACTAC  
CTGCGGGGCTGGTCAGCGGCCTGCGCTACCTGCACCAGCGGTGCATCCTGCACCGC

SEQ ID NO: 103\_AA210451\_M SGK384\_M

GGTCTGCTGCATGGATAATGGACTGGAACACAGAAAGACCATGCAGGGTTTCGGCTGTAGA  
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GGTTGTGAGCTGCCATGTTGAACCAAGCAGGTCACTGAGGGACACAGGCATGTGGATGGA  
AACCCTGCTGGGAGAAAAAAGAACTGCTGAAGGGACTGACATGGGACAGCAACATGGAA  
CCAGGAATGGTCTCACGCATAGAGAGCTCCCCCGGGGCGTGGGGCTGCTGCTCGCCATGG  
CCCTTATGAACGTGGCGCTCTACCTCTGCCTTGATCAGCTTTTCATCTCCCCTGGACGAT  
CCACCGCGGACTCTAGGCGCTGTCTCCGGGCTACTTCAGAATGGGGCGGATGAGAACT  
GCTCACGCTGGCTGTCTGTGAAGAGCTGAGGACAGAAGTCAGGCAGCTGAAGCGCGTTG  
GGGAGGGAGCCGTGAAGAGAGTCTTTCTGTCTGAATGGAAGGAACACAAAGTCGCTCTCT  
CCCGGCTCACAGGCTGGAGATGAAGGAGGACTTCCTGCATGGGCTGCAGATGCTGAAGT  
CTCTACAGAGTGAGCACGTGGTCACGCTGGTGGGCTACTGTGAGGAAGATGGCACTATTC  
TCACCGAATATCAACCTTAGGTTCTTTGAGCAACCTGGAAGAAACACTAAACCTTTCAA  
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TGCCCAAAACATTGTCCAGTACCTGCTAACAAGTAACTTCAGCATTTGTGGCAAACGACC  
TGGACGCTCTGCCCCTGGTAGACCATGACTCTGGGGTACTTATAAAGTGTGGCCACAGAG  
AGCTCCATGGGGATTTTGTGGCTCCAGAGCAGCTGTGGCCCTACGGAGAAGACACGCCCT  
TCCAAGACGATCTCATGCCTTCTTACAATGAGAAGGTTGACATCTGGAAGATTCCAGATG  
TCTCCAGTTTCTCTTGGGGCACGTGGAAGGGAGTGATATGGTTAGATTCCATTTGTTG  
ATATCCATAAGGCGTGCAAGAGCCAGATCCCGGCAGAAAGACCCACTGCTCAGAACGTGC

## FIGURE 2AAAA

TAGACGCTTACCAGAGGGTTTTCCATTCACTCCGAGACACTGTGATGTGCGAGACGAAAG  
AAATGCTGTAAAAATGAGCCATCGAGTGACGTGCTTGATGGCTGAATGGCATCCCAGCTG  
TTCCGCTCTTGATGATGGAAGAGCTTTGCATGGATGGATGTTGACCCTGGCTGTTACGCC  
ACGTAGGCCTCCTCTACGTCTGCCTGCATGTTTGAGTGTTCTGCTCTCCTGGCAGCCCCGG  
ATGGAAGCTGCCAAGCGAGAAAGCCTGGCTTCAGGATGCTCCCTGGTGAAGATGCAGAGG  
ATTCTGGATCTGCATAGTTTCAAGGGAGTGATCAAACGGTGACCTTGAAGACATGCTGCC  
TGCCTTGGTAACTTTTTATAGACTAGTAGGAAACAGAAATCTTTTGGGGGAGGGGGGGAC  
AACCCACTAGTTCCTCAGAGACAATTTCTTCTCATTAGAAAGCCCTGTTGGAAGCTGGG  
GATGTTTTAACTCCGTGGCAGGGCACTTGCCTAGTTGTGTGCAAAGCCTTGATCTGACC  
CATGGCATGTGCACACACAAATGCTCAAAGAAAATCCCAGACGCCAGAAGTGTGCCCC  
TTTCTTGTCAATAAGGTCAATGTTCAGTACCGGAGATGATTTTTTTTTATGAAGCGTTTATG  
CTGACTCGTGTCACTGAGCCAAGTGTGCATGGTTCGTTAGCTACTTTGTGGGTTCTTCTTT  
CTTTCTACCCTACTTCTTCCCTTCCACCCCTAACACTAGATAGGAGAGAGGAGAGAGA  
AAGGAAAGTGGGCACTGTTATATTGTTGGACGACTTCTTGCTGATTAAGGGGTGTCGAGT  
TCCTTGGAGCAATGATCTTTGCTGCCAAGATATCTCATTCTTCTTGTCTTCTTCTCGCC  
CACGACCACTTCACAAACACCGACCAACAGCAAACAACCCACCCCGCTTCTCGGGGG  
CCCTAGCACTTATGTACTTCTGAAAAGTCCCCAGAAATCCAATCATCACACACTCAGAG  
AACTGTCTGCTGCTGGCAAACTACACCCCTGCTAGAGCATGAGGCAAATCATAGTCAG  
CTGCTGTGGACAGTCTGAAGCAGCCTGGCATCCACACCTGAGATTAACAAACAAACATT  
CTTACCTGTGTTTTGTTTTGTTTTAAGAAACCAAAGTGCACCAAGATAGCATGCTCTTG  
AGATTGTGGCTGTCTAGAGATTTTTGGAACAGCAAGTTGAAGGAACTTTCTTACCTGCCCT  
TGAATGGTGCTTTGAACTTCTGCTGACCTGGAGTTTCTGTGTGAATATTTCTATCCAGT  
GTCCCCCTGTACCGGAAAGTACAAAGTCTGCTCTGGGCTTGCATGCCTGAACACTTTAAA  
ACACTGTGGAGCCAGGAATAATGGTACCCACCTGTAATCCCAGCACCTGGGAGACAGGAG  
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CAATAAAAAACAAAAAGGTC

SEQ ID NO: 104 SGK071\_2\_H

GAGGTGGTGGCTGTGCAGATGATGGTGGAAATGCATGGATGACCATTACGCCAGTCAGGCC  
CTGGAGGAGCTGATGCCACTGCTGAAGCTGCGGCACGCCCACATCTCTGTGTACCAGGAG  
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AATGAGCTCAGCTTCCAGGAGGTCAATGAGGATAAGAGGAAGGCAAAGAAAATCATTGAC  
TCTGAGTGGATGCAGAAATGTGCTGGGCCAGGTGCTGGACGCGCTGGAATACCTGCACCAT  
TTGGACATCATCCACAGGAATCTCAAACCCCTCCAACATCATCCTCATCAGCAGTGACCAC  
TGCAAACCTGCAGGACCTGAGTTCCAATGTGCTAATGACAGACAAAGCCAAATGGAATATT  
CGTGCGGAGGAAGACCCCTTTTCGTAAGTCTGGATGGCCCCCTGAAGCCCTCACTTCTCC  
TTCAGCCAGAAATCAGACATCTGGTCCCTGGGCTGCATCATTCTGGACATGACCAGCTGC  
TCCTTCATGGATGGCACAGAAGCCATGCATCTGCGGAAGTCCCTCCGCCAGAGCCCAGGC  
AGCCTGAAGGCCGTCTGAAGACAATGGAGGAGAAGCAGATCCCGGATGTGGAAACCTTC  
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GTGGTGCACATCACCTTCTTGAGAGGCTCCTTCAAGTCTCGTGCGTCTCTCTGACCCCTG  
CACCGGCAGATGGTGCCTGCCATCACCGACATGCTGTTAGAAGGCAACGTGGCCAGC  
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TTGGCATCCTATTGTTTAGTTCCAGAGGGTTCAATATTTATGCCCCCTGGCCTTGCTCCAC  
ATGCACGACCAGTGGCTCAGCTGTGACCAGGACAGAGTCCCTGGGAAGAGAGACTTTGCC  
TCCCTGGGGAACTAGGGAAGCTGTTGGGCCCCATCCCAAAGGGTCTGCCGTGGCCCCCG  
GAGCTGGTGGAGGTGGTGGTCACGACCATGGAGCTACATGACAGGGTCTCGATGTCCAG  
CTGTGTGCCTGCTCCCTGCTGCTGCACCTCCTGGGCCAAGCGCTGGTGCACCAACCCGGAA  
GCCAAGGCTCCCTGCAACCAAGCCATCACCTCCACCCTGCTGAGTGCTCTTACAGAGCCAC  
CCCGAGGAGGAGCCACTTCTTGTCAATGGTCTACAGCCTGCTAGCCATCACCACAACCCAG

## FIGURE 2BBBB

GAGTCAGAGTCACTGTCAGAGGAGCTGCAGAACGCTGGGCTGCTGGAGCACATCCTGGAG  
CACCTCAACAGCTCCCTCGAAAGCAGGGACGTCTGCGCCAGCGGCCTGGGCTGCTCTGG  
GCCCTCCTGCTGGACGACCCCATCTTGGCACTCCAGCGCCCCAGGAAAAAGAGAGCTCCA  
AACCACGGAAGCCCCGGGAAACCAAGAACCTGCCAGCACCCAAAGTATCATTTGTGAAC  
AAGGCCCCCTTGGAGAAGGTCCCGGACCTCATCAGCCAGGTGTTGGCCACCTACCCTGCG  
GATGGGGAAATGGCAGAAGCCAGCTGCGGAGTCTTCTGGCTGCTGTCCCTGCTGGGCTGC  
ATCAAGGAGCAGCAGTTTGAACAAGTGGTGGCGCTGCTCCTGCAAAGCATCCGGCTGTGC  
CAGGACAGAGCCCTGCTGGTGAACAATGCCTACCGGGGACTGGCCAGCCTGGTGAAGGTG  
TCAGAGCTGGCGGCCCTTCAAGGTGGTGGTGCAGGAGGAGGGCGGCAGTGGCCTCAGCCTC  
ATCAAGGAGACCTACCAGCTCCACAGGGACGACCCGGAGGTGGTGGAGAACGTGGGCATG  
CTGCTGGTCCACCTGGCTTCCTATGAGGAGATCCTGCCGGAGCTGGTGTCCAGTAGTATG  
AAGGCCCTGCTCCAGGAGATCAAGGAGCGCTTCACCTCCAGCCTGGTGAAGTACAGCAGC  
GCCTTCAGCAAACCAGGCCTCCCTCCAGGTGGAAGCCCCCAGCTGGGGTGCACCACGTCT  
GGGGGACTGGAATAG

SEQ ID NO: 105\_AA118352\_M SGK071\_M

CAGAAGAAGACCCCTGCCAGAAGTCTGGATGGCTCCTGAAGCTCTCAAATTCTCCTTCT  
CCACCAAATCCGACATCTGGTCTCTGGGCTGCATCATTCTAGACATGGCCACTTGCTCCT  
TCCTGAACGACACAGAAGCCATGCAACTGCCGAAGGCCATCCGCCATCATCCAGGCAGCC  
TGAAGCCCATCCTGAAAACCATGGAGGAGAAGCAAATCCCTGGTACAGATGTCTACTATT  
TGCTTCTGCCCTTCATGTTGCATATCAACCCCTCCGATCGACTGGCAATCAAGGATGTGA  
TGCAAGTCACCTTCATGAGCAACTCCTTCAAAGCTCCTCTGTTGCGCTGAATATGCAGC  
GGCAGAAGGTCCCCATCTTCATCACTGACGTGCTGCTTGAAGGCAACATGGCCAACATCT  
TAGGCAGCTGGCTGTGTGCTTCTTTGTGAACGACAGCAGGCACTGTGACTCAGGGATTG  
GCTCGCAGAGACTTGGGTTTGATTTTTCAGTCAGTCTCTTGGACAGAGCACCTCTGAAAG  
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TCAGCATCATAAAGCAGCATGGGCGGATCCTGGATATTCTGCTCAGCACCTGCTCCCTTC  
TGCTGCGTGTCTTGGCCAAGCACTGGCAAAGGACCCAGAAGCTGAGATCCCAAGGAGCA  
GTTTGATCATCTCCTTCTGATGGATACCTTGCGGAGCCATCCTAACTCTGAAAGGCTTG  
TTAATGTGGTCTACAACGTGCTTGCCATTATTTCCAGCCAAGGACAGATCTCAGAAGAGC  
TGGAAGAGGAGGGGTTGTTTCAGCTTGCCCAAGAGAACCCTGGAGCACTTCCAAGAGGACA  
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TGGACAAAGAGCCCTTGGAGCAGCTCTCTGGCATGGTACCTGGGTGCTGGCTACTCATC  
CGGAGGACGTGGAAATAGCAGAGGCTGGCTGTGCGGTGCTCTGGCTGCTGTCTTGTGG  
GCTGCATAAAGGAGAGTCAGTTTGAGCAGGTGGTAGTGCTGCTCCTGAGAAGCATCCAGC  
TGTGCCCTGGCAGAGTACTGCTGGTGAACAATGCATTCCGTGGCTTGGCCAGCCTCGCAA  
AGGTGTCCGAACCTGGTGGCCTTCCGAATAGTAGTACTGGAAGAGGGCAGCAGCGGCCTCC  
ACCTCATCCAAGATATCTACAAGCTCTACAAGGATGACCCTGAGGTGGTGGAGAACCCTCT  
GCATGCTGTTGGCCCATCTGACCTCCTACAAGGAGATCCTGCCAGAGATGGAGTCTGGAG  
GCATCAAAGACCTAGTCCAGGTGATCCGGGGGCGCTTTACCTCCAGCCTGGAGCTGATTT  
CTTACGCTGATGAGATACTCCAGGTACTGGAAGCAAATGCACAACCTGGCCTCCAGGAGG  
ATCAGCTTGAGCCTCCTGCAGGGCAGGAAGCCCCACTGCAGGGAGAGCCCCCTCTTCAGGC  
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TTTCGTACCCCATGGTGAATAATAAAGAAGCCCTAGGCTGTTTCTGGC

SEQ ID NO: 106\_018653.9\_H

GGCCGGGGTTCGGGGCGCGGGGCATGCGCGCGGGCTGGGCAGGGGGCCGGCGGGGCGCAGA  
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GCCGGCCGGGGGGAGGGGAGCGATGCGGCGCGGGCGGGCGGCAGTGGCCGCGGGTTTCTG



## FIGURE 2CCCC

CGCCTCCTTCCTGCTGGGCTCCGTCTCAACGTGCTCTTCGCTCCGGGTCCGAGCCTCCG  
AGGCCAGGCCAGTCCCCTGAGCCTTCGCCGGCCCCGGGTGCGGGCCGTGCGGGGGCCGC  
GGGGAGCTGGCCCGGCAGATCCGGGCGCGCTACGAGGAGGTGCAGCGCTATTCCCGCGGG  
GGCCCCGGGCCCGGGGCGGGCCGGCCGGAGCGGCGGCGCCTGATGGACCTGGCTCCGGGC  
GGGGCCGGCCTGCCGCGCCCCCGGCCCTTGGGGCCGGCCCTGTCCGACGGCGCCCCA  
GGCTGGCCCCCGGCTCCCGGCCAGGCTCCCCCGGCCGGGCCCGCGCCTGGGCTGCGCC  
GCGCTTCGCAACGTGTCCGGCGCGCAGTACATGGGCTCAGGCTACACCAAGGCCGTGTAC  
CGGGTCCGCCTGCCCGGCGGTGCCGCGGTGGCGCTCAAGGCGGTGGACTTTAGCGGCCAC  
GATCTGGGCAGCTGCGTGCGGAGTTCGGGGTACGGAGGGGCTGCTATCGGCTGGCGGCC  
CACAAGCTGCTTAAGGAGATGGTGCTGCTGGAGCGGTGCGGCACCCCAACGTGCTGCAG  
CTCTATGGCTACTGCTACCAGGACAGCGAGGACATCCAGACACCCTGACCACCATCACG  
GAGCTGGGCGCCCCCTGTAGAAATGATCCAGCTGCTGCAAACCTTCTGGGAGGATCGATT  
CGAATCTGCCTGAGCCTGGGCGCCCTCTCCACCACCTGGCCCACTCCCCACTGGGCTCC  
GTCACCTCTGCTGGACTTCCGCCCTCGGCAGTTTGTGCTGGTGGATGGGGAGCTCAAAGTG  
ACGGACCTGGATGACGCACGTGTGGAGGAGACGCCGTGTGCAGGCAGCACCGACTGCATA  
CTCGAGTTTCCGGCCAGGAACCTTACCCTGCCCTGCTCAGCCAGGGCTGGTGGAGGGC  
ATGAACGAGAAGCGGAACCTCTATAATGCCTACAGTTTTTCTTACATACCTCTGCCT  
CACAGTGCCCCGCCTTCACTGCGTCTCTGCTGGACAGCATCGTCAACGCCACAGGAGAG  
CTCGCCTGGGGGGTGGACGAGACCCTGGCCAGCTGGAGAAGGTGCTGCACCTGTACCGG  
AGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCA  
GACAGCACCATCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGC  
CTCCTTTCAGTGTTCAACCTGGCTGAGGCTGTGGATGTCTGTGAGAGCCATGCCAGTGT  
CGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTCCGCAGCTGGTCTTTTCAAG  
ACTGGATGGAGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGC  
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AACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAT  
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TGGGGACAATCCATCGTGGAGTGTCTCTCAGCTTAGGTCTGGACAGGAGACTTGGCGGG  
AGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTGACCTCCCGACAG  
GGGACACTCCAGGCCAGCCAGGGGTGAGGGGAGAGGTGCACACCTCAGCATGAGCCA  
AGACTGGGGTCAGGGAGCAGGTGTGGTTTGAGCCAGGACCTGGGGCGGGGTGGGGCCGG  
GGCCTTTCTGCCTCATTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACCAGGCTTTCC  
CCCTTCCTCGAGTTTGAATATCCAGAATCTTTGTACTTCTTGTGGTTAAATTGTTTAT  
TTTTGTAAAAATAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACCTCTCCC  
T

SEQ ID NO: 107\_AA396601\_M

CCACGCGTCCGGGCTGCGCCGCGCTCCGCAACGTGTCTGGCGCGCAGTACGTGGGCTCAG  
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CAGTGGACTTCAGCGGCCACGATCTGGGCAGCTGCGTGCGCGAGTTCCGGGCGCGAAGGG  
GCTGCTATCGCCTGGCGGCCACAAAGCTGCTCAAAGAGATGGTGCTGCTGGAGCGGCTGC  
GGCACCCCAACGTGCTGCAGCTCTATGGCTATTGCTACCAGGACAGTGAGGGCATCCCAG  
ACACGCTGACCACCATCACAGAGCTGGGTGCCCCTGTGGAGATGATCCAGCTGTTGCAGA  
CTTCCTGGGAGGATCGATTCCGAATCTGCCTCAGCCTTGGCCGCCTCCTCCACCACCTGG  
CCCACTCCCCGCTGGGCTCGGTACCCCTGCTTGACTTCCGCCCTCGGCAGTTTGTGCTAG  
TGAACGGGGAGCTGAAAGTGACAGACCTGGATGATGCCCGCGTGGAAGAGACACCGTGCA

## FIGURE 2DDDD

CCAGCAGTGCCGACTGCACGCTAGAGTTTCCAGCCAGGAACTTCAGCCTGCCCTGCTCGG  
CCCAGGGCTGGTGCGAGGGCATGAATGAGAAACGGAACCTCTACAATGCCTACAGGTTCT  
TCTTCACATACCTCCTGCCACACAGTGCCCCGCTTCCCTCCGACCTCTCCTGGATAGCA  
TCGTCAATGCCACGGGAGAGCTCGCCTGGGGGGTGGATGAGACCCTGGCCCAGCTGGAGA  
CAGCGCTACACTTGTTCCGAAGTGGGCAGTACCTGCAGAACTCTACAAGCAGCAGGGCTG  
AGTACCAGCGCATCCCGGACAGTGCCATCACACAGGAGGACTATCGCTGCTGGCCATCCT  
ATCACCACGGCGGCTGCCTCCTGTCCGTGTTCAACCTGGCTGAGGCTATAGATGTCTGTG  
AGAGCCATGCTCAGTGTCTGTCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTGCGA  
AGCTGGTCTTTTAAAGACTGGATGGAACCAAGTGGTCCCTGATGCCGCAAGACCACAT  
ATGTGAAGGCCCTGGTTGACTGGTTGTGGGCTCAGCTGACCAGCTGGGCTTGCCTGCTG  
CAGGCGTGACTTGCATCCACCTGGGAACCCCTGCAGACAAAAGCTAGCTCCCAGAGCAA  
CTGATGTGACCAGGACAAAACGTGCAATATGCAAAAATGTTAAAATGTGAGTTTGCCAGC  
TTCAGTCCCAGACTGGTTGGAACCCGATTGCCTCTCTGGAGCTGTAGGCTGTGAGCAGGG  
CTCAGGCTGGTCTTAACTGGGACAGTCCCGTGGGCAGCCATTACTGCATTTCATGCTTTG  
AGAATGTAGCCAGAACACTGCTGCTGCATAAGCCACCGTGGGCAGGAGCTGCCTGGGGAC  
AACCAGTCTCAGAGTGCTCTCTCAGCTCAGCTCCGCTCCAAATGGAGAGCGCGGGATGCG  
GAGATGTGAGTGAACCAGCACTGGGAAGAAGGCTCTCGGGCCTCTCCCTAGAGGTTGCTC  
CTAGGCCAGCCCCGAGGCCGTGGGCAGCAGTGCTCGCATCCATATGAGCCAAGACTAGAG  
TGGAGGAGCAGATTGCATTTGAGCCAGGACTGGGGTGGGGGTAGGGTCGGGGCCTCTCTG  
CCTCATTTGCTTTAGTGAAAGCCAGGGAGCAGCCGAGCCAGGCTCCTCCCCTCCTGG  
AGGCCAGGCTCCTCCCCCTCCTGGAGGCCAGGCTCCTCCCCCTCCTGGAGTTTGCGTACC  
CAGAAGCTTTTATACTTCTCGTTTATTAAATGTTTATTTTGTAAAAAATAATTAAT  
CAATTAATAAAATGATGTTTTGTGAC

SEQ ID NO: 108\_VRK3\_H

ATGATCTCCTTCTGTCCAGACTGTGGCAAAAGTATCCAAGCGGCATTCAAATTCTGCCCC  
TACTGTGGAAATTCTTTGCCTGTAGAGGAGCATGTAGGGTCCCAGACCTTTGTCAATCCA  
CATGTGTCATCCTTCCAAGGCTCAAAGAGAGGGCTGAACTCCAGTTTTGAAACCTCTCCT  
AAGAAAGTGAAATGGTCCAGCACCGTCACCTCTCCCCGATTATCCCTCTTCTCAGATGGT  
GACAGTTCTGAGTCTGAAGATACTCTGAGTTCTCTGAGAGATCCAAGGCTCCGGGAGC  
AGACCCCCAACCCCCAAAAGCAGCCCTCAGAAGACCAGGAAGAGCCCTCAGGTGACCAGG  
GGTAGCCCTCAGAAGACCAGCTGTAGCCCTCAGAAGACCAGGCAGAGCCCTCAGACGCTG  
AAGCGGAGCCGAGTGACCACCTCACTTGAAGCTTTGCCCACAGGGACAGTGCTGACAGAC  
AAGAGTGGGCGACAGTGGAAGCTGAAGTCCTTCCAGACCAGGGACAACCAGGGCATTCTC  
TATGAAGCTGCACCCACCTCCACCTCACCTGTGACTCAGGACCACAGAAGCAAAAGTTC  
TCACTCAAACCTGGATGCCAAGGATGGGCGCTTGTTCAATGAGCAGAACTTCTTCCAGCGG  
GCCGCCAAGCCTCTGCAAGTCAACAAGTGAAGAAGCTGTACTCGACCCCACTGCTGGCC  
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AGGTCTGTGCTGCAGGTGGCCTGCCGGCTGCTGGATGCCCTGGAGTTCCTCCATGAGAAT  
GAGTATGTTTCATGGAAATGTGACAGCTGAAAATATCTTTGTGGATCCAGAGGACCAGAGT  
CAGGTGACTTTGGCAGGCTATGGCTTCGCCCTCCGCTATTGCCCAAGTGGCAAACACGTG  
GCCTACGTGGAAGGCAGCAGGAGCCCTCACGAGGGGGACCTTGAGTTCATTAGCATGGAC  
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CTGAAGTGGCTCTACGGGTTTCTGCCATGGACAAATTGCCCTCCCAACACTGAGGACATC  
ATGAAGCAAAAACAGAAGTTTGTGATAAGCCGGGGCCCTTCGTGGGACCCCTGCGGTAC  
TGGATCAGGCCCTCAGAGACCCTGCAGAAGTACCTGAAGGTGGTGATGGCCCTCACGTAT  
GAGGAGAAGCCGCCCTACGCCATGCTGAGGAACAACCTAGAAGCTTTGCTGCAGGATCTG  
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## FIGURE 2EEEE

SEQ ID NO: 109\_S71575\_M VRK3\_M

CCATCCCCACCTGTATCGGCTTTGGCATTACACAGGACAAGTACAGGTTCTAGTATTCC  
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GCCAGGTGACCCTGGTGGGCTATGGCTTACCTACCGATACTGCCCAGGTGGCAAACACG  
TGGCCTACAAAGAAGGCAGCAGGAGTCCACACGATGGGGACTTGGAGTTCATTAGCATGG  
ACCTGCACAAGGGATGCGGACCCTCCCGCCGACGCGATCTCCAGACCTTGGGCTACTGTA  
TGCTCAAGTGGCTTTATGGGTCCCTGCCATGGACAAATTGCCTTCCCAACACCGAAAAGA  
TAAGTAGGCAGAAGCAGAAGTATCTGGACAGCCCCGAGCGCCTCGTGGGACTGTGTGGCC  
GCTGGAACAAGGCCTCAGAGACCCTGCGGGAGTACCTGAAGGTGGTGTATGGCCCTCAATT  
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TGCGGGTGTACCCCTATGACCCCTGAGCCTCCAGATGGTGCCTTAGATGGAATCCAGAG  
CTTCCGACTTGCAGCTTGAAGTAGAACATGAAGTAGTGTGACTGGAGGCCTGTTTGAAC  
CATAGCTCCTAAAAGAATCCCTTGAATGTGCATTCTCACCGCTCCCTTAGGACATATGAA  
TCAGCACTTGTGTTGGGGAACCTGAGTCATGTATGTAATGTGAACTCCTCCCTGTCTC  
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SEQ ID NO: 110\_AA45427\_H

ATGGGCCACGCGCTGTGTGTCTGCTCTCGGGGAAGTGCATCATTGACAATAAGCGCTAC  
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CATGATGGACACTTCTACGCCCTGAAGCGAATCCTGTGTCACGAGCAGCAGGACCGGGAG  
GAGGCCCAGCGAGAAGCCGACATGCATCGCCTCTTCAATCACCCCAACATCCTTCGCCTC  
GTGGCTTACTGTCTGAGGGAACGGGGTGCTAAGCATGAGGCCTGGCTGCTGCTACCATTC  
TTCAAGAGAGGTACGCTGTGGAATGAGATAGAAAGGCTGAAGGACAAAGGCAACTTCCTG  
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GCCAAGGGTTATGCCCACAGAGACTTGAAGCCCACCAATATATTGCTTGGAGATGAGGGG  
CAGCCAGTTTTTAATGGACTTGGGTTCCATGAATCAAGCATGCATCCATGTGGAGGGCTCC  
CGCCAGGCTCTGACCCTGCAGGACTGGGCAGCCGAGCGGTGCACCATCTCCTACCGAGCC  
CCAGAGCTCTTCTGTGTCAGAGTCACTGTGTCATCGATGAGCGGACTGATGTCTGGTCC  
CTAGGCTGCGTGCTATATGCCATGATGTTTGGGGAAGGCCCTTATGACATGGTGTTCCTAA  
AAGGGTGACAGTGTGGCCCTTGCTGTGTCAGAACCAACTCAGCATCCCAAGAGCCCGAGG  
CATTCTTCAGCATTGCGGCAGCTCCTGAACTCGATGATGACCGTGGACCCGCATCAGCGT  
CCTCACATTCCTCTCCTCCTCAGTCAGCTGGAGGCGCTGCAGCCCCCAGCTCCTGGCCAA  
CATACTACCCAAATCTGA

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CCCTGAGGCACCGCCCCAAGTTTGGTGTGACCGGCGGGGACGCGGTGGTGGCGGCAGC  
GACGGCTGCGGGGGACCGGGCCGCGGCGCCACCATGGCGGTGCGACAGGCGCTGGGCCG  
CGGCCTGCAGCTGGGTGAGCGCTGCTGCTGCGCTTACGGGCAAGCCCGGCCGGGCCTA  
CGGCTTGGGGCGGCGGGCCCGGCGGCGGGCTGTGTCCGCGGGGAGCGTCCAGGCTGGGC  
CGCAGGACCGGGCGCGGAGCCTCGCAGGGTGGGGCTCGGGCTCCCTAACCGTCTCCGCTT  
CTTCCGCCAGTCGGTGGCCGGGCTGGCGGCGCGGTGTCAGCGGCAGTTCGTGGTGGCGGC  
CTGGGGCTGCGCGGGCCCTTGCGGCGGGCAGTCTTCTGGCCTTCGGGCTAGGGCTGGG  
CCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGGCCTGTCAGGAGATCCA  
GGCAATTTTTTACCCAGAAAAGCAAGCCGGGGCCTGACCCGTTGGACACGAGACGCTTGCA  
GGGCTTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTAAGGGCTGCAGTGTCTG  
TGTGTATGAAGCCACCATGCCTACATTGCCCCAGAACCTGGAGGTGACAAAGAGCACCGG  
GTTGCTTCCAGGGAGAGGCCAGGTACAGTGCACAGGAGAAGGGCAGGAGCGAGCTCC

## FIGURE 2FFFF

GGGGGCCCCCTGCCTTCCCCTTGGCCATCAAGATGATGTGGAACATCTCGGCAGGTTCCCTC  
CAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAGCGAGCCGAGTGGCCTT  
GGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAGGTCCCAAGCAACTAGC  
CCCTCACCCCAACATCATCCGGGTTCTCCGCGCCTTCACCTCTTCCGTGCCGCTGCTGCC  
AGGGGCCCCCTGGTCGACTACCCTGATGTGCTGCCCTCACGCCTCCACCCTGAAGGCCTGGG  
CCATGGCCGGACGCTGTTCTCGTTATGAAGAACTATCCCTGTACCCTGCGCCAGTACCT  
TTGTGTGAACACACCCAGCCCCCGCCTCGCCGCCATGATGCTGCTGCAGCTGCTGGAAGG  
CGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGAAATCCGACAACATCCT  
TGTGGAGCTGGACCCAGACGGCTGCCCTGGCTGGTGATCGCAGATTTTGGCTGCTGCCCT  
GGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGCTGGTACGTGGATCGGGGCGG  
AAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCGTCCTGGCCCCAGGGCAGTGAT  
TGACTACAGCAAGGCTGATGCCTGGGCAGTGGGAGCCATCGCCTATGAAATCTTCGGGCT  
TGTCAATCCCTTCTACGGCCAGGGCAAGGCCACCTTGAAAGCCGAGCTACCAAGAGGC  
TCAGCTACCTGCACTGCCCGAGTCAGTGCCTCCAGACGTGAGACAGTTGGTGAGGGCACT  
GCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCGAGTAGCCGCAAATGTGCTTCATCT  
AAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGTTAGACAAGATGGTTGG  
CTGGCTCCTCCAACAATCGGCCGCCACTTTGTTGGCCAACAGGCTCACAGAGAAGTGTTG  
TGTGGAACAACAAAATGAAGATGCTCTTTCTGGCTAACCTGGAGTGTAACCGCTCTGCCA  
GGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTCCCTGCATGGAGCTGGT  
GAATTACTAAAAGAACATGGCATCCTCTGTGTCGTGATGGTCTGTGAATGGTGAGGGTGG  
GAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGAAAAGGCCTCGGGCTTGG  
CAAATGGAAGAACTTGAGTGAGAGTTAGTCTGCAGTCTCTGCTCACAGACATCTGAAA  
AGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGAGGGGTAGGCCTGCATC  
CACAGAGAGGATCCAGGCCAAGGCACTGGCTGTGAGTGGCAGAGTTTGGCTGTGACCTTT  
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GATGAAGGCAGACATCAACATGGGTGAGCACGTTTCAAGTACGGGAGTGGGAAATTACATG  
AGGCCTGGGCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGCTACTGAATTATTAATC  
TCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTAAGTGTGGGGATTTAAACTTGAG  
GGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAAATATTAAATGCAAATTTACA  
ACTGCAGATGACGTATGTGCCCTGAACTGAATATTTGGCTTTAAGAATGATTCTTCTTAT  
ACTCTGAAGGTGAGAATATTTTGTGGGCAGGTATCAACATTGGGGAAGAGATTTTCATGTC  
TAACTAATACTTTTATACATGATTTTTAGGAAGCTATTGCCTAAATCAGCGTCAACATG  
CAGTAAAGGTTGTCTTCAACTGACAAA

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AATGAGATGGAGAAGTACGAGCGGATCCGAGTGGTGGGGAGAGGTGCCTTCGGGATTGTG  
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CAGATGACCAAGGAAGAGCGGCAGGCAGCCAGAATGAGTGCCAGGTCTCAAGCTGCTC  
AACCACCCCAATGTCATTGAGTACTACGAGAACTTCCTGGAAGACAAAGCCCTTATGATC  
GCCATGGAATATGCACCAGGCGGCACTCTGGCTGAGTTCATCCAAAAGCGCTGTAATTCC  
CTGCTGGAGGAGGAGACCATCCTGCACTTCTTCGTGCAGATCCTGCTGCACTGCATCAT  
GTGCACACCCACCTCATCTGCACCGAGACCTCAAGACCCAGAACATCCTGCTTGACAAA  
CACCGCATGGTTCGTCAAGATCGGTGATTTCCGCATCTCCAAGATCCTTAGCAGCAAGAGC  
ACCCCATGCTATATCTCCCCTGAGCTGTGTGAGGGCAAGCCCTACAACCAGAAGAGTGAC  
ATCTGGGCCCCCTGGGCTGTGTCTCTACGAGCTGGCCAGCCTCAAGAGGGCTTTTCGAGGCT  
GCGAACTTGCCAGCACTGGTGCTGAAGATCATGAGTGGCACCTTTGCACCTATCTCTGAC  
CGGTACAGCCCTGAGCTTCGCCAGCTGGTCTGAGTCTACTCAGCCTGGAGCCTGCCCAG  
CGGCCACCACTCAGCCACATCATGGCACAGCCCTCTGCATCCGTGCCCTCCTCAACCTC  
CACACCGACGGCAGAGAAGTCCGTGGCCCCCAGCAACACAGGGAGCAGGACCACCAAGTGT  
CCGCTGCAGAGAGGCATCATCATGACATTCGGCAGCGGCAGCAATGGGTGCCTAGGCCAT

## FIGURE 2GGGG

GGCAGCCTCACTGACATCAGCCAGCCCACCATTTGTGGAGGCTTTGTTGGGCTATGAAATG  
GTGCAGCAAGTGGAGGAGGCCCTGAGCTTCACACTACTAGGCTCTGCACCCCTGGACCAG  
GAGCCTCTGCTGAGTATAGACCTGGGCACTGCTCACTCAGCTGCTGTGACTGGTGAGGAG  
GACTTGGGCTCTGGAGATGTAAACAGGTTACCCAGCTGGGAGAGAGGACATCTGCTGGCT  
GGTGTGGCGTCCAGCACTGATGTGTCTACCTTCTCTGAAGGTGACTGCAAGGAGCCTGAC  
AAGTGTCTGCTGGAGACACAAGCAGTGCCTGGGCACATCATCTACCCTTTTCGCTCTGAC  
TGTGTCCGCCACAGCCTGCACCTACACTCTGTCAACCCTGCAACTGTAATTCTAGGCTG  
AAGGACTCTTCAGAGGATAGCAGCAGCTCCCGGGGCGCGGGCCCAACCTGCTCCCATGTC  
ATCGAGTCCCCTTGCTTTGAGCTCACACCGGAGGAGGAGCATGTGGAGCGATTCCGGTAT  
GGCTGGTGCAAAAGCTACAGACCTGTCTCTGTGGCAGTGATCCACCATCCACTCTACCAT  
GAGTGTGGGGCAGATGATCTAAATGXAAAGAAGAGGAAGAGGAGGAGGAGGAAAAGCAAG  
CCCCCATCCCGACACAGGTGGGGCCCGCCACCGCCTCCCCTGACCTAGGCACCAGCATG  
GCCACTGGTACCCCTGACTCCACAGCGCCCATCACCATCTGGCGCTCTGAGAGCCCCACA  
GGGAAGGGTCAGGGCAGCAAGGTGATCAAGAAGGTAAAGAAGAAAAAGGAAAAAGAGAAA  
GACAAGGAGGAGATGGATGAGAAGGCAAAGCTGAAGAAAAAAGCCAAGAAAGGCCAGTTG  
ACTAAGAAGAAAAAGCCCGTTAAATTGGAGCCTTCCCGCCAGACGTGAGCCGATCATTA  
AGCGCAAGACAGCTGGCCAGGATGTCCGAGTCCAGCCAGAAAGCCGGGAAGAGCTGGAG  
AGCGAGGACAGTTACAATGGCCGGGGGCGAGGAGAACTGTCCAGCGAGGATATTGTGGAA  
TCATCATCGCCAGGAAGAGAGAGAAACACAGTCCAGGCCAAAAAGACAGGGGCAAAGCCC  
TCACAAGCCAGGAAGGTAAACAAGAGAAAAATCTCCCCAGGATCAAACCCCAACCTCAGT  
TGAGGCCAGGGTGGTTCAGGGTGCAGAATAAATGCCATCGAGCCTGTGGCTGGCCCTCTGC  
TGCTGTTCTCTCCCTCCAACCTGGCTGTTTCTTGCGGGGCAAGGGGTGGGCTCAGGGCTG  
CAGGGGTTTCTCAAAGGCAATCCAGCTTTCACAAAGGAAGCCCATGGGAAGGCAGGTGGG  
AGGGAAAGGAAGGGGCACAGCCCTATTTCTTCCCTACCTGCTAGGACAAGGTGGAAGAGTG  
TATCTGGGGTGGGAAGGAGGGCTTCCCTCTCTGCTGCGAGAGACTGGTCTGTGTGAAAT  
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CCC

SEQ ID NO: 113\_AA836348\_H

ATGTCGGTGCTGGGCGAGTACGAGCGACACTGCGATTCCATCAACTCGGACTTTGGGAGC  
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GGCGGCGGCGCGGCGGAGCAGGAGGAAGTGCCTACATCCCCATCCGCGTCTCTGGGCGCG  
GGCGCCTTCGGGGAAGCCACGCTGTACCGCCCGCACCAGGATGACTCACTGGTTGTGTGG  
AAGGAAGTCTGATTTGACCCGGCTGTCTGAGAAGGAACGTCGTGATGCCTTGAATGAGATA  
GTTATTCTGGCACTGCTGCAGCACGACAACATTATTGCCTACTACAATCACTTCATGGAC  
AATACCACGCTGCTGATTGAGCTGGAATATTGTAATGGAGGGAACCTGTATGACAAAATC  
CTTCGTGAGAAGGACAAGTTGTTGAGGAAGAGATGGTGGTGTGGTACCTATTTAGATT  
GTTTCAGCAGTGAGCTGCATCCATAAAGCTGGAATCCTTCATAGAGATATAAAGACATTA  
AATATTTTTCTGACCAAGGCAAACCTGATAAACTTGGAGATTATGGCCTAGCAAAGAAA  
CTTAATTCTGAGTATTCCATGGCTGAGACGCTTGTGGGAACCCCATATTACATGTCTCCA  
GAGCTCTGTCAAGGAGTAAAGTACAATTTCAAGTCTGATATCTGGGCAGTTGGCTGCGTC  
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GTGAAGATCGTGCAAGGAATTGCGGCCATGGAAGTTGACTCTAGCCAGTACTCTTTGGAA  
TTGATCCAAATGGTTCATTCGTGCCTTGACCAGGATCCTGAGCAGAGACCTACTGCAGAT  
GAACTTCTAGATCGCCCTCTTCTCAGGAAACGCAGGAGGTCAAGCACTGTGACTGAAGCA  
CCCATGCTGTAGTAACATCACGAACAGTGAAGTCTATGTTTGGGGTGGTGGAAAATCC  
ACCCCCAGAACTGGATGTTATCAAGAGTGGCTGTAGTGCCCGGCAGGTCTGTGCAGGG  
AATACCCACTTTGCTGTGGTTCACAGTGGAGAAGGAAGTGTACACTTGGGTGAACATGCAA  
GGAGGCACTAACTCCATGGTCAGCTGGGCCATGGAGACAAAGCCTCCTATCGACAGCCA  
AAGCATGTGGAAGGTTGCAAGGCAAAGCTATCCGTCAGGTGTCATGTGGTGATGATTTT

## FIGURE 2HHHH

ACTGTCTGTGTGACTGATGAGGGTCAGCTCTATGCCTTCGGATCAGATTATTATGGCTGC  
ATGGGGGTGGACAAAGTTGCTGGCCCTGAAGTGCTAGAACCCATGCAGCTGAACTTCTTC  
CTCAGCAATCCAGTGGAGCAGGTCTCCTGTGGAGATAATCATGTGGTGGTTCTGACACGA  
AACAAGGAAGTCTATTCTTGGGGCTGTGGCGAATATGGACGACTGGGTTTGGATTTCAGAA  
GAGGATTATTATACACCACAAAAGGTGGATGTTCCCAAGGCCTTGATTATTGTTGCAGTT  
CAATGTGGCTGTGATGGGACATTTCTGTTGACCCAGTCAGGCAAAGTGCTGGCCTGTGGA  
CTCAATGAATTCAATAAGCTGGGTCTGAATCAGTGCATGTCGGGAATTATCAACCATGAA  
GCATACCATGAAGTTCCCTACACAACGTCCTTTACCTTGGCCAAACAGTTGTCCTTTTAT  
AAGATCCGTACCATTGCCCCAGGCAAGACTCACACAGCTGCTATTGATGAGCGAGGCCGG  
CTGCTGACCTTTGGCTGCAACAAGTGTGGGCAGCTGGGCGTTGGGAACATAAGAAGCGT  
CTGGGAATCAACCTGTTGGGGGGACCCCTTGGTGGGAAGCAAGTGATCAGGGTCTCCTGC  
GGTGATGAGTTTACCATTGCTGCCACTGATGAGAAAGTATTGAATTCTAAGACCATCCGT  
TCCAATAGCAGTGGCTTATCCATTGGAAGTGTGTTTCAGAGCTCTAGCCCGGGAGGAGGC  
GGCGGGGGCGGCGGTGGTGAAGAAGAGGACAGTCAGCAGGAATCTGAAACTCCTGACCCA  
AGTGGAGGCTTCCGAGGAACAATGGAAGCAGACCGAGGAATGGAAGGTTTAATCAGTCCC  
ACAGAGGCCATGGGGAACAGTAATGGGGCCAGCAGCTCCTGTCCTGGCTGGCTTCGAAAG  
GAGCTGGAAAATGCAGAAATTTATCCCCATGCCTGACAGCCCATCTCCTCTCAGTGCAGCG  
TTTTCAGAATCTGAGAAAGATAACCTGCCCTATGAAGAGCTGCAAGGACTCAAAGTGGCC  
TCTGAAGCTCCTTTGGAACACAAACCCCAAGTAGAAGCCTCGGTAAGTGAAGCTTTTTGCC  
TTTGAATCACAAGTAGTCACCTCGGCTGAATCCTGCAGTAACCTGTGCTGGGAAGGGAAC  
ACCACTGACTCCTCCTGCGTGTGCGTGCAGCTCTCTGCAGGTGGAGGTTGA

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ATGAACTTGCTGCTCTCCTACCGCGATGTGCAGGACTACTCGGCCATCATTGAGCTGGTG  
GAGACGCTGCAGGCCCTTGCCACCTGTGATGTGGCCGAGCAGCATAATGTCTGCTTCCAC  
TACACTTTTGCCCTCAACCGGAGGAACAGGCCTGGGGACCGGGCGAAGGCCCTGTCTGTG  
CTGCTGCCGCTGGTACAGCTTGAGGGCTCTGTGGCGCCCGATCTGTACTGCATGTGTGGC  
CGTATCTACAAGGACATGTTCTTCAGCTCGGGTTTCCAGGATGCTGGGCACCGGGAGCAG  
GCCTATCACTGGTATCGCAAGGCTTTTGACGTAGAGCCCAGCCTTCACTCAGGCATCAAT  
GCAGCTGTGCTCCTCATTGCTGCCGGGCAGCACTTTGAGGATTCCAAAGAGCTCCGGCTA  
ATAGGCATGAAGCTGGGCTGCCTGCTGGCCCGCAAAGGCTGCGTGGAGAAGATGCAGTAT  
TACTGGGATGTGGGTTTCTACCTGGGAGCCAGATCCTCGCCAATGACCCACCCAGGTG  
GTGCTGGCTGCAGAGCAGCTGTATAAGCTCAATGCCCCATATGGTACCTGGTGTCCTGTG  
ATGGAGACCTTCTGCTCTACCAGCACTTCAGGCCCACGCCAGAGCCCCCTGGAGGGCCA  
CCACGCCGTGCCACTTCTGGCTCCACTTCTTGCTACAGTCTGCCAACCATTCAGACA  
GCCTGTGCCAGGGCGACCAGTGCTTGGTGCTGGTCTGAGATGAACAAGGTGCTGCTG  
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TGGGGACCCCTGAAGGACAACGAGAGCACCATCAGTTTCTACACCCGCCAGATCCTGCAG  
GGACTTGGCTACTTGCACGACAACCACATCGTGACAGGGACATAAAAGGGGACAATGTG  
CTGATCAACACCTTCAGTGGGCTGCTCAAGATTTCTGACTTCGGCACCTCCAAGCGGCTG  
GCAGGCATCACACCTTGCACTGAGACCTTCACAGGAACCTCTGCAGTATATGGCCCCAGAA

## FIGURE 2III

ATCATTGACCAGGGCCACGCGGGTATGGGAAAGCAGCTGACATCTGGTCACTGGGCTGC  
ACTGTCAATTGAGATGGCCACAGGTCGCCCCCCTTCCACGAGCTCGGGAGCCACAGGCT  
GCCATGTTTCAGGTGGGTATGTACAAGGTCCATCCGCCAATGCCAGCTCTCTGTCGGCC  
GAGGCCCAAGCCTTTCTCCTCCGAACCTTTGAGCCAGACCCCGCCTCCGAGCCAGCGCC  
CAGACACTGCTGGGGGACCCCTTCTGTCAGCCTGGGAAAAGGAGCCGCAGCCCCAGCTCC  
CCACGACATGCTCCACGGCCCTCAGATGCCCCCTTCTGCCAGTCCCACTCCTTCAGCCAAC  
TCAACCACCCAGTCTCAGACATTCCCGTGCCCTCAGGCACCCCTCTCAGCACCCACCCAGC  
CCCCGAAGCGCTGCCTCAGTTATGGGGGCACCAGCCAGCTCCGGGTGCCCGAGGAGCCT  
GCGGCCGAGGAGCCTGCGTCTCCGGAGGAGAGTTGCGGGCTGAGCCTGCTGCACCAGGAG  
AGCAAGCGTCGGGCCATGCTGGCCGCAGTATTGGAGCAGGAGCTGCCAGCGCTGGCGGAG  
AATCTGCACCAGGAGCAGAAGCAAGAGCAGGGGGCCCGTCTGGGCAGAAACCATGTGGAA  
GAGCTGCTGCGCTGCCTCGGGGCACACATCCACACTCCCAACCGCCGGCAGCTCGCCAG  
GAGCTGCGGGCGCTGCAAGGACGGCTGAGGGCCCAGGGCCTTGGGCCTGCGCTTCTGCAC  
AGACCGCTGTTTGCCCTTCCCGGATGCGGTGAAGCAGATCCTCCGCAAGCGCCAGATCCGT  
CCACACTGGATGTTTCTGTTCTGGACTCACTGCTCAGCCGTGCTGTGCGGGCAGCCCTGGGT  
GTGCTAGGACCGGAGGTGGAGAAGGAGGCGGTCTCACCAGGTCAGAGGAGCTGAGTAAT  
GAAGGGGACTCCCAGCAGAGCCCAGGCCAGCAGAGCCCGCTTCCGGTGGAGCCCGAGCAG  
GGCCCCGCTCCTCTGATGGTGCAGCTGAGCCTCTTGAGGGCAGAGACTGATCGGCTGCGC  
GAAATCCTGGCGGGGAAGGAACGGGAGTACCAGGCCCTGGTGCAGCGGGCTCTACAGCGG  
CTGAATGAGGAAGCCCGGACCTATGTCTGCCCCCAGAGCCTCCAACCTGCTCTTTCAACG  
GACCAGGGCCTGGTGCAGTGGCTACAGGAAGTGAATGTGGATTTCAGGCACCATCCAAATG  
CTGTTGAACCATAGCTTACCCCTCCACACTCTGCTCACCTATGCCACTCGAGATGACCTC  
ATCTACACCCGCATCAGGGGAGGGATGGTATGCCGCATCTGGAGGGCCATCTTGGCACAG  
CGAGCAGGATCCACACCAGTCACCTCTGGACCCTGA

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ATGTTTGGGAAGAAAAAGAAAAAGATTGAAATATCTGGCCCCGTCCAACCTTTGAACACAGG  
GTTCACTACTGGGTTTGATCCACAAGAGCAGAAGTTTACCGGCCTTCCCCAGCAGTGGCAC  
AGCCTGTAGCAGATACGGCCAAAGGCCAAAGCCTATGGTGGACCCCTCATGCATCACA  
CCCATCCAGCTGGCTCCTATGAAGACAATCGTTAGAGGAAACAAACCCTGCAAGGAAACC  
TCCATCAACGGCCTGCTAGAGGATTTTGACAACATCTCGGTGACTCGCTCCAACCTCCCTA  
AGGAAAGAAAGCCACCCACCCAGATCAGGGAGCCTCCAGCCACGGTCCAGGCCACGCG  
GAAGAAAATGGCTTCATCACCTTCTCCAGTATTCCAGCGAATCCGATACTACTGCTGAC  
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AGAGCCTCGAGTAGCTCCCCCTCTGGATTATTTCATTCCAATTTCACACCTTCTAGAAGTGA  
GGGACCAGCGGGTGCTCCAAGGAGAGCCTGGCGTACAGTGAAAGTGAATGGGGACCCAGC  
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ACCATGCGGCAGAGGTCCAGGTGAGGCTCGGGACTCCAGGAACCGATGATGCCATTTGGA  
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AGCCCAGGAGACCCAGGGAATACTTGGCCAACCTTTATCAAAATCGGGGAAGGCTCAACC  
GGCATCGTATGCATCGCCACCGAGAAACACAGGGAAACAAGTTGCAGTGAAGAAAATG

## FIGURE 2JJJJ

GACCTCCGGAAGCAACAGAGACGAGAACTGCTTTTCAATGAGGTCGTGATCATGCGGGAT  
TACCACCATGACAATGTGGTTGACATGTACAGCAGCTACCTTGTCGGCGATGAGCTCTGG  
GTGGTCATGGAGTTTCTAGAAGGTGGTGCCTTGACAGACATTGTGACTCACACCAGAATG  
AATGAAGAACAGATAGCTACTGTCTGCCTGTCAGTTCTGAGAGCTCTCTCCTACCTTCAT  
AACCAAGGAGTGATTACAGGGACATAAAAAGTGAATCCATCCTCCTGACAAGCGATGGC  
CGGATAAAGTTGTCTGATTTTGGTTTCTGTGCTCAAGTTTCCAAAGAGGTGCCGAAGAGG  
AAATCATTGGTTGGCACTCCCTACTGGATGGCCCCCTGAGGTGATTTCTAGGCTACCTTAT  
GGGACAGAGGTGGACATCTGGTCCCTCGGGATCATGGTGATAGAAATGATTGATGGCGAG  
CCCCCTACTTCAATGAGCCTCCCTCCAGGCGATGCGGAGGATCCGGGACAGTTTACCT  
CCAAGAGTGAAGGACCTACACAAGGTTTCTTCAGTGCTCCGGGGATTCTTAGACTTGATG  
TTGGTGAGGGAGCCCTCTCAGAGAGCAACAGCCCAGGAACTCCTCGGACATCCATTCTTA  
AAACTAGCAGGTCCACCGTCTTGCATCGTCCCCCTCATGAGACAATACAGGCATCACTGA

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ATGAATGATAGGAATGAGATTCAAATGGAAGCCAAACTCCAAAGTCTTACCATTATAGCA  
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CCTGAAGTCCCTCCTACCAGCATCCTAGAGCATCTCCAAAGAAGGAAAATCATGAAGAGA  
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CTGTCACTCTCACTTCTGCTGTCCCAGTCCCTAGAAATCCTGGGTAGAAGTGGTGGACCTG  
TGCAAAGGAGGTTTGAAGTCTGCAGTATTTGTTGGGGCATGGCACAAATAAGCTCATC  
CCTCCCGTCCGAGGCTAGTTTCTCTGGAACACATTTTATCTAGATGAAAATTTGGAA  
TGAAATGAAGGAATAGAAATCCAATAAAGAGTTGAAGGGAAAGAAAATTAAGGTTCTT  
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AGTTCTTCAGTCTGAGCCCTACATGTGGGGCTGGAGGAGAACTATAACGGAAAAACCTC  
TGAGTTTACCTTAGGTATAGATAAAGAAAGATGGTCCCCTTTTATCTGATTCTGAGAC  
AGGTAAATTCTGTTTGTACTACGTTTAATTAGAAGGTGGAGGAGTCATTCATGATTAA



## FIGURE 2KKKK

GAACATTCAACATGTATTGTTTCATTAAGCTAGCTTCCTAGTTCCGATTAGACTAAGGAGA  
CTAAGCCTAGAGAGTCAATGTTAGAACAGTGAAAAGAATTCTGTGTGTGTGTGTGTGTGT  
GTGTGTGTGTGCACAATAAATAGGAAATGTAGAAACCAAGCAAGAAGGCTTAGTAGCTCA  
GTCTTTAACAAGGGCTAGAAAAGAATGTAATCTGATATGGAAGGATAGCAGCTTCTAATT  
TTCAATCATCTGTTGATATACTGTGAACTTATTTTATTAAATTAATATTTATTAAATGG

SEQ ID NO: 117\_AA098024\_M

CTGCAGGAGAAGCACCTGTTTCATGGGGATGTGGCTGCCAGGAACATCCTGATCCAAAGT  
GACCTGACTCCCAAACCTTTGTCTCTGGGCCTGGCTTATGAAGTTCATGCCCATGGGGCC  
ATCTCCTCTGCTCGATCCAGCACCATCCCTCTCAAGTGGCTTGCTCCAGAAAGGCTTCTC  
CTGAGACCTGCAAGCATCAGGGGAGATATTTGGTCCTTTGGGATCCTGCTTTATGAGATG  
GTGACTCTAGGAGCACCACCATAACCTGAAGTCCCTCCCACCAGCATCCTACAATATCTT  
CAGAGAAAGAAAATCATGAAGAGACCCAGCAGCTGCTCACATGCCATGTACAACATCATG  
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GAAGAGGGCAGAGCCGTGCATGGGGCTGCTCCCCAGGACCTGAGCAGGAACCTGGAGTTT  
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## FIGURE 2LLLL

TCCACATTCTGTGGTACCCCTGAGTACTTGGCACCTGAAGTGCTTCGGAAAGAGCCTTAT  
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SEQ ID NO: 120\_CCRK\_H

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SEQ ID NO: 121\_TESK2\_H

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## FIGURE 2MMMM

CCCACCGCCTCCGCAGGCTAAGGAGCCGCTGCCACCAACGAGCTGTGAGGGTTACTATGC  
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